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(21) International Application Number: PCT/US00/08621 (22) International Filing Date: 31 March 2000 (31.03.00) (30) Priority Data: <table border="0"> <tr> <td>60/127,607</td> <td>31 March 1999 (31.03.99)</td> <td>US</td> </tr> <tr> <td>60/127,636</td> <td>2 April 1999 (02.04.99)</td> <td>US</td> </tr> <tr> <td>60/127,728</td> <td>5 April 1999 (05.04.99)</td> <td>US</td> </tr> <tr> <td>09/540,763</td> <td>30 March 2000 (30.03.00)</td> <td>US</td> </tr> </table> (63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Applications <table border="0"> <tr> <td>US</td> <td>60/127,607 (CIP)</td> </tr> <tr> <td>Filed on</td> <td>31 March 1999 (31.03.99)</td> </tr> <tr> <td>US</td> <td>60/127,636 (CIP)</td> </tr> <tr> <td>Filed on</td> <td>2 April 1999 (02.04.99)</td> </tr> <tr> <td>US</td> <td>60/127,728 (CIP)</td> </tr> <tr> <td>Filed on</td> <td>5 April 1999 (05.04.99)</td> </tr> <tr> <td>US</td> <td>09/540,763 (CIP)</td> </tr> <tr> <td>Filed on</td> <td>30 March 2000 (30.03.00)</td> </tr> </table> (71) Applicant (for all designated States except US): CURAGEN CORPORATION [US/US]; 555 Long Wharf Drive, 11th Floor, New Haven, CT 06511 (US).	60/127,607	31 March 1999 (31.03.99)	US	60/127,636	2 April 1999 (02.04.99)	US	60/127,728	5 April 1999 (05.04.99)	US	09/540,763	30 March 2000 (30.03.00)	US	US	60/127,607 (CIP)	Filed on	31 March 1999 (31.03.99)	US	60/127,636 (CIP)	Filed on	2 April 1999 (02.04.99)	US	60/127,728 (CIP)	Filed on	5 April 1999 (05.04.99)	US	09/540,763 (CIP)	Filed on	30 March 2000 (30.03.00)	(72) Inventors; and (75) Inventors/Applicants (for US only): SHIMKETS, Richard, A. [US/US]; 191 Leete Street, West Haven, CT 06516 (US). LEACH, Martin [GB/US]; 884 School Street, Webster, MA 01570 (US). (74) Agent: ELRIFI, Ivor, R.; Mintz, Levin, Cohn, Ferris, Glovsky and Popeo, P.C., One Financial Center, Boston, MA 02111 (US). (81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>
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(54) Title: NUCLEIC ACIDS INCLUDING OPEN READING FRAMES ENCODING POLYPEPTIDES; "ORFX" (57) Abstract <p>The present invention provides open reading frames ORFX, encoding isolated polypeptides, as well as polynucleotides encoding ORFX and antibodies that immunospecifically bind to ORFX or any derivative, variant, mutant, or fragment of the ORFX polypeptides, polynucleotides or antibodies. The invention additionally provides methods in which the ORFX polypeptide, polynucleotide and antibody are used in detection and treatment of a broad range of pathological states, as well as to other uses.</p>																													

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NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY

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BACKGROUND OF THE INVENTION

The invention relates generally to nucleic acids and polypeptides encoded thereby, and methods of using these nucleic acids and polypeptides.

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SUMMARY OF THE INVENTION

The invention is based in part on the discovery of nucleic acids that include open reading frames encoding novel polypeptides, and on the polypeptides encoded thereby. The nucleic acids and polypeptides are collectively referred to herein as "ORFX".

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Accordingly, in one aspect, the invention provides an isolated nucleic acid molecule (SEQ ID NO:2 n -1, wherein n is an integer between 1-3161), that encodes novel polypeptide, or a fragment, homolog, analog or derivative thereof. The nucleic acid can include, *e.g.*, a nucleic acid sequence encoding a polypeptide at least 85% identical to a polypeptide comprising the amino acid sequences of SEQ ID NO:2 n , wherein n is an integer between 1-3161. The nucleic acid can be, *e.g.*, a genomic DNA fragment, or a cDNA molecule.

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Also included in the invention is a vector containing one or more of the nucleic acids described herein, and a cell containing the vectors or nucleic acids described herein.

The invention is also directed to host cells transformed with a recombinant expression vector comprising any of the nucleic acid molecules described above.

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In another aspect, the invention includes a pharmaceutical composition that includes an ORFX nucleic acid and a pharmaceutically acceptable carrier or diluent.

In a further aspect, the invention includes a substantially purified ORF polypeptide, *e.g.*, any of the ORFX polypeptides encoded by an ORFX nucleic acid, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition that includes a ORFX polypeptide and a pharmaceutically acceptable carrier or diluent.

5 In a still a further aspect, the invention provides an antibody that binds specifically to an ORFX polypeptide. The antibody can be, *e.g.*, a monoclonal or polyclonal antibody, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition including ORFX antibody and a pharmaceutically acceptable carrier or diluent. The invention is also directed to isolated antibodies that bind to an epitope on a
10 polypeptide encoded by any of the nucleic acid molecules described above.

The invention also includes kits comprising any of the pharmaceutical compositions described above.

The invention further provides a method for producing an ORFX polypeptide by providing a cell containing a ORFX nucleic acid, *e.g.*, a vector that includes a ORFX nucleic
15 acid, and culturing the cell under conditions sufficient to express the ORFX polypeptide encoded by the nucleic acid. The expressed ORFX polypeptide is then recovered from the cell. Preferably, the cell produces little or no endogenous ORFX polypeptide. The cell can be, *e.g.*, a prokaryotic cell or eukaryotic cell.

The invention is also directed to methods of identifying an ORFX polypeptide or nucleic
20 acids in a sample by contacting the sample with a compound that specifically binds to the polypeptide or nucleic acid, and detecting complex formation, if present.

The invention further provides methods of identifying a compound that modulates the activity of a ORFX polypeptide by contacting ORFX polypeptide with a compound and determining whether the ORFX polypeptide activity is modified.

25 The invention is also directed to compounds that modulate ORFX polypeptide activity identified by contacting a ORFX polypeptide with the compound and determining whether the compound modifies activity of the ORFX polypeptide, binds to the ORFX polypeptide, or binds to a nucleic acid molecule encoding a ORFX polypeptide.

In a another aspect, the invention provides a method of determining the presence of or
30 predisposition of an ORFX-associated disorder in a subject. The method includes providing a sample from the subject and measuring the amount of ORFX polypeptide in the subject sample.

The amount of ORFX polypeptide in the subject sample is then compared to the amount of ORFX polypeptide in a control sample. An alteration in the amount of ORFX polypeptide in the subject protein sample relative to the amount of ORFX polypeptide in the control protein sample indicates the subject has a tissue proliferation-associated condition. A control sample is preferably taken from a matched individual, *i.e.*, an individual of similar age, sex, or other general condition but who is not suspected of having a tissue proliferation-associated condition. Alternatively, the control sample may be taken from the subject at a time when the subject is not suspected of having a tissue proliferation-associated disorder. In some embodiments, the ORFX is detected using a ORFX antibody.

10 In a further aspect, the invention provides a method of determining the presence of or predisposition of an ORFX-associated disorder in a subject. The method includes providing a nucleic acid sample, *e.g.*, RNA or DNA, or both, from the subject and measuring the amount of the ORFX nucleic acid in the subject nucleic acid sample. The amount of ORFX nucleic acid sample in the subject nucleic acid is then compared to the amount of an ORFX nucleic acid in a control sample. An alteration in the amount of ORFX nucleic acid in the sample relative to the amount of ORFX in the control sample indicates the subject has a tissue proliferation-associated disorder.

20 In a still further aspect, the invention provides method of treating or preventing or delaying a ORFX-associated disorder. The method includes administering to a subject in which such treatment or prevention or delay is desired a ORFX nucleic acid, a ORFX polypeptide, or an ORFX antibody in an amount sufficient to treat, prevent, or delay a tissue proliferation-associated disorder in the subject.

25 Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

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Other features and advantages of the invention will be apparent from the following detailed description and claims.

DETAILED DESCRIPTION OF THE INVENTION

The invention provides novel polypeptides and nucleotides encoded thereby. The polynucleotides and their encoded polypeptides can be grouped according to the functions played by their gene products. Such functions include, structural proteins, proteins from which associated with metabolic pathways fatty acid metabolism, glycolysis, intermediary metabolism, calcium metabolism, proteases, and amino acid metabolism, etc.

Included in the invention are 3161 novel nucleic acid sequences and their encoded polypeptides. The sequences are collectively referred to as “ORFX nucleic acids” or ORFX polynucleotides” and the corresponding encoded polypeptide is referred to as a “ORFX polypeptide” or ORFX protein”. For example, an ORFX nucleic acid according to the invention is a nucleic acid including an ORF1 nucleic acid, and an ORF polypeptide according to the invention is a polypeptide that includes the amino acid sequence of an ORF1 polypeptide. Unless indicated otherwise, “ORFX” is meant to refer to any of the ORF1-3161 sequences disclosed herein.

Table 1 provides a summary of the ORFX nucleic acids and their encoded polypeptides are summarized in Table 1. Nucleic acid sequences and polypeptide sequences for ORFX nucleic acids according to the invention is provided in the section of the specification entitled “Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences.”

Column 1 of Table 1, entitled “ORF #”, denotes an ORF number assigned to a nucleic acid containing an open reading frame according to the invention.

Column 2 of Table 1, entitled “Internal Identification number (Nucleic Acid Sequence Identification Number, Polypeptide Sequence Identification Number), provides an internal identification number for the indicated ORF, along with sequence identification numbers (SEQ ID NOs.) corresponding to the indicated ORF. In general, for an ORF n according to the invention (wherein n is any integer from 1 to 3161), a nucleic acid corresponding to the ORF is SEQ ID NO:2 n -1, and an amino acid sequence encoded by the ORF is SEQ ID NO:2 n . For example, a nucleic acid sequence corresponding to an ORF1 nucleic acid is SEQ ID NO:1, and a polypeptide sequence corresponding to an ORF1 polypeptide is SEQ ID NO:2. Similarly, a

nucleic acid sequence corresponding to an ORF4 nucleic acid is SEQ ID NO:7, and a polypeptide sequence corresponding to an ORF4 polypeptide is SEQ ID NO:8; a nucleic acid sequence corresponding to an ORF198 nucleic acid sequence is SEQ ID NO:395, and a polypeptide sequence corresponding to an ORF198 polypeptide is SEQ ID NO:396. Nucleic acid sequences and polypeptide sequences for ORFX nucleic acids according to the invention are provided in the section of the specification entitled "Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences."

Column 2 of Table 1, entitled "Protein Similarity", lists previously described proteins that are related to polypeptides encoded by the ORFs. Genbank identifiers for the previously described proteins are provided. These can be retrieved from <http://www.ncbi.nlm.nih.gov/>.

To determine similarity to previously described proteins, polypeptides encoded by ORFX DNA sequences were tested using the Framesearch Algorithm against a nonredundant version of the GenPept Database from NCBI/Genbank. DNA sequences that had a score of '90' or above (Framesearch algorithm score, Edelman et. al. GCG Genetics) to a known protein were selected. Open reading frames were extended beyond the region of the protein matched using standard DNA translation and codon tables. Novel proteins that lacked a protein match were translated against the standard genetic codons and proteins with an ORF at least 80 amino acids and containing a Methionine start are included in the Table.

Column 3 of Table 3, entitled "Protein Domains", lists previously described protein domains, designated by pfam entries, that are present in polypeptides encoded by the ORFs. Also included in column 3 are proteins in which these domains are present. The pfam entries can be retrieved from <http://pfam.wustl.edu/>. DNA sequences were translated in all six frames and tested using the Hmmer Algorithm against the Pfam Database (References to the algorithm and Pfam database can be found at <http://pfam.wustl.edu/>). Translated DNA sequences that matched a protein domain entry in the Pfam database AND had a score of '7.5' were selected.

Column 4 of Table 3, entitled "Protein Classification", lists the type of classification assigned for the protein, based on its homology. Examples of proteins in the classification include the following proteins:

Amylases

Amylase is responsible for endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides. Variations in amylase gene may be indicative of delayed maturation and of various amylase producing neoplasms and carcinomas.

5 Amyloid

The serum amyloid A (SAA) proteins comprise a family of vertebrate proteins that associate predominantly with high density lipoproteins (HDL). The synthesis of certain members of the family is greatly increased in inflammation. Prolonged elevation of plasma SAA levels, as in chronic inflammation, 15 results in a pathological condition, called amyloidosis, which affects the liver, kidney and spleen and which is characterized by the highly insoluble accumulation of SAA in these tissues. Amyloid selectively inhibits insulin-stimulated glucose utilization and glycogen deposition in muscle, while not affecting adipocyte glucose metabolism. Deposition of fibrillar amyloid proteins intraneuronally, as neurofibrillary tangles, extracellularly, as plaques and in blood vessels, is characteristic of both Alzheimer's disease and aged Down's syndrome. 15 Amyloid deposition is also associated with type II diabetes mellitus.

Angiopoeitin

Members of the angiopoetin/fibrinogen family have been shown to stimulate the generation of new blood vessels, inhibit the generation of new blood vessels, and perform several roles in blood clotting. This generation of new blood vessels, called angiogenesis, is also an 20 essential step in tumor growth in order for the tumor to get the blood supply it needs to expand. Variation in these genes may be predictive of any form of heart disease, numerous blood clotting disorders, stroke, hypertension and predisposition to tumor formation and metastasis. In particular, these variants may be predictive of the response to various antihypertensive drugs and chemotherapeutic and anti-tumor agents.

25 Apoptosis-related proteins

Active cell suicide (apoptosis) is induced by events such as growth factor withdrawal and toxins. It is controlled by regulators, which have either an inhibitory effect on programmed cell

death (anti-apoptotic) or block the protective effect of inhibitors (pro-apoptotic). Many viruses have found a way of countering defensive apoptosis by encoding their own anti-apoptosis genes preventing their target-cells from dying too soon. Variants of apoptosis related genes may be useful in formulation of anti-aging drugs.

5 **Cadherin, Cyclin, Polymerase, Oncogenes, Histones, Kinases**

Members of the cell division/cell cycle pathways such as cyclins, many transcription factors and kinases, DNA polymerases, histones, helicases and other oncogenes play a critical role in carcinogenesis where the uncontrolled proliferation of cells leads to tumor formation and eventually metastasis. Variation in these genes may be predictive of predisposition to any form
10 of cancer, from increased risk of tumor formation to increased rate of metastasis. In particular, these variants may be predictive of the response to various chemotherapeutic and anti-tumor agents.

Colony-stimulating factor-related proteins

Granulocyte/macrophage colony-stimulating factors are cytokines that act in
15 hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages.

Complement-related proteins

Complement proteins are immune associated cytotoxic agents, acting in a chain reaction to exterminate target cells to that were opsonized (primed) with antibodies, by forming a
20 membrane attack complex (MAC). The mechanism of killing is by opening pores in the target cell membrane. Variations in 20 complement genes or their inhibitors are associated with many autoimmune disorders. Modified serum levels of complement products cause edemas of various tissues, lupus (SLE), vasculitis, glomerulonephritis, renal failure, hemolytic anemia, thrombocytopenia, and arthritis. They interfere with mechanisms of ADCC (antibody dependent
25 cell cytotoxicity), severely impair immune competence and reduce phagocytic ability. Variants of complement genes may also be indicative of type I diabetes mellitus, meningitis neurological disorders such as nemaline myopathy, neonatal hypotonia, muscular disorders such as congenital myopathy and other diseases.

Cytochrome

The respiratory chain is a key biochemical pathway which is essential to all aerobic cells. There are five different cytochromes involved in the chain. These are heme bound proteins which serve as electron carriers. Modifications in these genes may be predictive of ataxia areflexia, dementia and myopathic and neuropathic changes in muscles. Also, association with various types of solid tumors.

Kinesins

Kinesins are tubulin molecular motors that function to transport organelles within cells and to move chromosomes along microtubules during cell division. Modifications of these genes may be indicative of neurological disorders such as Pick disease of the brain, tuberous sclerosis.

Cytokines, Interferon, Interleukin

Members of the cytokine families are known for their potent ability to stimulate cell growth and division even at low concentrations. Cytokines such as erythropoietin are cell-specific in their growth stimulation; erythropoietin is useful for the stimulation of the proliferation of erythroblasts. Variants in cytokines may be predictive for a wide variety of diseases, including cancer predisposition.

G-protein coupled receptors

G-protein coupled receptors (also called R7G) are an extensive group of hormones, neurotransmitters, odorants and light receptors which transduce extracellular signals by interaction with guanine nucleotide-binding (G) proteins. Alterations in genes coding for G-coupled proteins may be involved in and indicative of a vast number of physiological conditions. These include blood pressure regulation, renal dysfunctions, male infertility, dopamine associated cognitive, emotional, and endocrine functions, hypercalcemia, chondrodysplasia and osteoporosis, pseudohypoparathyroidism, growth retardation and dwarfism.

Thioesterases

Eukaryotic thiol proteases are a family of proteolytic enzymes which contain an active site cysteine. Catalysis proceeds through a thioester intermediate and is facilitated by a nearby histidine side chain; an asparagine completes the essential catalytic triad. Variants of thioester associated genes may be predictive of neuronal disorders and mental illnesses such as Ceroid Lipoffiscinosis, Neuronal 1, Infantile, Santavuori disease and more.

The key to the molecule type is as follows:

10	Abbrev:	Title:
	amylase	amylase protein
	amylaseinhib	amylase inhibitor
	amyloid	amyloid protein
15	apoptosis	apoptosis associated protein
	apoptosisinhib	apoptosis inhibitors
	apoptosisrecep	apoptosis receptors
	ATPase_associated	ATPase associated protein
	biotindep	biotin dependent enzyme/protein
20	cadherin	cadherin protein
	calcium_channel	calcium channel protein
	carboxylase	carboxylase protein
	cathepsin	cathepsin/carboxypeptidases
	cathepsininhib	cathepsin/carboxypeptidase inhibitor
25	chloride_channel	chloride channel protein
	collagen	collagen
	complement	complement protein
	complementrecept	complement receptor protein
	complementinhib	complement inhibitor
30	csf	colony stimulating factor
	csfrecept	colony stimulating factor receptor
	cyclin	cyclin protein
	cyto450	cytochrome p450 protein
	cytochrome	cytochrome related protein
35	deaminase	deaminase
	dehydrogenase	dehydrogenase
	desaturase	desaturase
	dna_ma_bind	DNA/RNA binding protein/factor
	dna_ma_inhib	DNA/RNA binding protein/factor inhibitor
40	dynein	dynein

	elastase	elastase
	elastaseinhib	elastase inhibitor
	eph	EPH family of tyrosine kinases
	esterase	esterase
5	esteraseinhib	esterase inhibitor
	fgf	fibroblast growth factor
	fgfreceptor	fibroblast growth factor receptor
	gaba	GABA receptor
	glucoamylase	glucoamylase
10	glucoronidase	glucoronidase
	glycoprotein	glycoprotein
	Guanylyl	guanylylate cyclase
	helicase	helicase
	histone	histone
15	HOM	homologous
	homeobox	homeobox protein
	hydrolase	hydrolase
	hydroxysteroid	hydroxysteroid associated protein
	hypoxanthine	hypoxanthine associated protein
20	immunoglob	immunoglobulin
	immunoglobrecept	immunoglobulin receptor
	interferon	interferon
	interleukin	interleukin
	interleukinrecept	interleukin receptor
25	isomerase	isomerase
	isomeraseinhibitor	isomerase inhibitor
	isomerasereceptor	isomerase receptor
	kinase	kinase
	kinaseinhibitor	kinase inhibitor
30	kinasereceptor	kinase receptor
	kinesin	kinesin
	laminin	laminin associated protein
	lipase	lipase
	metallothionein	metallothionein
35	MHC	major histocompatibility complex
	misc_channel	miscellaneous channel
	ngf	nerve growth factor
	nuci_recpt	nuclear receptor
	nuclease	nuclease
40	oncogene	oncogene associated protein
	oxidase	oxidase
	oxygenase	oxygenase
	peptidase	peptidase
	peroxidase	peroxidase
45	phosphatase	phosphatase
	phosphataseinhib	phosphatase inhibitor

	phosphorylase PIR	phosphorylase PIR DATABASE (release 56, 29-OCT-1998)
5	polymerase potassium_channel prostaglandin protease proteaseinhib reductase	polymerase potassium channel protein prostaglandin protease protease inhibitor reductase
10	ribosomalprot RTR	ribosomal associated protein EMBLDATABASE translated entries not to be incorporated into SWISS-PROT (20-JUL-1998)
15	SIM SPTR	similar EMBL DATABASE translated entries to be incorporated into SWISS-PROT (20-JUL-1998)
20	struct sulfotransferase SWP	structural associated protein sulfotransferase SWISS-PROT DATABASE (release 18-OCT-1998)
25	SWPN synthase tgf tgfreceptor thioesterase thiolase tm7	SWISS-PROT Update (release 11-NOV-98) synthase transforming growth factor transforming growth factor receptor thioesterase thiolase
30	tnf traffic tnfreceptor TRN	seven transmembrane domain G-protein coupled receptor necrosis factor receptor tumor necrosis factor tumor trafficking associated protein EMBL DATABASE translated entries update (20-JUL-1998)
35	transcriptfactor transferase transport tubulin ubiquitin	transcription factor transferase transport protein tubulin ubiquitin
40	unclassified water channel	Protein not categorized into one of the aforementioned protein families water channel protein

Column 5 of Table 1, entitled, "Cells or Tissues in Which Gene is Expressed", denotes tissues, represented by five digit numbers, in which RNA homologous to the ORF nucleic acid sequences is present. Tissues or cells corresponding to the numbers are provided in Table 2.

ORFX nucleic acids, and their encoded polypeptides, according to the invention are
 5 useful in a variety of applications and contexts. For example, various ORFX nucleic acids and polypeptides according to the invention are useful, *inter alia*, as novel members of the protein families indicated in Table 1, and/or according to the presence of domains and sequence relatedness to previously described proteins as summarized in Table 1.

ORFX nucleic acids and polypeptides according to the invention can also be used to
 10 identify cell types listed in Table 1 for an indicated ORFX according to the invention. Additional utilities for ORFX nucleic acids and polypeptides according to the invention are disclosed herein.

ORFX Nucleic Acids

15 The novel nucleic acids of the invention include those that encode an ORFX or ORFX-like protein, or biologically active portions thereof. The nucleic acids include nucleic acids encoding polypeptides that include the amino acid sequence of one or more of SEQ ID NO:2 n , wherein $n = 1$ to 3161. The encoded polypeptides can thus include, *e.g.*, the amino acid sequences of SEQ ID NO: 2, 4, 6, 8, 10, . . . , 6310, 6312, 6314, 6316, 6318, 6320, and/or 6322.

20 In some embodiments, a nucleic acid encoding a polypeptide having the amino acid sequence of one or more of SEQ ID NO:2 n (wherein $n = 1$ to 3161) includes the nucleic acid sequence of any of SEQ ID NO:2 $n-1$ (wherein $n = 1$ to 3161), or a fragment thereof. Additionally, the invention includes mutant or variant nucleic acids of any of SEQ ID NO:2 $n-1$ (wherein $n = 1$ to 3161), or a fragment thereof, any of whose bases may be changed from the
 25 disclosed sequence while still encoding a protein that maintains its ORFX-like activities and physiological functions. The invention further includes the complement of the nucleic acid sequence of any of SEQ ID NO:2 $n-1$ (wherein $n = 1$ to 3161), including fragments, derivatives,

analogues and homolog thereof. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications.

Also included are nucleic acid fragments sufficient for use as hybridization probes to identify ORFX-encoding nucleic acids (*e.g.*, ORFX mRNA) and fragments for use as
5 polymerase chain reaction (PCR) primers for the amplification or mutation of ORFX nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs thereof. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is
10 double-stranded DNA.

"Probes" refer to nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or as many as about, *e.g.*, 6,000 nt, depending on use. Probes are used in the detection of identical, similar, or complementary nucleic acid sequences. Longer length probes are usually obtained from a natural or recombinant source, are highly specific and
15 much slower to hybridize than oligomers. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization technologies, or ELISA-like technologies.

An "isolated" nucleic acid molecule is one that is separated from other nucleic acid molecules that are present in the natural source of the nucleic acid. Examples of isolated nucleic
20 acid molecules include, but are not limited to, recombinant DNA molecules contained in a vector, recombinant DNA molecules maintained in a heterologous host cell, partially or substantially purified nucleic acid molecules, and synthetic DNA or RNA molecules. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism
25 from which the nucleic acid is derived. For example, in various embodiments, the isolated ORFX nucleic acid molecule can contain less than about 50 kb, 25 kb, 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular
30 material or culture medium when produced by recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a complement of any of this nucleotide sequence, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequence of any
5 of SEQ ID NO:2*n*-1 (wherein *n*=1 to 3161) as a hybridization probe, ORFX nucleic acid sequences can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook *et al.*, eds., MOLECULAR CLONING: A LABORATORY MANUAL 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; and Ausubel, *et al.*, eds., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993.)

10 A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to ORFX nucleotide sequences can be prepared by standard synthetic techniques, *e.g.*, using an
15 automated DNA synthesizer.

As used herein, the term "oligonucleotide" refers to a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or
20 complementary DNA or RNA in a particular cell or tissue. Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at least 6 contiguous nucleotides of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a complement thereof. Oligonucleotides may be
25 chemically synthesized and may be used as probes.

In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence
30 shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a portion of this nucleotide sequence. A nucleic acid molecule that is complementary to the nucleotide sequence shown in

is one that is sufficiently complementary to the nucleotide sequence shown in of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) that it can hydrogen bond with little or no mismatches to the nucleotide sequence shown in of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161),, thereby forming a stable duplex.

5 As used herein, the term “complementary” refers to Watson-Crick or Hoogsteen base pairing between nucleotides units of a nucleic acid molecule, and the term “binding” means the physical or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, Von der Waals, hydrophobic interactions, etc. A physical interaction can be either direct or indirect.
10 Indirect interactions may be through or due to the effects of another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical intermediates.

 Moreover, the nucleic acid molecule of the invention can comprise only a portion of the
15 nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), *e.g.*, a fragment that can be used as a probe or primer, or a fragment encoding a biologically active portion of ORFX. Fragments provided herein are defined as sequences of at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, respectively,
20 and are at most some portion less than a full length sequence. Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice. Derivatives are nucleic acid sequences or amino acid sequences formed from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but
25 differs from it in respect to certain components or side chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild type.

 Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or
30 analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the

invention, in various embodiments, by at least about 70%, 80%, 85%, 90%, 95%, 98%, or even 99% identity (with a preferred identity of 80-99%) over a nucleic acid or amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the aforementioned proteins under stringent, moderately stringent, or low stringent conditions. See *e.g.* Ausubel, *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993, and below. An exemplary program is the Gap program (Wisconsin Sequence Analysis Package, Version 8 for UNIX, Genetics Computer Group, University Research Park, Madison, WI) using the default settings, which uses the algorithm of Smith and Waterman (Adv. Appl. Math., 1981, 2: 482-489, which is incorporated herein by reference in its entirety).

A "homologous nucleic acid sequence" or "homologous amino acid sequence," or variations thereof, refer to sequences characterized by a homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of ORFX polypeptide. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA. Alternatively, isoforms can be encoded by different genes. In the present invention, homologous nucleotide sequences include nucleotide sequences encoding for a ORFX polypeptide of species other than humans, including, but not limited to, mammals, and thus can include, *e.g.*, mouse, rat, rabbit, dog, cat cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence does not, however, include the nucleotide sequence encoding human ORFX protein. Homologous nucleic acid sequences include those nucleic acid sequences that encode conservative amino acid substitutions (see below) in any of SEQ ID NO:2 n (wherein $n = 1$ to 3161) as well as a polypeptide having ORFX activity. Biological activities of the ORFX proteins are described below. A homologous amino acid sequence does not encode the amino acid sequence of a human ORFX polypeptide.

The nucleotide sequence determined from the cloning of the human ORFX gene allows for the generation of probes and primers designed for use in identifying the cell types disclosed and/or cloning ORFX homologues in other cell types, *e.g.*, from other tissues, as well as ORFX homologues from other mammals. The probe/primer typically comprises a substantially purified

oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, 25, 50, 100, 150, 200, 250, 300, 350 or 400 or more consecutive sense strand nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161); or an anti-sense strand nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161);
 5 or of a naturally occurring mutant of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161).

Probes based on the human ORFX nucleotide sequence can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In various embodiments, the probe further comprises a label group attached thereto, *e.g.*, the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be
 10 used as a part of a diagnostic test kit for identifying cells or tissue which misexpress a ORFX protein, such as by measuring a level of a ORFX-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting ORFX mRNA levels or determining whether a genomic ORFX gene has been mutated or deleted.

"A polypeptide having a biologically active portion of ORFX" refers to polypeptides
 15 exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. A nucleic acid fragment encoding a "biologically active portion of ORFX" can be prepared by isolating a portion of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), that encodes a polypeptide having a ORFX biological activity (biological activities of the ORFX
 20 proteins are summarized in Table 1), expressing the encoded portion of ORFX protein (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of ORFX. For example, a nucleic acid fragment encoding a biologically active portion of ORFX can optionally include a domain as shown in Table 1, column 4.

25 **ORFX variants**

The invention further encompasses nucleic acid molecules that differ from the disclosed ORFX nucleotide sequences due to degeneracy of the genetic code. These nucleic acids thus encode the same ORFX protein as that encoded by the nucleotide sequence shown in SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, an isolated nucleic acid molecule of
 30 the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161).

In addition to the human ORFX nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of ORFX may exist within a population (*e.g.*, the human population). Such genetic polymorphism in the ORFX gene may exist among individuals within a population due to natural allelic variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding a ORFX protein, preferably a mammalian ORFX protein. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of the ORFX gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in ORFX that are the result of natural allelic variation and that do not alter the functional activity of ORFX are intended to be within the scope of the invention.

Moreover, nucleic acid molecules encoding ORFX proteins from other species, and thus that have a nucleotide sequence that differs from the human sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), are intended to be within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologues of the ORFX cDNAs of the invention can be isolated based on their homology to the human ORFX nucleic acids disclosed herein using the human cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions.

In another embodiment, an isolated nucleic acid molecule of the invention is at least 6 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, the nucleic acid is at least 10, 25, 50, 100, 250, 500 or 750 nucleotides in length. In another embodiment, an isolated nucleic acid molecule of the invention hybridizes to the coding region. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other.

Homologs (*i.e.*, nucleic acids encoding ORFX proteins derived from species other than human) or other related sequences (*e.g.*, paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

As used herein, the phrase "stringent hybridization conditions" refers to conditions under which a probe, primer or oligonucleotide will hybridize to its target sequence, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter sequences. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at excess, at T_m , 50% of the probes are occupied at equilibrium. Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes, primers or oligonucleotides (e.g., 10 nt to 50 nt) and at least about 60°C for longer probes, primers and oligonucleotides. Stringent conditions may also be achieved with the addition of destabilizing agents, such as formamide.

Stringent conditions are known to those skilled in the art and can be found in CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Preferably, the conditions are such that sequences at least about 65%, 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. A non-limiting example of stringent hybridization conditions is hybridization in a high salt buffer comprising 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 mg/ml denatured salmon sperm DNA at 65°C. This hybridization is followed by one or more washes in 0.2X SSC, 0.01% BSA at 50°C. An isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequence of any of SEQ ID NO:2n-1 (wherein $n = 1$ to 3161) corresponds to a naturally occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein).

In a second embodiment, a nucleic acid sequence that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2n-1 (wherein $n = 1$ to 3161), or fragments, analogs or derivatives thereof, under conditions of moderate stringency is provided. A non-limiting example of moderate stringency hybridization conditions are

hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55°C, followed by one or more washes in 1X SSC, 0.1% SDS at 37°C. Other conditions of moderate stringency that may be used are well known in the art. See, *e.g.*, Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and
5 Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY.

In a third embodiment, a nucleic acid that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or fragments, analogs or derivatives thereof, under conditions of low stringency, is provided. A
10 non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40°C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50°C. Other conditions of low stringency that may be used are well known in the art (*e.g.*, as
15 employed for cross-species hybridizations). See, *e.g.*, Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY; Shilo and Weinberg, 1981, *Proc Natl Acad Sci USA* 78: 6789-6792.

Conservative mutations

20 In addition to naturally-occurring allelic variants of the ORFX sequence that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), thereby leading to changes in the amino acid sequence of the encoded ORFX protein, without altering the functional ability of the ORFX protein. For example, nucleotide substitutions
25 leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of ORFX without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. For example, amino acid residues that are conserved among the ORFX proteins of the present
30 invention, are predicted to be particularly unamenable to alteration.

Amino acid residues that are conserved among members of an ORFX family members are predicted to be less amenable to alteration. For example, an ORFX protein according to the present invention can contain at least one domain (*e.g.*, as shown in Table 1) that is a typically conserved region in an ORFX family member. As such, these conserved domains are not likely to be amenable to mutation. Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-conserved among members of the ORFX family) may not be as essential for activity and thus are more likely to be amenable to alteration.

Another aspect of the invention pertains to nucleic acid molecules encoding ORFX proteins that contain changes in amino acid residues that are not essential for activity. Such ORFX proteins differ in amino acid sequence from any of any of SEQ ID NO:2 n (wherein $n = 1$ to 3161), yet retain biological activity. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 75% homologous to the amino acid sequence of any of SEQ ID NO:2 n (wherein $n = 1$ to 3161). Preferably, the protein encoded by the nucleic acid is at least about 80% homologous to any of SEQ ID NO:2 n (wherein $n = 1$ to 3161), more preferably at least about 90%, 95%, 98%, and most preferably at least about 99% homologous to SEQ ID NO:2.

An isolated nucleic acid molecule encoding a ORFX protein homologous to the protein of any of SEQ ID NO:2 n (wherein $n = 1$ to 3161) can be created by introducing one or more nucleotide substitutions, additions or deletions into the corresponding nucleotide sequence, *i.e.* SEQ ID NO:2 n -1 for the corresponding n , such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein.

Mutations can be introduced into SEQ ID NO:2 n -1 (wherein $n = 1$ to 3161) by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline,

phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in ORFX is replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of a ORFX coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for ORFX biological activity to identify mutants that retain activity. Following mutagenesis of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), the encoded protein can be expressed by any recombinant technology known in the art and the activity of the protein can be determined.

In one embodiment, a mutant ORFX protein can be assayed for (1) the ability to form protein:protein interactions with other ORFX proteins, other cell-surface proteins, or biologically active portions thereof, (2) complex formation between a mutant ORFX protein and a ORFX receptor; (3) the ability of a mutant ORFX protein to bind to an intracellular target protein or biologically active portion thereof; (*e.g.*, avidin proteins); (4) the ability to bind BRA protein; or (5) the ability to specifically bind an anti-ORFX protein antibody.

Antisense

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire ORFX coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a ORFX protein of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) or antisense nucleic acids complementary to a ORFX nucleic acid sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding ORFX. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid

residues (*e.g.*, the protein coding region of a human ORFX that corresponds to any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161)). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding ORFX. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding ORFX disclosed herein (*e.g.*, SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161)), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of ORFX mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of ORFX mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of ORFX mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (*v*), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (*v*), 5-methyl-2-thiouracil,

3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest,
5 described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a ORFX protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide
10 complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For
15 example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules,
20 vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the
25 strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

Ribozymes and PNA moieties

30 Such modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are

carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme.

5 Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave ORFX mRNA transcripts to thereby inhibit translation of ORFX mRNA. A ribozyme having specificity for a ORFX-encoding
10 nucleic acid can be designed based upon the nucleotide sequence of a ORFX DNA disclosed herein (*i.e.*, SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161)). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a ORFX-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742.
15 Alternatively, ORFX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, ORFX gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the ORFX (*e.g.*, the ORFX promoter and/or
20 enhancers) to form triple helical structures that prevent transcription of the ORFX gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of ORFX can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of
25 the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has
30 been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide

synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of ORFX can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of ORFX can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of ORFX can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of ORFX can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or

the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

ORFX polypeptides

The novel protein of the invention includes the ORFX-like protein whose sequence is provided in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residue shown in FIG. 1 while still encoding a protein that maintains its ORFX-like activities and physiological functions, or a functional fragment thereof. For example, the invention includes the polypeptides encoded by the variant ORFX nucleic acids described above. In the mutant or variant protein, up to 20% or more of the residues may be so changed.

In general, an ORFX -like variant that preserves ORFX-like function includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further include the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above. Furthermore, without limiting the scope of the invention, positions of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) may be substituted such that a mutant or variant protein may include one or more substitutions

The invention also includes isolated ORFX proteins, and biologically active portions thereof, or derivatives, fragments, analogs or homologs thereof. Also provided are polypeptide fragments suitable for use as immunogens to raise anti-ORFX antibodies. In one embodiment, native ORFX proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, ORFX proteins are produced by recombinant DNA techniques. Alternative to recombinant expression, a ORFX

protein or polypeptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the ORFX protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of ORFX protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of ORFX protein having less than about 30% (by dry weight) of non-ORFX protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-ORFX protein, still more preferably less than about 10% of non-ORFX protein, and most preferably less than about 5% non-ORFX protein. When the ORFX protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of ORFX protein in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of ORFX protein having less than about 30% (by dry weight) of chemical precursors or non-ORFX chemicals, more preferably less than about 20% chemical precursors or non-ORFX chemicals, still more preferably less than about 10% chemical precursors or non-ORFX chemicals, and most preferably less than about 5% chemical precursors or non-ORFX chemicals.

Biologically active portions of a ORFX protein include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequence of the ORFX protein, *e.g.*, the amino acid sequence shown in SEQ ID NO:2 that include fewer amino acids than the full length ORFX proteins, and exhibit at least one activity of a ORFX protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the ORFX protein. A biologically active portion of a ORFX protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length.

A biologically active portion of a ORFX protein of the present invention may contain at least one of the above-identified domains conserved between the FGF family of proteins.

Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native ORFX protein.

In an embodiment, the ORFX protein has an amino acid sequence shown in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). In other embodiments, the ORFX protein is substantially homologous to any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) and retains the functional activity of the protein of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161), yet differs in amino acid sequence due to natural allelic variation or mutagenesis, as described in detail below.

Accordingly, in another embodiment, the ORFX protein is a protein that comprises an amino acid sequence at least about 45% homologous, and more preferably about 55, 65, 70, 75, 80, 85, 90, 95, 98 or even 99% homologous to the amino acid sequence of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) and retains the functional activity of the ORFX proteins of the corresponding polypeptide having the sequence of SEQ ID NO:2*n* (wherein *n* = 1 to 3161).

Determining homology between two or more sequences

To determine the percent homology of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in either of the sequences being compared for optimal alignment between the sequences). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity").

The nucleic acid sequence homology may be determined as the degree of identity between two sequences. The homology may be determined using computer programs known in the art, such as GAP software provided in the GCG program package. See, *Needleman and Wunsch* 1970 *J Mol Biol* 48: 443-453. Using GCG GAP software with the following settings for nucleic acid sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3, the coding region of the analogous nucleic acid sequences referred to above exhibits a

degree of identity preferably of at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99%, with the CDS (encoding) part of the DNA sequence shown in SEQ ID NO:2n-1 (wherein n = 1 to 3161).

The term "sequence identity" refers to the degree to which two polynucleotide or polypeptide sequences are identical on a residue-by-residue basis over a particular region of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, U, or I, in the case of nucleic acids) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The term "substantial identity" as used herein denotes a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 80 percent sequence identity, preferably at least 85 percent identity and often 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison region. The term "percentage of positive residues" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical and conservative amino acid substitutions, as defined above, occur in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of positive residues.

Chimeric and fusion proteins

The invention also provides ORFX chimeric or fusion proteins. As used herein, a ORFX "chimeric protein" or "fusion protein" includes a ORFX polypeptide operatively linked to a non-ORFX polypeptide. A "ORFX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to ORFX, whereas a "non-ORFX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially homologous to the ORFX protein, *e.g.*, a protein that is different from the ORFX protein and that is derived from the same or a different organism. Within a ORFX fusion protein the ORFX polypeptide can correspond to all or a portion of a ORFX protein. In one embodiment, a ORFX fusion protein comprises at least one biologically active portion of a ORFX protein. In another embodiment, a ORFX fusion protein comprises at least two biologically active portions of a

ORFX protein. Within the fusion protein, the term "operatively linked" is intended to indicate that the ORFX polypeptide and the non-ORFX polypeptide are fused in-frame to each other. The non-ORFX polypeptide can be fused to the N-terminus or C-terminus of the ORFX polypeptide.

5 For example, in one embodiment a ORFX fusion protein comprises a ORFX polypeptide operably linked to the extracellular domain of a second protein. Such fusion proteins can be further utilized in screening assays for compounds that modulate ORFX activity (such assays are described in detail below).

10 In another embodiment, the fusion protein is a GST-ORFX fusion protein in which the ORFX sequences are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences. Such fusion proteins can facilitate the purification of recombinant ORFX.

15 In yet another embodiment, the fusion protein is a ORFX protein containing a heterologous signal sequence at its N-terminus. For example, the native ORFX signal sequence can be removed and replaced with a signal sequence from another protein. In certain host cells (e.g., mammalian host cells), expression and/or secretion of ORFX can be increased through use of a heterologous signal sequence.

20 In another embodiment, the fusion protein is a ORFX-immunoglobulin fusion protein in which the ORFX sequences comprising one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The ORFX-immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ORFX ligand and a ORFX protein on the surface of a cell, to thereby suppress ORFX-mediated signal transduction *in vivo*. In one nonlimiting example, a contemplated ORFX ligand of the invention is an ORFX receptor. The ORFX-immunoglobulin fusion proteins can be used to modulate the bioavailability of a ORFX cognate ligand. Inhibition of the ORFX ligand/ORFX interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, as well as modulating (e.g., promoting or inhibiting) cell survival. Moreover, the ORFX-immunoglobulin fusion proteins of the invention can be used as immunogens to produce anti-ORFX antibodies in a subject, to purify ORFX ligands, and in screening assays to identify molecules that inhibit the interaction of
30 ORFX with a ORFX ligand.

A ORFX chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). A ORFX-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the ORFX protein.

ORFX agonists and antagonists

The present invention also pertains to variants of the ORFX proteins that function as either ORFX agonists (mimetics) or as ORFX antagonists. Variants of the ORFX protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the ORFX protein. An agonist of the ORFX protein can retain substantially the same, or a subset of, the biological activities of the naturally occurring form of the ORFX protein. An antagonist of the ORFX protein can inhibit one or more of the activities of the naturally occurring form of the ORFX protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the ORFX protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function. In one embodiment, treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein has fewer side effects in a subject relative to treatment with the naturally occurring form of the ORFX proteins.

Variants of the ORFX protein that function as either ORFX agonists (mimetics) or as ORFX antagonists can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the ORFX protein for ORFX protein agonist or antagonist activity. In one

embodiment, a variegated library of ORFX variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of ORFX variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential ORFX sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (e.g., for phage display) containing the set of ORFX sequences therein. There are a variety of methods which can be used to produce libraries of potential ORFX variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential ORFX sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, e.g., Narang (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu Rev Biochem* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucl Acid Res* 11:477.

Polypeptide libraries

In addition, libraries of fragments of the ORFX protein coding sequence can be used to generate a variegated population of ORFX fragments for screening and subsequent selection of variants of a ORFX protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of a ORFX coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA that can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal and internal fragments of various sizes of the ORFX protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of ORFX proteins. The most widely used techniques, which are amenable to high throughput analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors,

transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique that enhances the frequency of functional mutants in the libraries, can
5 be used in combination with the screening assays to identify ORFX variants (Arkin and Yourvan (1992) PNAS 89:7811-7815; Delgrave *et al.* (1993) Protein Engineering 6:327-331).

Anti-ORFX Antibodies

The invention further encompasses antibodies and antibody fragments, such as F_{ab} or $(F_{ab})_2$, that bind immunospecifically to any of the proteins of the invention.

10 An isolated ORFX protein, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that bind ORFX using standard techniques for polyclonal and monoclonal antibody preparation. Full-length ORFX protein can be used. Alternatively, the invention provides antigenic peptide fragments of ORFX for use as immunogens. The antigenic peptide of ORFX comprises at least 4 amino acid residues of the amino acid sequence shown in
15 any of SEQ ID NO:2*n* (wherein $n = 1$ to 3161). The antigenic peptide encompasses an epitope of ORFX such that an antibody raised against the peptide forms a specific immune complex with ORFX. The antigenic peptide may comprise at least 6 aa residues, at least 8 aa residues, at least 10 aa residues, at least 15 aa residues, at least 20 aa residues, or at least 30 aa residues. In one embodiment of the invention, the antigenic peptide comprises a polypeptide comprising at least 6
20 contiguous amino acids of any of SEQ ID NO:2*n* (wherein $n = 1$ to 3161).

In an embodiment of the invention, epitopes encompassed by the antigenic peptide are regions of ORFX that are located on the surface of the protein, *e.g.*, hydrophilic regions. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example,
25 the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each incorporated herein by reference in their entirety.

As disclosed herein, an ORFX protein sequence of any of SEQ ID NO:2*n* (wherein $n = 1$ to 3161), or derivatives, fragments, analogs or homologs thereof, may be utilized as
30 immunogens in the generation of antibodies that immunospecifically-bind these protein components. The term "antibody" as used herein refers to immunoglobulin molecules and

immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen, such as ORFX. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} and $F_{(ab)2}$ fragments, and an F_{ab} expression library. In a specific embodiment, antibodies to human ORFX proteins are disclosed. Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies to a ORFX protein sequence of any of SEQ ID NO:2n (wherein $n = 1$ to 3161) or derivative, fragment, analog or homolog thereof. Some of these proteins are discussed below.

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by injection with the native protein, or a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, recombinantly expressed ORFX protein or a chemically synthesized ORFX polypeptide. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against ORFX can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as protein A chromatography to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of ORFX. A monoclonal antibody composition thus typically displays a single binding affinity for a particular ORFX protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular ORFX protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the hybridoma technique (see Kohler & Milstein, 1975 *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (see Kozbor, *et al.*, 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND

CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND
 5 CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Each of the above citations are incorporated herein by reference in their entirety

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to a ORFX protein (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, *et al.*,
 10 1989 *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a ORFX protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See *e.g.*, U.S. Patent No. 5,225,539. Each of the above citations are incorporated herein by reference. Antibody fragments that contain the idiotypes to a ORFX protein may be produced by
 15 techniques known in the art including, but not limited to: (i) an F_{(ab')₂} fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an F_{(ab')₂} fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

Additionally, recombinant anti-ORFX antibodies, such as chimeric and humanized
 20 monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent
 25 Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Pat. No. 4,816,567; European Patent Application No. 125,023; Better *et al.* (1988) *Science* 240:1041-1043; Liu *et al.* (1987) *PNAS* 84:3439-3443; Liu *et al.* (1987) *J Immunol.* 139:3521-3526; Sun *et al.* (1987) *PNAS* 84:214-218; Nishimura *et al.* (1987) *Cancer Res* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446-449; Shaw *et al.* (1988), *J.*
 30 *Natl Cancer Inst* 80:1553-1559; Morrison (1985) *Science* 229:1202-1207; Oi *et al.* (1986) *BioTechniques* 4:214; U.S. Pat. No. 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525;

Verhoeyan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J Immunol* 141:4053-4060. Each of the above citations are incorporated herein by reference.

In one embodiment, methods for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art. In a specific embodiment, selection of antibodies that are specific to a particular domain of a ORFX protein is facilitated by generation of hybridomas that bind to the fragment of a ORFX protein possessing such a domain. Antibodies that are specific for one or more domains within a ORFX protein, *e.g.*, the domain spanning the first fifty amino-terminal residues specific to ORFX when compared to FGF-9, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

Anti-ORFX antibodies may be used in methods known within the art relating to the localization and/or quantitation of a ORFX protein (*e.g.*, for use in measuring levels of the ORFX protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for ORFX proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody derived binding domain, are utilized as pharmacologically-active compounds [hereinafter "Therapeutics"].

An anti-ORFX antibody (*e.g.*, monoclonal antibody) can be used to isolate ORFX by standard techniques, such as affinity chromatography or immunoprecipitation. An anti-ORFX antibody can facilitate the purification of natural ORFX from cells and of recombinantly produced ORFX expressed in host cells. Moreover, an anti-ORFX antibody can be used to detect ORFX protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the ORFX protein. Anti-ORFX antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or

phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

ORFX Recombinant Vectors and Host Cells

5 Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding ORFX protein, or derivatives, fragments, analogs or homologs thereof. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can
10 be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are
15 replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the
20 invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

 The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the
25 recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, that is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner that allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation
30 system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements

(*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the
5 nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as
10 described herein (*e.g.*, ORFX proteins, mutant forms of ORFX, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of ORFX in prokaryotic or eukaryotic cells. For example, ORFX can be expressed in bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors) yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, GENE EXPRESSION TECHNOLOGY:
15 METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or
20 non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: (1) to increase expression of recombinant protein; (2) to increase the solubility of the recombinant protein; and (3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is
25 introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, Mass.) and
30 pRIT5 (Pharmacia, Piscataway, N.J.) that fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amrann *et al.*, (1988) *Gene* 69:301-315) and pET 11d (Studier *et al.*, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 60-89).

5 One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein. See, Gottesman, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 119-128. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons
10 for each amino acid are those preferentially utilized in *E. coli* (Wada *et al.*, (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the ORFX expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*,
15 (1987) *EMBO J* 6:229-234), pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), pYES2 (Invitrogen Corporation, San Diego, Calif.), and picZ (InVitrogen Corp, San Diego, Calif.).

Alternatively, ORFX can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*,
20 SF9 cells) include the pAc series (Smith *et al.* (1983) *Mol Cell Biol* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J*
25 6: 187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells. See, *e.g.*, Chapters 16 and 17 of Sambrook *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory,
30 Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv Immunol* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, *e.g.*, the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to ORFX mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen that direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen that direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub *et al.*, "Antisense RNA as a molecular tool for genetic analysis," Reviews--Trends in Genetics, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant

host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, ORFX protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding ORFX or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) ORFX protein. Accordingly, the invention further provides methods for producing ORFX protein using the host cells of the invention. In one embodiment,

the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding ORFX has been introduced) in a suitable medium such that ORFX protein is produced. In another embodiment, the method further comprises isolating ORFX from the medium or the host cell.

5 **Transgenic animals**

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which ORFX-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous ORFX sequences
10 have been introduced into their genome or homologous recombinant animals in which endogenous ORFX sequences have been altered. Such animals are useful for studying the function and/or activity of ORFX and for identifying and/or evaluating modulators of ORFX activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal
15 includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal develops and that remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous
20 recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous ORFX gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing ORFX-encoding
25 nucleic acid into the male pronuclei of a fertilized oocyte, *e.g.*, by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. The human ORFX DNA sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) can be introduced as a transgene into the genome of a non-human animal. Alternatively, a nonhuman homologue of the human ORFX gene, such as a mouse ORFX gene, can be isolated based on hybridization to
30 the human ORFX cDNA (described further above) and used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of

expression of the transgene. A tissue-specific regulatory sequence(s) can be operably linked to the ORFX transgene to direct expression of ORFX protein to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Pat.

5 Nos. 4,736,866; 4,870,009; and 4,873,191; and Hogan 1986, In: MANIPULATING THE MOUSE EMBRYO, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the ORFX transgene in its genome and/or expression of ORFX mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed
10 additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene encoding ORFX can further be bred to other transgenic animals carrying other transgenes.

To create a homologous recombinant animal, a vector is prepared which contains at least a portion of a ORFX gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the ORFX gene. The ORFX gene can be a human gene
15 (*e.g.*, SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161)), but more preferably, is a non-human homologue of a human ORFX gene. For example, a mouse homologue of human ORFX gene of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) can be used to construct a homologous recombination vector suitable for altering an endogenous ORFX gene in the mouse genome. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous
20 ORFX gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector).

Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous ORFX gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous
25 ORFX protein). In the homologous recombination vector, the altered portion of the ORFX gene is flanked at its 5' and 3' ends by additional nucleic acid of the ORFX gene to allow for homologous recombination to occur between the exogenous ORFX gene carried by the vector and an endogenous ORFX gene in an embryonic stem cell. The additional flanking ORFX nucleic acid is of sufficient length for successful homologous recombination with the
30 endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector. See *e.g.*, Thomas *et al.* (1987) *Cell* 51:503 for a description of

homologous recombination vectors. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced ORFX gene has homologously recombined with the endogenous ORFX gene are selected (see e.g., Li *et al.* (1992) *Cell* 69:915).

5 The selected cells are then injected into a blastocyst of an animal (e.g., a mouse) to form aggregation chimeras. See e.g., Bradley 1987, In: TERATOCARCINOMAS AND EMBRYONIC STEM CELLS: A PRACTICAL APPROACH, Robertson, ed. IRL, Oxford, pp. 113-152. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously recombined
10 DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley (1991) *Curr Opin Biotechnol* 2:823-829; PCT International Publication Nos.: WO 90/11354; WO 91/01140; WO 92/0968; and WO 93/04169.

In another embodiment, transgenic non-humans animals can be produced that contain
15 selected systems that allow for regulated expression of the transgene. One example of such a system is the cre/loxP recombinase system of bacteriophage P1. For a description of the cre/loxP recombinase system, see, e.g., Lakso *et al.* (1992) *PNAS* 89:6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman *et al.* (1991) *Science* 251:1351-1355. If a cre/loxP recombinase system is used to regulate
20 expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced
25 according to the methods described in Wilmut *et al.* (1997) *Nature* 385:810-813. In brief, a cell, e.g., a somatic cell, from the transgenic animal can be isolated and induced to exit the growth cycle and enter G₀ phase. The quiescent cell can then be fused, e.g., through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops to morula or
30 blastocyte and then transferred to pseudopregnant female foster animal. The offspring borne of

this female foster animal will be a clone of the animal from which the cell, *e.g.*, the somatic cell, is isolated.

Pharmaceutical Compositions

5 The ORFX nucleic acid molecules, ORFX proteins, and anti-ORFX antibodies (also referred to herein as "active compounds") of the invention, and derivatives, fragments, analogs and homologs thereof, can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein, "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, 10 antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Suitable carriers are described in the most recent edition of Remington's Pharmaceutical Sciences, a standard reference text in the field, which is incorporated herein by reference. Preferred examples of such carriers or diluents include, but are not limited to, water, saline, finger's solutions, dextrose solution, and 5% human 15 serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

20 A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent 25 such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with 30 acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringeability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, a ORFX protein or anti-ORFX antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation are vacuum drying and freeze-drying that yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use

as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder
5 such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

10 For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated
15 are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

20 The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible
25 polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as
30 pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Pat. No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved.

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by any of a number of routes, *e.g.*, as described in U.S. Patent Nos. 5,703,055. Delivery can thus also include, *e.g.*, intravenous injection, local administration (see U.S. Pat. No. 5,328,470) or stereotactic injection (see *e.g.*, Chen *et al.* (1994) *PNAS* 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells that produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

Additional Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, and antibodies described herein can be used in one or more of the following methods: (a) screening assays; (b) detection assays (*e.g.*, chromosomal mapping, cell and tissue typing, forensic biology), (c) predictive medicine (*e.g.*, diagnostic assays, prognostic assays, monitoring clinical trials, and pharmacogenomics); and (d) methods of treatment (*e.g.*, therapeutic and prophylactic).

The isolated nucleic acid molecules of the invention can be used to express ORFX protein (*e.g.*, via a recombinant expression vector in a host cell in gene therapy applications), to detect ORFX mRNA (*e.g.*, in a biological sample) or a genetic lesion in a ORFX gene, and to modulate ORFX activity, as described further below. In addition, the ORFX proteins can be used to screen drugs or compounds that modulate the ORFX activity or expression as well as to treat disorders characterized by insufficient or excessive production of ORFX protein, for

example proliferative or differentiative disorders, or production of ORFX protein forms that have decreased or aberrant activity compared to ORFX wild type protein. In addition, the anti-ORFX antibodies of the invention can be used to detect and isolate ORFX proteins and modulate ORFX activity.

5 This invention further pertains to novel agents identified by the above described screening assays and uses thereof for treatments as described herein.

Screening Assays

 The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides,
10 peptidomimetics, small molecules or other drugs) that bind to ORFX proteins or have a stimulatory or inhibitory effect on, for example, ORFX expression or ORFX activity.

 In one embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of a ORFX protein or polypeptide or biologically active portion thereof. The test compounds of the present invention can be obtained
15 using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are
20 applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam (1997) *Anticancer Drug Des* 12:145).

 Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc Natl Acad Sci U.S.A.* 90:6909; Erb *et al.* (1994) *Proc Natl Acad Sci U.S.A.* 91:11422; Zuckermann *et al.* (1994) *J Med Chem* 37:2678; Cho *et al.* (1993)
25 *Science* 261:1303; Carrell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2059; Carell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2061; and Gallop *et al.* (1994) *J Med Chem* 37:1233.

 Libraries of compounds may be presented in solution (*e.g.*, Houghten (1992) *Biotechniques* 13:412-421), or on beads (Lam (1991) *Nature* 354:82-84), on chips (Fodor (1993) *Nature* 364:555-556), bacteria (Ladner U.S. Pat. No. 5,223,409), spores (Ladner USP '409),
30 plasmids (Cull *et al.* (1992) *Proc Natl Acad Sci USA* 89:1865-1869) or on phage (Scott and

Smith (1990) *Science* 249:386-390; Devlin (1990) *Science* 249:404-406; Cwirla *et al.* (1990) *Proc Natl Acad Sci U.S.A.* 87:6378-6382; Felici (1991) *J Mol Biol* 222:301-310; Ladner above.).

In one embodiment, an assay is a cell-based assay in which a cell which expresses a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface is contacted with a test compound and the ability of the test compound to bind to a ORFX protein determined. The cell, for example, can be of mammalian origin or a yeast cell. Determining the ability of the test compound to bind to the ORFX protein can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the ORFX protein or biologically active portion thereof can be determined by detecting the labeled compound in a complex. For example, test compounds can be labeled with ^{125}I , ^{35}S , ^{14}C , or ^3H , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, test compounds can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. In one embodiment, the assay comprises contacting a cell which expresses a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the test compound to preferentially bind to ORFX or a biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ORFX protein or biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ORFX or a biologically active portion thereof can be accomplished, for example, by determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule. As used herein, a "target molecule" is a molecule with which a ORFX protein binds or interacts in nature, for example, a molecule on the surface of a cell which expresses a ORFX interacting protein, a molecule on the surface of a second cell, a molecule in the extracellular milieu, a molecule

associated with the internal surface of a cell membrane or a cytoplasmic molecule. A ORFX target molecule can be a non-ORFX molecule or a ORFX protein or polypeptide of the present invention. In one embodiment, a ORFX target molecule is a component of a signal transduction pathway that facilitates transduction of an extracellular signal (*e.g.*, a signal generated by binding
5 of a compound to a membrane-bound ORFX molecule) through the cell membrane and into the cell. The target, for example, can be a second intercellular protein that has catalytic activity or a protein that facilitates the association of downstream signaling molecules with ORFX.

Determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule can be accomplished by one of the methods described above for determining direct
10 binding. In one embodiment, determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule can be accomplished by determining the activity of the target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (*i.e.* intracellular Ca^{2+} , diacylglycerol, IP_3 , etc.), detecting catalytic/enzymatic activity of the target an appropriate substrate, detecting the
15 induction of a reporter gene (comprising a ORFX-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker, *e.g.*, luciferase), or detecting a cellular response, for example, cell survival, cellular differentiation, or cell proliferation.

In yet another embodiment, an assay of the present invention is a cell-free assay comprising contacting a ORFX protein or biologically active portion thereof with a test
20 compound and determining the ability of the test compound to bind to the ORFX protein or biologically active portion thereof. Binding of the test compound to the ORFX protein can be determined either directly or indirectly as described above. In one embodiment, the assay comprises contacting the ORFX protein or biologically active portion thereof with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test
25 compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the test compound to preferentially bind to ORFX or biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-free assay comprising contacting ORFX protein
30 or biologically active portion thereof with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ORFX protein or

biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ORFX can be accomplished, for example, by determining the ability of the ORFX protein to bind to a ORFX target molecule by one of the methods described above for determining direct binding. In an alternative embodiment, determining the ability of the test compound to modulate the activity of ORFX can be accomplished by determining the ability of the ORFX protein further modulate a ORFX target molecule. For example, the catalytic/enzymatic activity of the target molecule on an appropriate substrate can be determined as previously described.

In yet another embodiment, the cell-free assay comprises contacting the ORFX protein or biologically active portion thereof with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the ORFX protein to preferentially bind to or modulate the activity of a ORFX target molecule.

The cell-free assays of the present invention are amenable to use of both the soluble form or the membrane-bound form of ORFX. In the case of cell-free assays comprising the membrane-bound form of ORFX, it may be desirable to utilize a solubilizing agent such that the membrane-bound form of ORFX is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton[®] X-100, Triton[®] X-114, Thesit[®], Isotridecypoly(ethylene glycol ether)_n, N-dodecyl--N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl)dimethylamminiol-1-propane sulfonate (CHAPS), or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either ORFX or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to ORFX, or interaction of ORFX with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For

example, GST-ORFX fusion proteins or GST-target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, that are then combined with the test compound or the test compound and either the non-adsorbed target protein or ORFX protein, and the mixture is incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of ORFX binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either ORFX or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated ORFX or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with ORFX or target molecules, but which do not interfere with binding of the ORFX protein to its target molecule, can be derivatized to the wells of the plate, and unbound target or ORFX trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the ORFX or target molecule, as well as enzyme-linked assays that rely on detecting an enzymatic activity associated with the ORFX or target molecule.

In another embodiment, modulators of ORFX expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of ORFX mRNA or protein in the cell is determined. The level of expression of ORFX mRNA or protein in the presence of the candidate compound is compared to the level of expression of ORFX mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of ORFX expression based on this comparison. For example, when expression of ORFX mRNA or protein is greater (statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of ORFX mRNA or protein expression. Alternatively, when expression of ORFX mRNA or protein is less (statistically significantly less) in the presence of the candidate

compound than in its absence, the candidate compound is identified as an inhibitor of ORFX mRNA or protein expression. The level of ORFX mRNA or protein expression in the cells can be determined by methods described herein for detecting ORFX mRNA or protein.

In yet another aspect of the invention, the ORFX proteins can be used as "bait proteins" in a two-hybrid assay or three hybrid assay (see, *e.g.*, U.S. Pat. No. 5,283,317; Zervos *et al.* (1993) Cell 72:223-232; Madura *et al.* (1993) J Biol Chem 268:12046-12054; Bartel *et al.* (1993) Biotechniques 14:920-924; Iwabuchi *et al.* (1993) Oncogene 8:1693-1696; and Brent WO94/10300), to identify other proteins that bind to or interact with ORFX ("ORFX-binding proteins" or "ORFX-bp") and modulate ORFX activity. Such ORFX-binding proteins are also likely to be involved in the propagation of signals by the ORFX proteins as, for example, upstream or downstream elements of the ORFX pathway.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for ORFX is fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming a ORFX-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) that is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the protein which interacts with ORFX.

This invention further pertains to novel agents identified by the above-described screening assays and uses thereof for treatments as described herein.

Detection Assays

Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For example, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a

minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample.

The ORFX sequences of the present invention can also be used to identify individuals from minute biological samples. In this technique, an individual's genomic DNA is digested
5 with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identification. The sequences of the present invention are useful as additional DNA markers for RFLP ("restriction fragment length polymorphisms," described in U.S. Pat. No. 5,272,057).

Furthermore, the sequences of the present invention can be used to provide an alternative technique that determines the actual base-by-base DNA sequence of selected portions of an
10 individual's genome. Thus, the ORFX sequences described herein can be used to prepare two PCR primers from the 5' and 3' ends of the sequences. These primers can then be used to amplify an individual's DNA and subsequently sequence it.

Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, as each individual will have a unique set of such DNA
15 sequences due to allelic differences. The sequences of the present invention can be used to obtain such identification sequences from individuals and from tissue. The ORFX sequences of the invention uniquely represent portions of the human genome. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. It is estimated that allelic variation between individual humans occurs with a frequency
20 of about once per each 500 bases. Much of the allelic variation is due to single nucleotide polymorphisms (SNPs), which include restriction fragment length polymorphisms (RFLPs).

Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in the noncoding regions, fewer sequences are necessary to
25 differentiate individuals. The noncoding sequences of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), as described above, can comfortably provide positive individual identification with a panel of perhaps 10 to 1,000 primers that each yield a noncoding amplified sequence of 100 bases. If predicted coding sequences are used, a more appropriate number of primers for positive individual identification would be 500-2,000.

Predictive Medicine

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining ORFX protein and/or nucleic acid expression as well as ORFX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ORFX expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ORFX protein, nucleic acid expression or activity. For example, mutations in a ORFX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ORFX protein, nucleic acid expression or activity.

Another aspect of the invention provides methods for determining ORFX protein, nucleic acid expression or ORFX activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX in clinical trials.

Use of Partial ORFX Sequences in Forensic Biology

DNA-based identification techniques can also be used in forensic biology. Forensic biology is a scientific field employing genetic typing of biological evidence found at a crime scene as a means for positively identifying, for example, a perpetrator of a crime. To make such an identification, PCR technology can be used to amplify DNA sequences taken from very small biological samples such as tissues, *e.g.*, hair or skin, or body fluids, *e.g.*, blood, saliva, or semen

found at a crime scene. The amplified sequence can then be compared to a standard, thereby allowing identification of the origin of the biological sample.

The sequences of the present invention can be used to provide polynucleotide reagents, *e.g.*, PCR primers, targeted to specific loci in the human genome, that can enhance the reliability of DNA-based forensic identifications by, for example, providing another "identification marker" (*i.e.* another DNA sequence that is unique to a particular individual). As mentioned above, actual base sequence information can be used for identification as an accurate alternative to patterns formed by restriction enzyme generated fragments. Sequences targeted to noncoding regions of SEQ ID NOs:___ are particularly appropriate for this use as greater numbers of polymorphisms occur in the noncoding regions, making it easier to differentiate individuals using this technique. Examples of polynucleotide reagents include the ORFX sequences or portions thereof, *e.g.*, fragments derived from the noncoding regions of one or more of SEQ ID NO:2*n*-1 (where *n* = 1 to 3161), having a length of at least 20 bases, preferably at least 30 bases.

The ORFX sequences described herein can further be used to provide polynucleotide reagents, *e.g.*, labeled or label-able probes that can be used, for example, in an *in situ* hybridization technique, to identify a specific tissue, *e.g.*, brain tissue, etc. This can be very useful in cases where a forensic pathologist is presented with a tissue of unknown origin. Panels of such ORFX probes can be used to identify tissue by species and/or by organ type.

In a similar fashion, these reagents, *e.g.*, ORFX primers or probes can be used to screen tissue culture for contamination (*i.e.* screen for the presence of a mixture of different types of cells in a culture).

Predictive Medicine

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining ORFX protein and/or nucleic acid expression as well as ORFX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ORFX expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ORFX protein, nucleic

acid expression or activity. For example, mutations in a ORFX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ORFX protein, nucleic acid expression or activity.

5 Another aspect of the invention provides methods for determining ORFX protein, nucleic acid expression or ORFX activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the
10 individual examined to determine the ability of the individual to respond to a particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX in clinical trials.

These and other agents are described in further detail in the following sections.

Diagnostic Assays

15 Other conditions in which proliferation of cells plays a role include tumors, restenosis, psoriasis, Dupuytren's contracture, diabetic complications, Kaposi's sarcoma and rheumatoid arthritis.

An ORFX polypeptide may be used to identify an interacting polypeptide a sample or tissue. The method comprises contacting the sample or tissue with ORFX, allowing formation of
20 a complex between the ORFX polypeptide and the interacting polypeptide, and detecting the complex, if present.

The proteins of the invention may be used to stimulate production of antibodies specifically binding the proteins. Such antibodies may be used in immunodiagnostic procedures to detect the occurrence of the protein in a sample. The proteins of the invention may be used to
25 stimulate cell growth and cell proliferation in conditions in which such growth would be favorable. An example would be to counteract toxic side effects of chemotherapeutic agents on, for example, hematopoiesis and platelet formation, linings of the gastrointestinal tract, and hair follicles. They may also be used to stimulate new cell growth in neurological disorders including, for example, Alzheimer's disease. Alternatively, antagonistic treatments may be
30 administered in which an antibody specifically binding the ORFX-like proteins of the invention

would abrogate the specific growth-inducing effects of the proteins. Such antibodies may be useful, for example, in the treatment of proliferative disorders including various tumors and benign hyperplasias.

Polynucleotides or oligonucleotides corresponding to any one portion of the ORFX
5 nucleic acids of SEQ ID NO:2 n -1 (wherein $n = 1$ to 3161) may be used to detect DNA
containing a corresponding ORF gene, or detect the expression of a corresponding ORFX gene,
or ORFX-like gene. For example, an ORFX nucleic acid expressed in a particular cell or tissue,
as noted in Table 2, can be used to identify the presence of that particular cell type.

An exemplary method for detecting the presence or absence of ORFX in a biological
10 sample involves obtaining a biological sample from a test subject and contacting the biological
sample with a compound or an agent capable of detecting ORFX protein or nucleic acid (*e.g.*,
mRNA, genomic DNA) that encodes ORFX protein such that the presence of ORFX is detected
in the biological sample. An agent for detecting ORFX mRNA or genomic DNA is a labeled
15 nucleic acid probe capable of hybridizing to ORFX mRNA or genomic DNA. The nucleic acid
probe can be, for example, a full-length ORFX nucleic acid, such as the nucleic acid of SEQ ID
NO:2 n -1 (wherein $n = 1$ to 3161), or a portion thereof, such as an oligonucleotide of at least 15,
30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under
stringent conditions to ORFX mRNA or genomic DNA, as described above. Other suitable
probes for use in the diagnostic assays of the invention are described herein.

20 An agent for detecting ORFX protein is an antibody capable of binding to ORFX protein,
preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably,
monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or F(ab')₂) can be used. The
term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of
the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or
25 antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent
that is directly labeled. Examples of indirect labeling include detection of a primary antibody
using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin
such that it can be detected with fluorescently labeled streptavidin. The term "biological sample"
is intended to include tissues, cells and biological fluids isolated from a subject, as well as
30 tissues, cells and fluids present within a subject. That is, the detection method of the invention
can be used to detect ORFX mRNA, protein, or genomic DNA in a biological sample *in vitro* as

well as *in vivo*. For example, *in vitro* techniques for detection of ORFX mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of ORFX protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. *In vitro* techniques for detection of ORFX genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of ORFX protein include introducing into a subject a labeled anti-ORFX antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

In one embodiment, the biological sample contains protein molecules from the test subject. Alternatively, the biological sample can contain mRNA molecules from the test subject or genomic DNA molecules from the test subject. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject.

In another embodiment, the methods further involve obtaining a control biological sample from a control subject, contacting the control sample with a compound or agent capable of detecting ORFX protein, mRNA, or genomic DNA, such that the presence of ORFX protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of ORFX protein, mRNA or genomic DNA in the control sample with the presence of ORFX protein, mRNA or genomic DNA in the test sample.

The invention also encompasses kits for detecting the presence of ORFX in a biological sample. For example, the kit can comprise: a labeled compound or agent capable of detecting ORFX protein or mRNA in a biological sample; means for determining the amount of ORFX in the sample; and means for comparing the amount of ORFX in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect ORFX protein or nucleic acid.

Prognostic Assays

The diagnostic methods described herein can furthermore be utilized to identify subjects having or at risk of developing a disease or disorder associated with aberrant ORFX expression or activity. For example, the assays described herein, such as the preceding diagnostic assays or the following assays, can be utilized to identify a subject having or at risk of developing a disorder associated with ORFX protein, nucleic acid expression or activity in, *e.g.*, proliferative or differentiative disorders such as hyperplasias, tumors, restenosis, psoriasis, Dupuytren's

contracture, diabetic complications, or rheumatoid arthritis, etc.; and glia-associated disorders such as cerebral lesions, diabetic neuropathies, cerebral edema, senile dementia, Alzheimer's disease, etc. Alternatively, the prognostic assays can be utilized to identify a subject having or at risk for developing a disease or disorder. Thus, the present invention provides a method for
5 identifying a disease or disorder associated with aberrant ORFX expression or activity in which a test sample is obtained from a subject and ORFX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) is detected, wherein the presence of ORFX protein or nucleic acid is diagnostic for a subject having or at risk of developing a disease or disorder associated with aberrant ORFX expression or activity. As used herein, a "test sample" refers to a biological sample obtained
10 from a subject of interest. For example, a test sample can be a biological fluid (*e.g.*, serum), cell sample, or tissue.

Furthermore, the prognostic assays described herein can be used to determine whether a subject can be administered an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to treat a disease or disorder
15 associated with aberrant ORFX expression or activity. For example, such methods can be used to determine whether a subject can be effectively treated with an agent for a disorder, such as a proliferative disorder, differentiative disorder, glia-associated disorders, etc. Thus, the present invention provides methods for determining whether a subject can be effectively treated with an agent for a disorder associated with aberrant ORFX expression or activity in which a test sample
20 is obtained and ORFX protein or nucleic acid is detected (*e.g.*, wherein the presence of ORFX protein or nucleic acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with aberrant ORFX expression or activity.)

The methods of the invention can also be used to detect genetic lesions in a ORFX gene, thereby determining if a subject with the lesioned gene is at risk for, or suffers from, a
25 proliferative disorder, differentiative disorder, glia-associated disorder, etc. In various embodiments, the methods include detecting, in a sample of cells from the subject, the presence or absence of a genetic lesion characterized by at least one of an alteration affecting the integrity of a gene encoding a ORFX-protein, or the mis-expression of the ORFX gene. For example, such genetic lesions can be detected by ascertaining the existence of at least one of (1) a deletion
30 of one or more nucleotides from a ORFX gene; (2) an addition of one or more nucleotides to a ORFX gene; (3) a substitution of one or more nucleotides of a ORFX gene, (4) a chromosomal

rearrangement of a ORFX gene; (5) an alteration in the level of a messenger RNA transcript of a ORFX gene, (6) aberrant modification of a ORFX gene, such as of the methylation pattern of the genomic DNA, (7) the presence of a non-wild type splicing pattern of a messenger RNA transcript of a ORFX gene, (8) a non-wild type level of a ORFX-protein, (9) allelic loss of a ORFX gene, and (10) inappropriate post-translational modification of a ORFX-protein. As described herein, there are a large number of assay techniques known in the art which can be used for detecting lesions in a ORFX gene. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

10 In certain embodiments, detection of the lesion involves the use of a probe/primer in a polymerase chain reaction (PCR) (see, *e.g.*, U.S. Pat. Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR) (see, *e.g.*, Landegran *et al.* (1988) *Science* 241:1077-1080; and Nakazawa *et al.* (1994) *PNAS* 91:360-364), the latter of which can be particularly useful for detecting point mutations in the ORFX-gene (see Abravaya *et al.* (1995) *Nucl Acids Res* 23:675-682). This method can include the steps of
15 collecting a sample of cells from a patient, isolating nucleic acid (*e.g.*, genomic, mRNA or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers that specifically hybridize to a ORFX gene under conditions such that hybridization and amplification of the ORFX gene (if present) occurs, and detecting the presence or absence of an
20 amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (Guatelli
25 *et al.*, 1990, *Proc Natl Acad Sci USA* 87:1874-1878), transcriptional amplification system (Kwoh, *et al.*, 1989, *Proc Natl Acad Sci USA* 86:1173-1177), Q-Beta Replicase (Lizardi *et al.*, 1988, *BioTechnology* 6:1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such
30 molecules are present in very low numbers.

In an alternative embodiment, mutations in a ORFX gene from a sample cell can be identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and compared.

5 Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes (see, for example, U.S. Pat. No. 5,493,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

10 In other embodiments, genetic mutations in ORFX can be identified by hybridizing a sample and control nucleic acids, *e.g.*, DNA or RNA, to high density arrays containing hundreds or thousands of oligonucleotides probes (Cronin *et al.* (1996) *Human Mutation* 7: 244-255; Kozal *et al.* (1996) *Nature Medicine* 2: 753-759). For example, genetic mutations in ORFX can be identified in two dimensional arrays containing light-generated DNA probes as described in Cronin *et al.* above. Briefly, a first hybridization array of probes can be used to scan through
15 long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This step is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one
20 complementary to the wild-type gene and the other complementary to the mutant gene.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the ORFX gene and detect mutations by comparing the sequence of the sample ORFX with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on techniques developed by Maxim and Gilbert (1977) *PNAS*
25 74:560 or Sanger (1977) *PNAS* 74:5463. It is also contemplated that any of a variety of automated sequencing procedures can be utilized when performing the diagnostic assays (Naeve *et al.*, (1995) *Biotechniques* 19:448), including sequencing by mass spectrometry (see, *e.g.*, PCT International Publ. No. WO 94/16101; Cohen *et al.* (1996) *Adv Chromatogr* 36:127-162; and Griffin *et al.* (1993) *Appl Biochem Biotechnol* 38:147-159).

30 Other methods for detecting mutations in the ORFX gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA

heteroduplexes (Myers *et al.* (1985) *Science* 230:1242). In general, the art technique of "mismatch cleavage" starts by providing heteroduplexes of formed by hybridizing (labeled) RNA or DNA containing the wild-type ORFX sequence with potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent that
5 cleaves single-stranded regions of the duplex such as which will exist due to basepair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S1 nuclease to enzymatically digesting the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest
10 mismatched regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of mutation. See, for example, Cotton *et al* (1988) *Proc Natl Acad Sci USA* 85:4397; Saleeba *et al* (1992) *Methods Enzymol* 217:286-295. In an embodiment, the control DNA or RNA can be labeled for detection.

15 In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in ORFX cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T
20 mismatches (Hsu *et al.* (1994) *Carcinogenesis* 15:1657-1662). According to an exemplary embodiment, a probe based on a ORFX sequence, *e.g.*, a wild-type ORFX sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like. See, for example, U.S. Pat. No. 5,459,039.

25 In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in ORFX genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Orita *et al.* (1989) *Proc Natl Acad Sci USA*: 86:2766, see also Cotton (1993) *Mutat Res* 285:125-144; Hayashi (1992) *Genet Anal Tech Appl* 9:73-79). Single-stranded DNA fragments
30 of sample and control ORFX nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting

alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA, rather than DNA, in which the secondary structure is more sensitive to a change in sequence. In one embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility. See, *e.g.*, Keen *et al.* (1991) *Trends Genet* 7:5.

In yet another embodiment the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE). See, *e.g.*, Myers *et al* (1985) *Nature* 313:495. When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA. See, *e.g.*, Rosenbaum and Reissner (1987) *Biophys Chem* 265:12753.

Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions that permit hybridization only if a perfect match is found. See, *e.g.*, Saiki *et al.* (1986) *Nature* 324:163; Saiki *et al.* (1989) *Proc Natl Acad. Sci USA* 86:6230. Such allele specific oligonucleotides are hybridized to PCR amplified target DNA or a number of different mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology that depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation of interest in the center of the molecule (so that amplification depends on differential hybridization) (Gibbs *et al.* (1989) *Nucleic Acids Res* 17:2437-2448) or at the extreme 3' end of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prossner (1993) *Tibtech* 11:238). In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection. See, *e.g.*, Gasparini *et al* (1992) *Mol Cell Probes* 6:1. It is anticipated that in certain embodiments amplification may also be performed using Taq ligase

for amplification. See, *e.g.*, Barany (1991) *Proc Natl Acad Sci USA* 88:189. In such cases, ligation will occur only if there is a perfect match at the 3' end of the 5' sequence, making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of amplification.

5 The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid or antibody reagent described herein, which may be conveniently used, *e.g.*, in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving a ORFX gene.

10 Furthermore, any cell type or tissue, preferably peripheral blood leukocytes, in which ORFX is expressed may be utilized in the prognostic assays described herein. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

Pharmacogenomics

15 Agents, or modulators that have a stimulatory or inhibitory effect on ORFX activity (*e.g.*, ORFX gene expression), as identified by a screening assay described herein can be administered to individuals to treat (prophylactically or therapeutically) disorders (*e.g.*, neurological, cancer-related or gestational disorders) associated with aberrant ORFX activity. In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be
20 considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate
25 dosages and therapeutic regimens. Accordingly, the activity of ORFX protein, expression of ORFX nucleic acid, or mutation content of ORFX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

30 Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See *e.g.*, Eichelbaum, 1996, *Clin Exp Pharmacol Physiol*, 23:983-985 and Linder, 1997, *Clin Chem*, 43:254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic

conditions transmitted as a single factor altering the way drugs act on the body (altered drug action) or genetic conditions transmitted as single factors altering the way the body acts on drugs (altered drug metabolism). These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is haemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, PM show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. The other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the activity of ORFX protein, expression of ORFX nucleic acid, or mutation content of ORFX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with a ORFX modulator, such as a modulator identified by one of the exemplary screening assays described herein.

Monitoring Clinical Efficacy

Monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX (*e.g.*, the ability to modulate aberrant cell proliferation and/or differentiation) can be applied in basic drug screening and in clinical trials. For example, the effectiveness of an agent
5 determined by a screening assay as described herein to increase ORFX gene expression, protein levels, or upregulate ORFX activity, can be monitored in clinical trials of subjects exhibiting decreased ORFX gene expression, protein levels, or downregulated ORFX activity.

Alternatively, the effectiveness of an agent determined by a screening assay to decrease ORFX gene expression, protein levels, or downregulate ORFX activity, can be monitored in clinical
10 trials of subjects exhibiting increased ORFX gene expression, protein levels, or upregulated ORFX activity. In such clinical trials, the expression or activity of ORFX and, preferably, other genes that have been implicated in, for example, a proliferative or neurological disorder, can be used as a "read out" or marker of the responsiveness of a particular cell.

For example, genes, including ORFX, that are modulated in cells by treatment with an
15 agent (*e.g.*, compound, drug or small molecule) that modulates ORFX activity (*e.g.*, identified in a screening assay as described herein) can be identified. Thus, to study the effect of agents on cellular proliferation disorders, for example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of ORFX and other genes implicated in the disorder. The levels of gene expression (*i.e.*, a gene expression pattern) can be quantified by
20 Northern blot analysis or RT-PCR, as described herein, or alternatively by measuring the amount of protein produced, by one of the methods as described herein, or by measuring the levels of activity of ORFX or other genes. In this way, the gene expression pattern can serve as a marker, indicative of the physiological response of the cells to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the
25 agent.

In one embodiment, the invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, protein, peptide, nucleic acid, peptidomimetic, small molecule, or other drug candidate identified by the screening assays described herein) comprising the steps of (*i*) obtaining a pre-administration sample from a
30 subject prior to administration of the agent; (*ii*) detecting the level of expression of a ORFX protein, mRNA, or genomic DNA in the preadministration sample; (*iii*) obtaining one or more

post-administration samples from the subject; (iv) detecting the level of expression or activity of the ORFX protein, mRNA, or genomic DNA in the post-administration samples; (v) comparing the level of expression or activity of the ORFX protein, mRNA, or genomic DNA in the pre-administration sample with the ORFX protein, mRNA, or genomic DNA in the post administration sample or samples; and (vi) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of ORFX to higher levels than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent may be desirable to decrease expression or activity of ORFX to lower levels than detected, *i.e.*, to decrease the effectiveness of the agent.

Methods of Treatment

The present invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant ORFX expression or activity.

Diseases and disorders that are characterized by increased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that antagonize (*i.e.*, reduce or inhibit) activity. Therapeutics that antagonize activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to, (i) a ORFX polypeptide, or analogs, derivatives, fragments or homologs thereof; (ii) antibodies to a ORFX peptide; (iii) nucleic acids encoding a ORFX peptide; (iv) administration of antisense nucleic acid and nucleic acids that are "dysfunctional" (*i.e.*, due to a heterologous insertion within the coding sequences of coding sequences to a ORFX peptide) that are utilized to "knockout" endogenous function of a ORFX peptide by homologous recombination (see, *e.g.*, Capecchi, 1989, *Science* 244: 1288-1292); or (v) modulators (*i.e.*, inhibitors, agonists and antagonists, including additional peptide mimetic of the invention or antibodies specific to a peptide of the invention) that alter the interaction between a ORFX peptide and its binding partner.

Diseases and disorders that are characterized by decreased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that increase (*i.e.*, are agonists to) activity. Therapeutics that upregulate activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized

include, but are not limited to, a ORFX peptide, or analogs, derivatives, fragments or homologs thereof; or an agonist that increases bioavailability.

Increased or decreased levels can be readily detected by quantifying peptide and/or RNA, by obtaining a patient tissue sample (*e.g.*, from biopsy tissue) and assaying it *in vitro* for RNA or peptide levels, structure and/or activity of the expressed peptides (or mRNAs of a ORFX peptide). Methods that are well-known within the art include, but are not limited to, immunoassays (*e.g.*, by Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis, immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs (*e.g.*, Northern assays, dot blots, *in situ* hybridization, etc.).

In one aspect, the invention provides a method for preventing, in a subject, a disease or condition associated with an aberrant ORFX expression or activity, by administering to the subject an agent that modulates ORFX expression or at least one ORFX activity. Subjects at risk for a disease that is caused or contributed to by aberrant ORFX expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the ORFX aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending on the type of ORFX aberrancy, for example, a ORFX agonist or ORFX antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein.

Another aspect of the invention pertains to methods of modulating ORFX expression or activity for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of ORFX protein activity associated with the cell. An agent that modulates ORFX protein activity can be an agent as described herein, such as a nucleic acid or a protein, a naturally-occurring cognate ligand of a ORFX protein, a peptide, a ORFX peptidomimetic, or other small molecule. In one embodiment, the agent stimulates one or more ORFX protein activity. Examples of such stimulatory agents include active ORFX protein and a nucleic acid molecule encoding ORFX that has been introduced into the cell. In another embodiment, the agent inhibits one or more ORFX protein activity. Examples of such inhibitory agents include antisense ORFX nucleic acid molecules and anti-ORFX antibodies. These modulatory methods can be performed *in vitro*

(*e.g.*, by culturing the cell with the agent) or, alternatively, *in vivo* (*e.g.*, by administering the agent to a subject). As such, the present invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant expression or activity of a ORFX protein or nucleic acid molecule. In one embodiment, the method involves administering an agent (*e.g.*, an agent identified by a screening assay described herein), or combination of agents that modulates (*e.g.*, upregulates or downregulates) ORFX expression or activity. In another embodiment, the method involves administering a ORFX protein or nucleic acid molecule as therapy to compensate for reduced or aberrant ORFX expression or activity.

Determination of the Biological Effect of a Therapeutic

In various embodiments of the present invention, suitable *in vitro* or *in vivo* assays are utilized to determine the effect of a specific Therapeutic and whether its administration is indicated for treatment of the affected tissue.

In various specific embodiments, *in vitro* assays may be performed with representative cells of the type(s) involved in the patient's disorder, to determine if a given Therapeutic exerts the desired effect upon the cell type(s). Compounds for use in therapy may be tested in suitable animal model systems including, but not limited to rats, mice, chicken, cows, monkeys, rabbits, and the like, prior to testing in human subjects. Similarly, for *in vivo* testing, any of the animal model system known in the art may be used prior to administration to human subjects.

Malignancies

Some ORFX polypeptides are expressed in cancerous cells (*see, e.g.*, Tables 1 and 2). Accordingly, the corresponding ORF protein is involved in the regulation of cell proliferation. Accordingly, Therapeutics of the present invention may be useful in the therapeutic or prophylactic treatment of diseases or disorders that are associated with cell hyperproliferation and/or loss of control of cell proliferation (*e.g.*, cancers, malignancies and tumors). For a review of such hyperproliferation disorders, *see e.g.*, Fishman, *et al.*, 1985. MEDICINE, 2nd ed., J.B. Lippincott Co., Philadelphia, PA.

Therapeutics of the present invention may be assayed by any method known within the art for efficacy in treating or preventing malignancies and related disorders. Such assays include,

but are not limited to, *in vitro* assays utilizing transformed cells or cells derived from the patient's tumor, as well as *in vivo* assays using animal models of cancer or malignancies. Potentially effective Therapeutics are those that, for example, inhibit the proliferation of tumor-derived or transformed cells in culture or cause a regression of tumors in animal models,
5 in comparison to the controls.

In the practice of the present invention, once a malignancy or cancer has been shown to be amenable to treatment by modulating (*i.e.*, inhibiting, antagonizing or agonizing) activity, that cancer or malignancy may subsequently be treated or prevented by the administration of a Therapeutic that serves to modulate protein function.

10 Premalignant conditions

The Therapeutics of the present invention that are effective in the therapeutic or prophylactic treatment of cancer or malignancies may also be administered for the treatment of pre-malignant conditions and/or to prevent the progression of a pre-malignancy to a neoplastic or malignant state. Such prophylactic or therapeutic use is indicated in conditions known or
15 suspected of preceding progression to neoplasia or cancer, in particular, where non-neoplastic cell growth consisting of hyperplasia, metaplasia or, most particularly, dysplasia has occurred. For a review of such abnormal cell growth see *e.g.*, Robbins & Angell, 1976. BASIC PATHOLOGY, 2nd ed., W.B. Saunders Co., Philadelphia, PA.

Hyperplasia is a form of controlled cell proliferation involving an increase in cell number
20 in a tissue or organ, without significant alteration in its structure or function. For example, it has been demonstrated that endometrial hyperplasia often precedes endometrial cancer. Metaplasia is a form of controlled cell growth in which one type of mature or fully differentiated cell substitutes for another type of mature cell. Metaplasia may occur in epithelial or connective tissue cells. Dysplasia is generally considered a precursor of cancer, and is found mainly in the
25 epithelia. Dysplasia is the most disorderly form of non-neoplastic cell growth, and involves a loss in individual cell uniformity and in the architectural orientation of cells. Dysplasia characteristically occurs where there exists chronic irritation or inflammation, and is often found in the cervix, respiratory passages, oral cavity, and gall bladder.

Alternatively, or in addition to the presence of abnormal cell growth characterized as hyperplasia, metaplasia, or dysplasia, the presence of one or more characteristics of a transformed or malignant phenotype displayed either *in vivo* or *in vitro* within a cell sample derived from a patient, is indicative of the desirability of prophylactic/therapeutic administration of a Therapeutic that possesses the ability to modulate activity of An aforementioned protein.

Characteristics of a transformed phenotype include, but are not limited to: (i) morphological changes; (ii) looser substratum attachment; (iii) loss of cell-to-cell contact inhibition; (iv) loss of anchorage dependence; (v) protease release; (vi) increased sugar transport; (vii) decreased serum requirement; (viii) expression of fetal antigens, (ix) disappearance of the 250 kDal cell-surface protein, and the like. See *e.g.*, Richards, *et al.*, 1986. MOLECULAR PATHOLOGY, W.B. Saunders Co., Philadelphia, PA.

In a specific embodiment of the present invention, a patient that exhibits one or more of the following predisposing factors for malignancy is treated by administration of an effective amount of a Therapeutic: (i) a chromosomal translocation associated with a malignancy (*e.g.*, the Philadelphia chromosome (*bcr/abl*) for chronic myelogenous leukemia and t(14;18) for follicular lymphoma, etc.); (ii) familial polyposis or Gardner's syndrome (possible forerunners of colon cancer); (iii) monoclonal gammopathy of undetermined significance (a possible precursor of multiple myeloma) and (iv) a first degree kinship with persons having a cancer or pre-cancerous disease showing a Mendelian (genetic) inheritance pattern (*e.g.*, familial polyposis of the colon, Gardner's syndrome, hereditary exostosis, polyendocrine adenomatosis, Peutz-Jeghers syndrome, neurofibromatosis of Von Recklinghausen, medullary thyroid carcinoma with amyloid production and pheochromocytoma, retinoblastoma, carotid body tumor, cutaneous melanocarcinoma, intraocular melanocarcinoma, xeroderma pigmentosum, ataxia telangiectasia, Chediak-Higashi syndrome, albinism, Fanconi's aplastic anemia and Bloom's syndrome).

In another embodiment, a Therapeutic of the present invention is administered to a human patient to prevent the progression to breast, colon, lung, pancreatic, or uterine cancer, or melanoma or sarcoma.

Hyperproliferative and dysproliferative disorders

In one embodiment of the present invention, a Therapeutic is administered in the therapeutic or prophylactic treatment of hyperproliferative or benign dysproliferative disorders. The efficacy in treating or preventing hyperproliferative diseases or disorders of a Therapeutic of the present invention may be assayed by any method known within the art. Such assays include *in vitro* cell proliferation assays, *in vitro* or *in vivo* assays using animal models of hyperproliferative diseases or disorders, or the like. Potentially effective Therapeutics may, for example, promote cell proliferation in culture or cause growth or cell proliferation in animal models in comparison to controls.

Specific embodiments of the present invention are directed to the treatment or prevention of cirrhosis of the liver (a condition in which scarring has overtaken normal liver regeneration processes); treatment of keloid (hypertrophic scar) formation causing disfiguring of the skin in which the scarring process interferes with normal renewal; psoriasis (a common skin condition characterized by excessive proliferation of the skin and delay in proper cell fate determination); benign tumors; fibrocystic conditions and tissue hypertrophy (*e.g.*, benign prostatic hypertrophy).

Neurodegenerative disorders

Some ORFX proteins are found in cell types have been implicated in the deregulation of cellular maturation and apoptosis, which are both characteristic of neurodegenerative disease. Accordingly, Therapeutics of the invention, particularly but not limited to those that modulate (or supply) activity of an aforementioned protein, may be effective in treating or preventing neurodegenerative disease. Therapeutics of the present invention that modulate the activity of an aforementioned protein involved in neurodegenerative disorders can be assayed by any method known in the art for efficacy in treating or preventing such neurodegenerative diseases and disorders. Such assays include *in vitro* assays for regulated cell maturation or inhibition of apoptosis or *in vivo* assays using animal models of neurodegenerative diseases or disorders, or any of the assays described below. Potentially effective Therapeutics, for example but not by way of limitation, promote regulated cell maturation and prevent cell apoptosis in culture, or reduce neurodegeneration in animal models in comparison to controls.

Once a neurodegenerative disease or disorder has been shown to be amenable to treatment by modulation activity, that neurodegenerative disease or disorder can be treated or prevented by administration of a Therapeutic that modulates activity. Such diseases include all degenerative disorders involved with aging, especially osteoarthritis and neurodegenerative disorders.

Disorders related to organ transplantation

Some ORFX can be associated with disorders related to organ transplantation, in particular but not limited to organ rejection. Therapeutics of the invention, particularly those that modulate (or supply) activity, may be effective in treating or preventing diseases or disorders related to organ transplantation. Therapeutics of the invention (particularly Therapeutics that modulate the levels or activity of an aforementioned protein) can be assayed by any method known in the art for efficacy in treating or preventing such diseases and disorders related to organ transplantation. Such assays include *in vitro* assays for using cell culture models as described below, or *in vivo* assays using animal models of diseases and disorders related to organ transplantation, see *e.g.*, below. Potentially effective Therapeutics, for example but not by way of limitation, reduce immune rejection responses in animal models in comparison to controls.

Accordingly, once diseases and disorders related to organ transplantation are shown to be amenable to treatment by modulation of activity, such diseases or disorders can be treated or prevented by administration of a Therapeutic that modulates activity.

Cardiovascular Disease

GENX has been implicated in cardiovascular disorders, including in atherosclerotic plaque formation. Diseases such as cardiovascular disease, including cerebral thrombosis or hemorrhage, ischemic heart or renal disease, peripheral vascular disease, or thrombosis of other major vessel, and other diseases, including diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage disease, systemic lupus erythematosus, homocysteinemia, and familial protein or lipid processing diseases, and the like, are either directly or indirectly associated with atherosclerosis. Accordingly, Therapeutics of the invention, particularly those that modulate (or supply) activity or formation may be effective in treating or preventing

atherosclerosis-associated diseases or disorders. Therapeutics of the invention (particularly Therapeutics that modulate the levels or activity) can be assayed by any method known in the art, including those described below, for efficacy in treating or preventing such diseases and disorders.

5 A vast array of animal and cell culture models exist for processes involved in atherosclerosis. A limited and non-exclusive list of animal models includes knockout mice for premature atherosclerosis (Kurabayashi and Yazaki, 1996, *Int. Angiol.* 15: 187-194), transgenic mouse models of atherosclerosis (Kappel *et al.*, 1994, *FASEB J.* 8: 583-592), antisense oligonucleotide treatment of animal models (Callow, 1995, *Curr. Opin. Cardiol.* 10: 569-576),
 10 transgenic rabbit models for atherosclerosis (Taylor, 1997, *Ann. N.Y. Acad. Sci.* 811: 146-152), hypercholesterolemic animal models (Rosenfeld, 1996, *Diabetes Res. Clin. Pract.* 30 Suppl.: 1-11), hyperlipidemic mice (Paigen *et al.*, 1994, *Curr. Opin. Lipidol.* 5: 258-264), and inhibition of lipoxygenase in animals (Sigal *et al.*, 1994, *Ann. N.Y. Acad. Sci.* 714: 211-224). In addition, *in vitro* cell models include but are not limited to monocytes exposed to low density lipoprotein
 15 (Frostegard *et al.*, 1996, *Atherosclerosis* 121: 93-103), cloned vascular smooth muscle cells (Suttles *et al.*, 1995, *Exp. Cell Res.* 218: 331-338), endothelial cell-derived chemoattractant exposed T cells (Katz *et al.*, 1994, *J. Leukoc. Biol.* 55: 567-573), cultured human aortic endothelial cells (Farber *et al.*, 1992, *Am. J. Physiol.* 262: H1088-1085), and foam cell cultures (Libby *et al.*, 1996, *Curr Opin Lipidol* 7: 330-335). Potentially effective Therapeutics, for
 20 example but not by way of limitation, reduce foam cell formation in cell culture models, or reduce atherosclerotic plaque formation in hypercholesterolemic mouse models of atherosclerosis in comparison to controls.

 Accordingly, once an atherosclerosis-associated disease or disorder has been shown to be amenable to treatment by modulation of activity or formation, that disease or disorder can be
 25 treated or prevented by administration of a Therapeutic that modulates activity.

Cytokine and Cell Proliferation/Differentiation Activity

A GENX protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered

to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D,
 5 DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods: Assays for T-cell or thymocyte proliferation include without limitation those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan *et al.*, Greene Publishing
 10 Associates and Wiley-Interscience (Chapter 3 and Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bertagnoli *et al.*, *J Immunol* 145:1706-1712, 1990; Bertagnoli *et al.*, *Cell Immunol* 133:327-341, 1991; Bertagnoli, *et al.*, *J Immunol* 149:3778-3783, 1992; Bowman *et al.*, *J Immunol* 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or
 15 thymocytes include, without limitation, those described by Kruisbeek and Shevach, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1, pp. 3.12.1-14, John Wiley and Sons, Toronto 1994; and by Schreiber, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan eds. Vol 1 pp. 6.8.1-8, John Wiley and Sons, Toronto 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells
 20 include, without limitation, those described by Bottomly *et al.*, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto 1991; deVries *et al.*, *J Exp Med* 173:1205-1211, 1991; Moreau *et al.*, *Nature* 336:690-692, 1988; Greenberger *et al.*, *Proc Natl Acad Sci U.S.A.* 80:2931-2938, 1983; Nordan, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.6.1-5, John Wiley and Sons,
 25 Toronto 1991; Smith *et al.*, *Proc Natl Acad Sci U.S.A.* 83:1857-1861, 1986; Measurement of human Interleukin 11-Bennett, *et al.* In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto 1991; Ciarletta, *et al.*, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto 1991.

30 Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and

cytokine production) include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds., Greene Publishing Associates and Wiley-Interscience (Chapter 3Chapter 6, Chapter 7); Weinberger *et al.*, *Proc Natl Acad Sci USA* 77:6091-6095, 1980; Weinberger *et al.*, *Eur J Immun* 11:405-411, 1981; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A GENX protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by vital (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by vital, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania species., malaria species. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response.

The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or energy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon re-exposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to energize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the

immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc Natl Acad Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and auto-antibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of auto-antibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the

patient. Another method of enhancing anti-vital immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be
5 capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a
10 subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression
15 of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells.
20 In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on
25 the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a
30 B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor

specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods: Suitable assays for thymocyte or splenocyte cytotoxicity include, without
5 limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981; Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981;
10 Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bowman *et al.*, *J Virology* 61:1992-1998; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *Cell Immunol* 133:327-341, 1991; Brown *et al.*, *J Immunol* 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which
15 will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, *J Immunol* 144:3028-3033, 1990; and Mond and Brunswick In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, (eds.) Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins
20 that generate predominantly Th1 and CTL responses) include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *J Immunol* 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by
25 dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery *et al.*, *J Immunol* 134:536-544, 1995; Inaba *et al.*, *J Exp Med* 173:549-559, 1991; Macatonia *et al.*, *J Immunol* 154:5071-5079, 1995; Porgador *et al.*, *J Exp Med* 182:255-260, 1995; Nair *et al.*, *J Virol* 67:4062-4069, 1993; Huang *et al.*, *Science* 264:961-965, 1994; Macatonia *et al.*, *J Exp Med* 169:1255-1264, 1989; Bhardwaj *et al.*, *J Clin Investig* 94:797-807, 1994; and Inaba *et al.*, *J*
30 *Exp Med* 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz *et al.*, *Cytometry* 13:795-808, 1992; Gorczyca *et al.*, *Leukemia* 7:659-670, 1993; Gorczyca *et al.*, *Cancer Res* 53:1945-1951, 1993; Itoh *et al.*, *Cell* 66:233-243, 1991; Zacharchuk, *J Immunol* 145:4037-4045, 1990; Zamai *et al.*, *Cytometry* 14:891-897, 1993; Gorczyca *et al.*, *Internat J Oncol* 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica *et al.*, *Blood* 84:111-117, 1994; Fine *et al.*, *Cell Immunol* 155: 111-122, 1994; Galy *et al.*, *Blood* 85:2770-2778, 1995; Toki *et al.*, *Proc Nat Acad Sci USA* 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A GENX protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, *e.g.* in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (*i.e.*, in conjunction with bone marrow

transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

5 Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

 Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson *et al.* *Cellular Biology* 15:141-151, 1995; Keller *et al.*, *Mol. Cell.*
10 *Biol.* 13:473-486, 1993; McClanahan *et al.*, *Blood* 81:2903-2915, 1993.

 Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama *et al.*,
15 *Proc Natl Acad Sci USA* 89:5907-5911, 1992; McNiece and Briddeli, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben *et al.*, *Exp Hematol* 22:353-359, 1994; Ploemacher, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Spoonceret *et al.*, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.*, (eds.) Vol pp.
20 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Sutherland, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.*, (eds.) Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

Tissue Growth Activity

 A GENX protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for
25 wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

 A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation
30 employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation

induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendonitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein

may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with
5 the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular
10 insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such
15 tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions
20 resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the
25 following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

30 Assays for wound healing activity include, without limitation, those described in: Winter, EPIDERMAL WOUND HEALING, pp. 71-112 (Maibach and Rovee, eds.), Year Book Medical

Publishers, Inc., Chicago, as modified by Eaglstein and Menz, *J. Invest. Dermatol* 71:382-84 (1978).

Activin/Inhibin Activity

A GENX protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-b group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale *et al.*, *Endocrinology* 91:562-572, 1972; Ling *et al.*, *Nature* 321:779-782, 1986; Vale *et al.*, *Nature* 321:776-779, 1986; Mason *et al.*, *Nature* 318:659-663, 1985; Forage *et al.*, *Proc Natl Acad Sci USA* 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (*e.g.*, act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example,

attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

5 Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by following methods:

10 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Coligan *et al.*,
15 eds. (Chapter 6.12, MEASUREMENT OF ALPHA AND BETA CHEMOKINES 6.12.1-6.12.28); Taub *et al. J Clin Invest* 95:1370-1376, 1995; Lind *et al. APMIS* 103:140-146, 1995; Muller *et al., Eur J Immunol* 25: 1744-1748; Gruber *et al. J Immunol* 152:5860-5867, 1994; Johnston *et al., J Immunol* 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

20 A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for
25 treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (*e.g.*, stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

30 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet *et al., J. Clin. Pharmacol.* 26:131-140, 1986; Burdick *et al., Thrombosis Res.*

45:413-419, 1987; Humphrey *et al.*, *Fibrinolysis* 5:71-79 (1991); Schaub, *Prostaglandins* 35:467-474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor
5 ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and
ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and
their ligands, receptor phosphatases and their ligands, receptors involved in cell—cell
interactions and their ligands (including without limitation, cellular adhesion molecules (such as
selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation,
10 antigen recognition and development of cellular and humoral immune responses). Receptors and
ligands are also useful for screening of potential peptide or small molecule inhibitors of the
relevant receptor/ligand interaction. A protein of the present invention (including, without
limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of
receptor/ligand interactions.

15 The activity of a protein of the invention may, among other means, be measured by the
following methods:

Suitable assays for receptor-ligand activity include without limitation those described in:
CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan, *et al.*, Greene Publishing Associates and
Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions
20 7.28.1-7.28.22), Takai *et al.*, *Proc Natl Acad Sci USA* 84:6864-6868, 1987; Bierer *et al.*, *J. Exp.*
Med. 168:1145-1156, 1988; Rosenstein *et al.*, *J. Exp. Med.* 169:149-160 1989; Stoltenborg *et al.*,
J Immunol Methods 175:59-68, 1994; Stitt *et al.*, *Cell* 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The
25 anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the
inflammatory response, by inhibiting or promoting cell—cell interactions (such as, for example,
cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory
process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production
of other factors which more directly inhibit or promote an inflammatory response. Proteins
30 exhibiting such activities can be used to treat inflammatory conditions including chronic or acute

conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from
5 over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit
10 tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote
15 tumor growth.

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing
20 or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or
25 elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other
30 than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting

deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or
5 entity which is cross-reactive with such protein.

Neural disorders in general include Parkinson's disease, Alzheimer's disease, Huntington's disease, multiple sclerosis, amyotrophic lateral sclerosis (ALS), peripheral neuropathy, tumors of the nervous system, exposure to neurotoxins, acute brain injury, peripheral nerve trauma or injury, and other neuropathies, epilepsy, and/or tremors.

10 EQUIVALENTS

From the foregoing detailed description of the specific embodiments of the invention, it should be apparent that particular novel compositions and methods involving nucleic acids, polypeptides, antibodies, detection and treatment have been described. Although these particular
15 embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims that follow. In particular, it is contemplated by the inventors that various substitutions, alterations, and modifications may be made as a matter of routine for a person of ordinary skill in the art to the invention without departing from the spirit and scope of the invention as defined by the claims. Indeed, various modifications of the invention in addition to
20 those described herein will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

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Table 1

ORF#	Internal Identification Number	Protein similarity	Protein domain	Protein Classification	Cells or Tissues in which Gene is Expressed
1	13076366 (1, 2)	Novel Protein sim. GBank gi 4691395 emb CAB41562.1 - (AL049727) putative large secreted protein [Streptomyces coelicolor]		UNCLASSIFIED	264636
2	60248091 (3, 4)	Novel Protein sim. GBank gi 2829508 sp P71559 SUCC_MYCTU - SUCCINYL-COA SYNTHETASE BETA CHAIN (SCS-BETA)	Contains protein domain (PF00549) - CoA-ligases	UNCLASSIFIED	264907, 264600, 264602, 264762, 264769, 264689, 264638, 264587
3	80415924 (5, 6)			UNCLASSIFIED	264910, 264604, 264634, 264905, 264636, 264691, 264907, 264692, 264629
4	82018837 (7, 8)			UNCLASSIFIED	264908, 264909, 264760, 264628, 264635
5	79970035 (9, 10)			UNCLASSIFIED	22279002, 264583
6	79842462 (11, 12)		Contains protein domain (PF00127) - Copper binding proteins, plastocyanin/azurin family	UNCLASSIFIED	264908
7	85515576 (13, 14)	Novel Protein sim. GBank gi 4415926 gb AAD20157 - (AC006282) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	20281099, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265006, 264512, 265009, 264910, 264595, 264596, 264758, 264603, 264604, 264760, 264762, 264883, 264768, 264767, 264689, 35695917, 264690, 264692, 264693, 33657109, 264628, 264629, 35698423, 55811578, 35695855, 264630, 264631, 264632, 264634, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264566, 264486
8	56924278 (15, 16)	Novel Protein sim. GBank gi 585562 sp Q06458 NIRB_KLEPN - NITRITE REDUCTASE (NAD(P)H) LARGE SUBUNIT		reductase	264807
9	79394457 (17, 18)			UNCLASSIFIED	265007, 265019, 263972
10	79558459 (19, 20)			UNCLASSIFIED	264906
11	20414027 (21, 22)				264605
12	94141210 (23, 24)	Novel Protein sim. GBank gi 3878145 emb CAA99871 - (Z75543) similar to potassium channel protein [Caenorhabditis elegans]		misc_channel	264259, 265007, 83373044
13	20750551 (25, 26)			UNCLASSIFIED	264556, 264557, 264564
14	95105114 (27, 28)	Novel Protein sim. GBank gi 2832781 emb CAA12645 - (AJ225805) inward potassium channel alpha subunit [Egeria densa]	Contains protein domain (PF00023) - Ank repeat	potassium_channel	35698288, 35696052, 264510, 35695917, 264691, 264628, 35698423, 264555, 264558, 264559, 83373044
15	20458307 (29, 30)	Novel Protein sim. GBank gi 1710791 sp Q10234 RT05_SCHPO - PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S5	Contains protein domain (PF00333) - Ribosomal protein S5	ribosomalprot	264604
16	20760356 (31, 32)				264555

17	20282744 (33, 34)	Novel Protein sim. GBank gij1174884 sp P44391 URE1_HAEIN - UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE)	Contains protein domain (PF00449) - Urease		284600
18	80246804 (35, 36)	Novel Protein sim. GBank gij2281102 (AC002333) - SF16 isolog [Arabidopsis thaliana]			29331827, 284555, 284557, 284638, 284558
19	80076624 (37, 38)				
20	20724558 (39, 40)	Novel Protein sim. GBank gij2506112 sp P43672 UUP_ECOLI - ABC TRANSPORTER ATP-BINDING PROTEIN UUP	UNCLASSIFIED transport		22278986, 284907, 284910, 284600, 284693 284602
21	80417554 (41, 42)	Novel Protein sim. GBank gij1730203 sp P50442 GATM_RAT - GLYCINE AMIDINOTRANSFERASE PRECURSOR (L- ARGININE:GLYCINE AMIDINOTRANSFERASE) (TRANSAMIDINASE) (AT)	UNCLASSIFIED		22278985, 284906, 265008, 265010, 265011, 284602, 284605, 284768, 284688, 21908764, 284691, 18108376, 284636, 18108387, 284486
22	11705858 (43, 44)				284685
23	80419176 (45, 46)	Novel Protein sim. GBank gij1877329 emb CAB07077 - (282771) fadE25 [Mycobacterium tuberculosis]	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	dehydrogenase	284488, 284907, 284909, 284600, 284602, 284603, 284605, 284682, 284768, 32833986, 284636, 284486
24	20291697 (47, 48)				284600
25	80253774 (49, 50)				264593
26	80255394 (51, 52)				22278986, 56182435, 265018, 264566
27	80235785 (53, 54)	Novel Protein sim. GBank gij4808369 emb CAB42783.1 - (AL049841) putative 30S ribosomal protein S14 [Streptomyces coelicolor]	Contains protein domain (PF00253) - Ribosomal protein S14p/S29e	ribosomal prot	18108370, 35898423, 264635, 264555
28	79483581 (55, 56)				284638
29	82448765 (57, 58)	Novel Protein sim. GBank gij122280 sp O08333 K6PF_STRCO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)	Contains protein domain (PF00365) - Phosphofructokinase	kinase	284601, 284762, 284768, 284769, 284638
30	79189333 (59, 60)				284908, 285019, 284687, 21906764, 21908768
31	18848158 (61, 62)				284534
32	82449495 (63, 64)	Novel Protein sim. GBank gij3560504 (AF027770) - unknown [Mycobacterium smegmatis]			284905, 284605, 284762, 284768, 284687, 284689
33	79582628 (65, 66)	Novel Protein sim. GBank gij2129003 pir G64507 - hypothetical protein MJ1685 - Methanococcus jannaschii			264687
34	87467657 (67, 68)				
35	85005170 (69, 70)	Novel Protein sim. GBank gij5420387 emb CAB46678.1 - (AJ243459) proteophosphoglycan [Leishmania major]			60432289, 284600, 284602, 284760, 18108357, 284769, 265020, 284691
36	18642042 (71, 72)	Novel Protein sim. GBank gij3287739 sp P73538 BIOS_SYN3 - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)			264600, 284687, 264558, 264639
37	20368215 (73, 74)	Novel Protein sim. GBank gij2313134 gb AAD07126.1 - (AE000527) delta-1-pyrroline-5-carboxylate dehydrogenase [Helicobacter pylori 26695]		synthase dehydrogenase	264566 284803

36	20466334 (75, 76)	Novel Protein sim. GBank gij3805970[embjCAA05231] - (AJ004933) periplasmic nitrate reductase, large subunit [Rhodospseudomonas sp.]		reductase	264605
39	94300715 (77, 78)	Novel Protein sim. GBank gij1929449 (L63543) - endodermin [Xenopus laevis]	Contains protein domain (PF00207) - Alpha-2-macroglobulin family	complement	264905, 264908, 264907, 66712502, 264908, 264909, 264511, 265009, 264910, 55812038, 264758, 265011, 264762, 264882, 264763, 264764, 264768, 265022, 264893, 264828, 264831, 264634, 264635, 264555, 264638, 18108381, 264558, 18108385, 264482
40	20635625 (79, 80)			UNCLASSIFIED	264592
41	80023287 (81, 82)	Novel Protein sim. GBank gij854065[embjCAA58337] - (X83413) U88 [Human herpesvirus 6]			264591, 35895917
42	20724568 (83, 84)			UNCLASSIFIED	264602
43	20467069 (85, 86)	Novel Protein sim. GBank gij3820584 (AF086791) - carbamoylphosphate synthetase large subunit [Zymomonas mobilis]		synthase	264605
44	13085297 (87, 88)	Novel Protein sim. GBank gij2494764[sp]Q50729[GUA_MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)]	Contains protein domain (PF00958) - GMP synthase C terminal domain	synthase	264769, 264638
45	39384711 (89, 90)	Novel Protein sim. GBank gij1881738 (U89688) - myosin-I binding protein Acan125 [Acanthamoeba castellanii]		UNCLASSIFIED	264769, 264510, 264508
46	95003398 (91, 92)			ngf	264566
47	11698624 (93, 94)			UNCLASSIFIED	264689
48	79407218 (95, 96)				18108385, 264635, 264828
49	21659844 (97, 98)			UNCLASSIFIED	264603
50	80503998 (99, 100)				264508, 264603, 264769, 264689, 264636, 264558, 264488
51	80255569 (101, 102)	Novel Protein sim. GBank gij3411177 (AF076240) - MocC [Rhizobium leguminosarum bv. viciae]		UNCLASSIFIED	264593, 18108387
52	79208528 (103, 104)	Novel Protein sim. GBank gij3914992[sp]Q26284[SM41_HEMPU - 41 KD SPICULE MATRIX PROTEIN PRECURSOR (HSM41) (HPSMC)]		stud	264634
53	36996970 (105, 106)	Novel Protein sim. GBank gij3980411 (AC004561) - putative proline-rich protein [Arabidopsis thaliana]		UNCLASSIFIED	264762
54	79570897 (107, 108)			UNCLASSIFIED	264630, 264909, 264768
55	80202703 (109, 110)	Novel Protein sim. GBank gij1633372 (U52064) - Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus]			29331824, 264102, 265018, 18108376
56	8758408 (111, 112)	Novel Protein sim. GBank gij4321580[gbjAAD15785] - (AF050114) alginate lyase [Pseudomonas sp. W7]			264604
57	11223386 (113, 114)		Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264557

58	91227508 (115, 116)	Novel Protein sim. GBank gi 5616074 gb AAD45616.1 AF08194 - (AF081943) protate- derived STE20-like kinase PSK [Homo sapiens]	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	56182575, 264259, 60432049, 35696052, 66712502, 264909, 265008, 265010, 265011, 264661, 29148784, 35695917, 60170615, 264691, 264692, 264693, 18108374, 35696423, 56182323, 60432113 264600, 264689, 264638
59	80077371 (117, 118)	Novel Protein sim. GBank gi 1172920 sp P45830 RFE_MYCLE - PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N- ACETYLGUCOSAMINYL TRANSFERASE	Contains protein domain (PF00953) - transferase Glycosyl transferase	
60	12958341 (119, 120)			264689
61	80426806 (121, 122)	Novel Protein sim. GBank gi 1710216 (U79260) - unknown [Homo sapiens]		264766
62	13504866 (123, 124)			264630
63	16474553 (125, 126)			265019
64	20724578 (127, 128)	Novel Protein sim. GBank gi 420845 p j A47041 - transposase homolog (insertion element [SAE1]) - Alcaligenes eutrophus	UNCLASSIFIED UNCLASSIFIED	264602
65	79326308 (129, 130)	Novel Protein sim. GBank gi 3122312 sp O08134 KPYK_MYCTU - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) - kinase Pyruvate kinase	264563
66	46854384 (131, 132)	Novel Protein sim. GBank gi 3928723 emb CAA22219 - (AL034355) putative ABC transporter [Streptomyces coelicolor]	transport	22278996, 264558
67	78952543 (133, 134)	Novel Protein sim. GBank gi 231885 sp P30234 DHA_MYCTU - ALANINE DEHYDROGENASE (40 KD ANTIGEN)	dehydrogenase	265021
68	78817382 (135, 136)			264909
69	79841764 (137, 138)			264908
70	79871329 (139, 140)			264908, 264908
71	65897458 (141, 142)			264602, 265021
72	87734977 (143, 144)	Novel Protein sim. GBank gi 4415926 gb AAD20157 - (AC006282) unknown protein [Arabidopsis thaliana]	UNCLASSIFIED UNCLASSIFIED	264488, 264905, 264906, 264907, 264908, 264511, 265008, 264910, 264758, 87168474, 264682, 264768, 264688, 264689, 35695917, 265021, 60170615, 264691, 33657023, 264692, 264693, 264629, 264631, 264639, 22279000
73	60025241 (145, 146)		UNCLASSIFIED	60424179, 264508, 264908, 265007, 264603, 264687, 264689, 264692, 16108387
74	20377410 (147, 148)			264805
75	11819032 (149, 150)	Novel Protein sim. GBank gi 2853098 emb CAA16914 - (AL021767) vacuolar protein sorting [Schizosaccharomyces pombe]	UNCLASSIFIED UNCLASSIFIED	264689
76	95105303 (151, 152)	Novel Protein sim. GBank gi 4468811 emb CAB38212 - (AL035601) putative protein [Arabidopsis thaliana]	UNCLASSIFIED	83373044, 264906, 264557
77	10144718 (153, 154)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [human herpesvirus 6]	UNCLASSIFIED	264563
78	6758256 (155, 156)		UNCLASSIFIED	264604

79	94140190 (157, 158)	Novel Protein sim. GBank gl 5688453 dbj BAA83010.1 - (AB028981) KIAA1058 protein [Homo sapiens]	Contains protein domain (PF00169) - PH domain		35696286, 22278998, 29331822, 29331824, 29331825, 29331827, 264905, 264906, 264907, 66712502, 264908, 264909, 265008, 265009, 264910, 60170831, 55812038, 33109954, 265017, 265018, 264288, 264768, 56181562, 21906765, 21906769, 29148784, 265020, 264690, 264691, 264692, 264693, 60431528, 35698423, 264631, 264632, 264634, 264636, 264639, 83373044, 264564, 264566, 264567
80	82314840 (159, 160)			UNCLASSIFIED	264769, 264801, 265008, 264910, 264604, 264605, 264634, 264635, 264905, 264762, 264637, 264592, 264628, 264907, 264691, 264908, 264567, 264908, 264768
81	20467247 (161, 162)	Novel Protein sim. GBank gl 1723442 sp Q10258 YD2A_SCHPO - HYPOTHETICAL 89.0 KD PROTEIN C56F8.10 IN CHROMOSOME I		reductase	264605
82	16331388 (163, 164)	Novel Protein sim. GBank gl 2895666 (AF045770) - methylmalonate semi-aldelyde dehydrogenase [Oryza sativa]		dehydrogenase	264567
83	94741180 (165, 166)	Novel Protein sim. GBank gl 3402673 (AC004697) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 264508, 264509, 264905, 264808, 264909, 264511, 264591, 264593, 264594, 264595, 264596, 264758, 264603, 264760, 264681, 18108351, 264762, 264682, 264764, 264684, 264766, 264686, 264632, 264637, 264557, 264638, 264639, 18108385, 264566
84	80355375 (167, 168)	Novel Protein sim. GBank gl 1173364 sp P45380 SAT1_RAT - SULFATE ANION TRANSPORTER 1 (CANALICULAR SULFATE TRANSPORTER) (SULFATE/CARBONATE ANTIPORTER)		transport	264508, 264908, 264907, 264908, 264909, 264910, 264760, 264763, 264764, 264766, 264768, 264769, 35695855, 264636, 264637
85	80498600 (169, 170)	Novel Protein sim. GBank gl 2120998 pir S70882 - glycosyltransferase homolog - Bordetella pertussis		transferase	264605, 264762, 264687, 264769, 18108374, 264636, 264486
86	39558043 (171, 172)	Novel Protein sim. GBank gl 3256023 emb CAA17228.1 - (AL021897) hypothetical protein Rv1112 [Mycobacterium tuberculosis]			264910
87	13856808 (173, 174)			UNCLASSIFIED	264093

188	85344718 (175, 176)	Novel Protein sim. GBank gi 559703 dbj BAA07552 - (D38549) ha1025 is new [Homo sapiens]			52644507, 52646365, 18108398, 65274572, 58182575, 56994075, 35698286, 22278997, 22278998, 22278999, 264092, 264093, 264094, 264095, 264259, 29331822, 29331824, 56182181, 66714117, 29331825, 29331826, 60432289, 29331827, 29331828, 35696052, 33658970, 264105, 264508, 264905, 264908, 264907, 264908, 29331830, 66712502, 52844045, 58182435, 265007, 265009, 264910, 60170831, 264592, 60431735, 60433356, 33657402, 264757, 60433438, 55812038, 264758, 21906754, 52846317, 33109954, 52844296, 87168474, 265011, 87168559, 264801, 265017, 265018, 264604, 265019, 264448, 264368, 264288, 264768, 52844229, 21906788, 21906787, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 60170615, 52844150, 33657023, 65274820, 33657109, 27486261, 27486264, 33657349, 35695763, 264628, 263972, 18108374, 55810764, 35698423, 55811578, 65274791, 35695855, 60431850, 264638, 52844332, 58182323, 60170394, 83373044, 18108385, 18108387, 18108388, 56526488, 87168518, 60432113, 22279000, 22279002, 264482, 264564, 264488
89	80077389 (177, 178)	Novel Protein sim. GBank gi 1710383 sp P48352 RIPX_BACSU - PROBABLE INTEGRASE/RECOMBINASE RIPX			264600
90	82115998 (179, 180)	Novel Protein sim. GBank gi 2499891 sp P76403 YEGQ_ECOLI - PUTATIVE PROTEASE IN BAER-GRK INTERGENIC REGION	UNCLASSIFIED		264760
91	78908950 (181, 182)	Novel Protein sim. GBank gi 3367754 emb CAA20079 - (AL031155) hypothetical protein SC3A7.16c [Streptomyces coelicolor]	protease		265006
92	79554871 (183, 184)	Novel Protein sim. GBank gi 2895095 (AF011337) - putative E1-E2 ATPase [Mus musculus]	UNCLASSIFIED		264691
93	80496778 (185, 186)	Novel Protein sim. GBank gi 1171919 sp P46920 OPUA_BACSU - GLYCINE BETAINES TRANSPORT ATP-BINDING PROTEIN OPUAA	ATPase_associated		264907, 264908, 264910, 265009, 264605, 264789
94	79846649 (187, 188)	Novel Protein sim. GBank gi 1171919 sp P46920 OPUA_BACSU - GLYCINE BETAINES TRANSPORT ATP-BINDING PROTEIN OPUAA	Contains protein domain (PF00571) - transport CBS domain		264908
95	11090238 (189, 190)				264594

96	94322125 (191, 192)	Novel Protein sim. GBank gij4589560[dbj BAA76802.1] - (AB023175) KIAA0958 protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278999, 284259, 29331822, 29331826, 35896052, 29146498, 284509, 284806, 284907, 284908, 284909, 285007, 285008, 284910, 285009, 284593, 285010, 285017, 284604, 285019, 18108351, 284288, 284766, 284768, 284769, 21906765, 21906767, 21906769, 285020, 284692, 33657182, 35895783, 284628, 284629, 18108379, 284831, 284636, 18108381, 284559, 18108382, 83373044, 22278002, 284508
97	79805200 (193, 194)	Novel Protein sim. GBank gij4583559[emb CAB40388.1] - (AJ005255) OxyR [Erwinia chrysanthemi]		UNCLASSIFIED	
98	79427000 (195, 196)	Novel Protein sim. GBank gij1001693[dbj BAA10430] - (D84002) hypothetical protein [Synecococcus sp.]		UNCLASSIFIED	284909
99	20465524 (197, 198)	Novel Protein sim. GBank gij1169479[sp P43925 EFG_HAEIN - ELONGATION FACTOR G (EF-G)]		UNCLASSIFIED	284805
100	79840113 (199, 200)	Novel Protein sim. GBank gij480897[pir S37485 - gene msg1 protein - mouse]		UNCLASSIFIED	284693
101	80203298 (201, 202)	Novel Protein sim. GBank gij2894166[emb CAA11773.1] - (AJ223998) PCZA381.18 [Amycolatopsis orientalis]		UNCLASSIFIED	285020, 284102, 263972
102	20467259 (203, 204)	Novel Protein sim. GBank gij1731040[sp P54509 YQHH_BACSU - HYPOTHETICAL HELICASE IN SINI-GCVT INTERGENIC REGION]		synthase	264605
103	20466368 (205, 206)	Novel Protein sim. GBank gij1731040[sp P54509 YQHH_BACSU - HYPOTHETICAL HELICASE IN SINI-GCVT INTERGENIC REGION]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	264605
104	80247572 (207, 208)	Novel Protein sim. GBank gij854065[emb CAA58337] - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	284591, 284595, 284602
105	79605206 (209, 210)	Novel Protein sim. GBank gij1685117 (U70770) - furrowed [Drosophila melanogaster]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	complement	284508
106	28382058 (211, 212)	Novel Protein sim. GBank gij1705505[sp P54729 BS4_MOUSE - BS4 PROTEIN]	Contains protein domain (PF00627) - UBA domain	UNCLASSIFIED	284511, 285009
107	80057791 (213, 214)	Novel Protein sim. GBank gij4887229[gb AAD32244.1 AF15075 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]		ATPase-associated	29331824, 284591, 21906754, 285019
108	80237936 (215, 216)	Novel Protein sim. GBank gij263577[emb CAB15264] - (Z99120) similar to ABC transporter (ATP-binding protein) [Bacillus subtilis]	Contains protein domain (PF00005) - ABC transporter	transport	18108374, 35895917, 22278996, 264113, 284600, 284602, 284603, 285017, 284910, 284906, 284636, 284768
109	95184148 (217, 218)	Novel Protein sim. GBank gij2330791[emb CAB11265] - (Z98601) carboxypeptidase s precursor [Schizosaccharomyces pombe]		UNCLASSIFIED	284758, 284603, 284630, 284636, 284637
110	79582823 (219, 220)				284887
111	39585456 (221, 222)				284584
112	79856038 (223, 224)			UNCLASSIFIED	284908
113	17859439 (225, 226)			UNCLASSIFIED	285007
114	80502101 (227, 228)			UNCLASSIFIED	284769

115	80251003 (229, 230)	Novel Protein sim. GBank gj2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	52845158, 52845080, 33656970, 284592, 21908754, 27486284, 18108379, 35698423, 284635, 52844332, 18108382
116	81288689 (231, 232)				284805, 284906, 284907, 284908, 284909, 284910, 284758, 285010, 284763, 284882, 284764, 284768, 284885, 284886, 284788, 284789, 33657023, 284693, 33657109, 284628, 18108374, 284631, 284632, 284634, 284636, 284637, 284638, 284639, 56526486, 284585, 284586
117	79636695 (233, 234)				284639, 284893
118	80222170 (235, 236)		Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	283974
119	91013071 (237, 238)	Novel Protein sim. GBank gj732526 (U22327) - alpha2(IV) collagen [Caenorhabditis elegans]		UNCLASSIFIED	22278996, 28331824, 60432289, 265007, 60433438, 284603, 284605, 18108351, 284769, 284889, 285020, 284534, 27486281, 284558, 83373044, 18108385, 284584
120	8756491 (239, 240)	Novel Protein sim. GBank gj2131219 [pir]S50157 - cyclin-dependent kinase chain SRB10 - yeast (Saccharomyces cerevisiae)		kinase	284603
121	80028153 (241, 242)				284595
122	20457620 (243, 244)	Novel Protein sim. GBank gj2052147 [emb]CAB08137] - (Z94752) tsgA [Mycobacterium tuberculosis]	Contains protein domain (PF00398) - Ribosomal RNA adenine dimethylases	transferase	284605
123	8758278 (245, 246)				284604
124	79104017 (247, 248)	Novel Protein sim. GBank gj2833385 [sp]Q43134 [UGST_SORBI - GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR		synthase	18108394, 18108397, 285006, 285007, 285008, 285010, 285011, 18108355, 18108379, 18108380, 18108384
125	87797988 (249, 250)	Novel Protein sim. GBank gj475542 (U08255) - glutamate receptor delta-1 subunit [Rattus norvegicus]	Contains protein domain (PF00080) - Ligand-gated ion channel	misc_channel	284508, 284906, 285009, 284598, 22279002
126	56701283 (251, 252)	Novel Protein sim. GBank gj5102785 [emb]CAB45200.1] - (AL078308) putative transcriptional regulator [Streptomyces coelicolor]			284511
127	20467267 (253, 254)			UNCLASSIFIED	284605
128	80248473 (255, 256)	Novel Protein sim. GBank gj130120 [sp]P23620 [PHOB_PSEAE - PHOSPHATE REGULON TRANSCRIPTIONAL REGULATORY PROTEIN PHOB	Contains protein domain (PF00072) - Response regulator receiver domain	phosphatase	284907, 284909, 284910, 284600, 284601, 284603, 284605, 18108351, 284693, 284557
129	95290543 (257, 258)	Novel Protein sim. GBank gj2508493 [sp]P38036 [YGC8_ECOLI - HYPOTHETICAL 100.5 KD PROTEIN IN IAP-CYSH INTERGENIC REGION	Contains protein domain (PF00270) - DEAD/DEAH box helicase	UNCLASSIFIED	35686423, 35695855, 284600, 284602, 284603, 284604, 284605, 284508, 284908, 284564, 284628, 284682, 284595, 284683
130	80085583 (259, 260)	Novel Protein sim. GBank gj854085 [emb]CAA58337] - (X83413) U88 [Human herpesvirus 6]			284634
131	84995022 (261, 262)	Novel Protein sim. GBank gj1076038 [pir]S54860 - ABC transporter PstC-2 chain - Mycobacterium tuberculosis	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	transport	18108376, 284769, 28331826, 284689, 22278986, 285021, 284600, 284511, 284601, 284602, 284605, 284905, 284636

132	10887692 (263, 284)	Novel Protein sim. GBank gi 1877340 emb CAB07058 - (Z92771) accA3 [Mycobacterium tuberculosis]	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)	carboxylase	264636 264905, 264689
133	94630883 (265, 286)	Novel Protein sim. GBank gi 4585838 emb CAB40932.1 - (AL049630) putative NADH dehydrogenase [Streptomyces coelicolor]		dehydrogenase	264905, 264605, 265021
134	79834680 (267, 288)	Novel Protein sim. GBank gi 1460074 emb CAB01049 - (Z77250) hypothetical protein Rv2586 [Mycobacterium tuberculosis]			264634
135	19885057 (269, 270)	Novel Protein sim. GBank gi 2125896 emb CAA73511 - (Y13070) folypolyglutamate synthase [Streptomyces coelicolor]		synthase	264508
136	79846083 (271, 272)				264683, 264685, 264686, 264691, 264692, 264693
137	79819770 (273, 274)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	18108374, 18108385, 33657109, 33657182, 265010, 22278998, 265008, 265007, 265008, 265009, 264693
138	79835971 (275, 276)	Novel Protein sim. GBank gi 5688912 emb CAB52075.1 - (AL108732) putative mutase [Streptomyces coelicolor A3(2)]	Contains protein domain (PF01817) - Chorismate mutase	dehydrogenase	22278998, 265007, 264910, 60433358, 265010, 264602, 264605, 264768, 264688, 264769, 264693, 32833986, 18108374, 18108387
139	86688076 (277, 278)			UNCLASSIFIED	264908
140	79825759 (279, 280)				264600
141	20700084 (281, 282)	Novel Protein sim. GBank gi 3581916 emb CAA20855 - (AL031545) mutS family DNA mismatch repair protein [Schizosaccharomyces pombe]		nuclease	264602, 265017
142	80028104 (283, 284)				
143	11072274 (285, 286)	Novel Protein sim. GBank gi 3334127 sp P97303 BAC2_MOUSE - TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOLOG 2)		UNCLASSIFIED	264600
144	85008102 (287, 288)	Novel Protein sim. GBank gi 3757569 emb CAA21315 - (AL031883) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=66.31; 1-evidence_end [Drosophila melanogaster]			263878, 264600, 264910, 264632, 264508, 264563, 264564, 264591, 264556, 264908, 264629, 264639
145	80027058 (289, 290)	Novel Protein sim. GBank gi 140807 sp P24536 Y121_BURCE - INSERTION ELEMENT IS402 HYPOTHETICAL 24 KD PROTEIN		UNCLASSIFIED	22278998, 264602
146	13085862 (291, 292)	Novel Protein sim. GBank gi 2827608 emb CAA16663 - (AL021848) uvrD2 [Mycobacterium tuberculosis]	Contains protein domain (PF01675) - Transposase		264687
147	94320368 (293, 294)			helicase	264905, 264906, 264909, 264510, 265009, 60433358, 264600, 264601, 264604, 264605, 264687, 264769, 18108385, 65274791, 18108387
148	80248804 (295, 296)	Novel Protein sim. GBank gi 2916947 emb CAA17585 - (AL021999) hypothetical protein Rv0986 [Mycobacterium tuberculosis]		transport	265008, 265010, 264600, 264602, 264603, 264604, 264605, 264683, 33657109, 264636

149	80249373 (297, 298)	Novel Protein sim. GBank gi 1723073 sp Q11040 Y081_MYCTU - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CY50.01	Contains protein domain (PF00005) - ABC transporter	transport	265010, 264600, 264601, 264603, 264604, 27486265, 264636
150	20294748 (299, 300)	Novel Protein sim. GBank gi 3724125 emb CAA11805 - (AJ224340) maltosephosphorylase [Lactobacillus sanfrancisco]			264600
151	20726398 (301, 302)	Novel Protein sim. GBank gi 729312 sp P07651 DEOB_ECOLI - PHOSPHOPENTOMUTASE (PHOSPHODEOXYRIBOMUTASE)	Contains protein domain (PF01676) - Metalloenzyme superfamily	UNCLASSIFIED	264602
152	95002877 (303, 304)	Novel Protein sim. GBank gi 2497952 sp P55667 Y4TM_RHISN - HYPOTHETICAL HYDROLASE/PEPTIDASE Y4TM		peptidase	264602
153	80256665 (305, 306)	Novel Protein sim. GBank gi 3123021 sp Q90508 MT1_FUNHE - VITELLOGENIN I PRECURSOR (VTG I) (CONTAINS: LIPOVITELLIN 1 (LV1); PHOSVITIN (PV); LIPOVITELLIN 2 (LV2))		UNCLASSIFIED	264593
154	82305968 (307, 308)				264810, 264762, 264691, 264634
155	20429859 (309, 310)	Novel Protein sim. GBank gi 419897 pir JUN0443 - transcription Initiation factor sigma homolog hrdB - Streptomyces aureofaciens	Contains protein domain (PF00140) - Sigma-70 factor	mapolymerase	264605
156	39564742 (311, 312)	Novel Protein sim. GBank gi 628710 pir S41739 - hypothetical protein - Escherichia coli		UNCLASSIFIED	264565
157	10358887 (313, 314)	Novel Protein sim. GBank gi 3895013 (AF052586) - CtrA [Pseudomonas aeruginosa]	Contains protein domain (PF00142) - 4Fe-4S iron sulfur cluster binding proteins, Nif-HfrxC family	hydrolase	264691
158	78761838 (315, 316)	Novel Protein sim. GBank gi 1073072 pir C55543 - cnaU protein - Pseudomonas syringae pv. syringae		UNCLASSIFIED	264805
159	7890376 (317, 318)				265008
160	11075119 (318, 320)			UNCLASSIFIED	264605
161	80055007 (321, 322)	Novel Protein sim. GBank gi 173023 sp P46789 RL30_STRCO - 50S RIBOSOMAL PROTEIN L30	Contains protein domain (PF00400) - WD domain, G-beta repeat		
162	80016371 (323, 324)	Novel Protein sim. GBank gi 5304869 emb CAB46028.1 - (AL031685) dJ963K23.2 (novel protein) [Homo sapiens]	Contains protein domain (PF00327) - Ribosomal protein L30p/L7e	ribosomal prot	22278996, 264600, 264603, 35695917, 32833986, 35698423, 264636
163	11692306 (325, 326)		Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	interleukin	264112, 264532, 22279002
164	80077902 (327, 328)			UNCLASSIFIED	264639
165	10856067 (328, 330)			UNCLASSIFIED	264905, 264907, 264600
166	88095003 (331, 332)	Novel Protein sim. GBank gi 2661691 emb CAA15785 - (AL009204) putative protease [Streptomyces coelicolor]		UNCLASSIFIED	264681
167	16395460 (333, 334)	Novel Protein sim. GBank gi 4416478 gb AAD20378 - (AF125999) transposase [Mycobacterium avium]		UNCLASSIFIED	264605, 264486
168	80079362 (335, 336)	Novel Protein sim. GBank gi 76177 pir JQCECF - hypothetical 38.8K protein (ftsI 5' region) - Escherichia coli		UNCLASSIFIED	265010
169	80239581 (337, 338)				264600
					264556, 264557, 264558, 264559

170	78612384 (339, 340)	Novel Protein sim. GBank gij140888 sp P27847 YIGK_ECOLI - HYPOTHETICAL 15.4 KD PROTEIN IN RECQ-PLDB INTERGENIC REGION (F138)	Contains protein domain (PF01810) - LysE type translocator		284908 284595, 284604
171	85283073 (341, 342)				
172	37797007 (343, 344)	Novel Protein sim. GBank gij4210905 gb AAD12048.1 - (AF045609) AgtG [Sinorhizobium meliloti]	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	transport	284789
173	57528660 (345, 346)	Novel Protein sim. GBank gij132854 sp P02387 RL2_ECOLI - 50S RIBOSOMAL PROTEIN L2	Contains protein domain (PF00181) - Ribosomal Proteins L2	ribosomalprot	284769
174	95293078 (347, 348)	Novel Protein sim. GBank gij1881350 dbj BAA19377 - (AB001488) PROBABLE TRANSPORT PROTEIN, SIMILAR TO ANTIBIOTIC TRANSPORT-ASSOCIATED PROTEIN ACTII IN STREPTOMYCES COELICOLOR. [Bacillus subtilis]		transport	284510, 284593, 284602, 284603, 284605, 284782, 284693
175	79756270 (349, 350)	Novel Protein sim. GBank gij2072722 emb CAB08328 - (Z85121) manA [Mycobacterium tuberculosis]		isomerase	284565
176	80068898 (351, 352)	Novel Protein sim. GBank gij1055198 (U40187) - similar to PIR:A41724 chicken LD (limb deformity) gene product and to formin; also P-rich region similar to collagen [Caenorhabditis elegans]		UNCLASSIFIED	284907, 284910, 284881, 284558
177	86884852 (353, 354)	Novel Protein sim. GBank gij2328738 emb CAB10952 - (Z99288) hypothetical protein Rv1695 [Mycobacterium tuberculosis]	Contains protein domain (PF01513) - Domain of unknown function	UNCLASSIFIED	284788, 60424179, 284887, 284888, 284789, 29331828, 60432289, 18108376, 284889, 18108387, 32833886, 22278996, 265020, 284600, 284801, 284802, 284803, 284604, 284605, 284635, 284762, 284636, 284906, 284564, 284637, 284638, 284486, 60433358, 284788
178	78559526 (355, 356)	Novel Protein sim. GBank gij1906596 (U81788) - kinesin-73 [Drosophila melanogaster]		struc1	284693, 33857109, 284635
179	20263112 (357, 358)			UNCLASSIFIED	284583
180	80488958 (359, 360)	Novel Protein sim. GBank gij1169367 sp P45256 DNAB_HAEIN - REPLICATIVE DNA HELICASE		helicase	284789
181	78585369 (361, 362)	Novel Protein sim. GBank gij3170615 (AF059485) - DOCA [Mus musculus]		UNCLASSIFIED	21908767, 284635, 284638, 18108384
182	80577899 (363, 364)			UNCLASSIFIED	284259, 35896052, 58182435, 284511, 285018, 33857109, 284555, 284568
183	11614017 (365, 366)	Novel Protein sim. GBank gij1076627 pir S54172 - Inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco		UNCLASSIFIED	284680
184	10174167 (367, 368)	Novel Protein sim. GBank gij4371280 gb AAD18138 - (AC006260) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	284510

185	21660822 (369, 370)	Novel Protein sim. GBank gjl3008178[embjCAA18398.1] - (AL022304) putative mma transport regulator [Schizosaccharomyces pombe]		UNCLASSIFIED	264604	
186	80070328 (371, 372)	Novel Protein sim. GBank gjl2829802[sp P84408 YCLE_BACSU - HYPOTHETICAL 53.3 KD PROTEIN IN SFP-GERKA INTERGENIC REGION]		transport	264595	
187	80186611 (373, 374)					
188	20464942 (375, 376)	Novel Protein sim. GBank gjl3150260[embjCAA19179] - (AL023634) cyclin [Schizosaccharomyces pombe]		UNCLASSIFIED	264369	
189	82338215 (377, 378)	Novel Protein sim. GBank gjl2145853[ptrj S72938 - hIX protein - Mycobacterium leprae]		kinase	264605	
190	80086821 (379, 380)	Novel Protein sim. GBank gjl1881244[dbj BAA19271] - (AB001488) SIMILAR TO PYRUVATE OXIDASE AND ACETOLACTATE SYNTHASE. [Bacillus subtilis]		UNCLASSIFIED	35896052, 264602, 264605, 284762, 264689, 35895917, 18108370, 18108372, 264638, 264585	
191	88095012 (381, 382)	Novel Protein sim. GBank gjl120226[sp P28725 FKBP_STRCH - FK506-BINDING PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PIPIASE) (ROTAMASE)]	Contains protein domain (PF00205) - Thiamine pyrophosphate enzymes	synthase	264583	
192	16333379 (383, 384)		Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	isomerase	264508, 264604, 284605, 284769, 284555	
193	79910127 (385, 386)				264567	
194	20464949 (387, 388)				264808, 264693	
195	13518389 (389, 390)	Novel Protein sim. GBank gjl4980892[gb AAD35474.1 AE00171 - (AE001718) ABC transporter, ATP-binding protein [Thermotoga maritima]		transport	264605	
196	95005569 (391, 392)	Novel Protein sim. GBank gjl1705461[sp P53656 BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)]	Contains protein domain (PF00202) - gamma Amino transferases class-III pyridoxal phosphate		264600, 264689, 284638	
197	80248665 (393, 394)	Novel Protein sim. GBank gjl3122305[sp Q27778 K6PF_SCHMA - 6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE)]	Contains protein domain (PF00365) - kinase	kinase	264602, 264682, 284692, 18108374	
198	79163635 (395, 396)				264638	
199	78690715 (397, 398)	Novel Protein sim. GBank gjl1781203[embj CAB06110] - (Z83859) gnd [Mycobacterium tuberculosis]	Contains protein domain (PF00393) - 6-phosphogluconate dehydrogenases		265008	
200	79413849 (399, 400)	Novel Protein sim. GBank gjl2842222 (AF030885) - telomere-associated recQ-like helicase [Ustilago maydis]		UNCLASSIFIED	284595, 264588	
201	86945924 (401, 402)	Novel Protein sim. GBank gjl2894379[embj CAA74911.1] - (Y14573) ring finger protein [Hordeum vulgare]		UNCLASSIFIED	29331826, 265007, 264512, 33657402, 284598, 265017, 18108351, 264682, 264683, 284767, 284629, 55810784, 264634, 264635, 56182323, 60432113, 22279000	

202	79588048 (403, 404)	Novel Protein sim. GBank gi 231772 sp P30588 CHS1_USTMA - CHITIN SYNTHASE 1 (CHITIN-UDP ACETYL-GLUCOSAMINYL TRANSFERASE 1)	Contains protein domain (PF01644) - Chitin synthase	264600	
203	79843927 (405, 406)	Novel Protein sim. GBank gi 1504042 dbj BAA13220 - (D88984) similar to yeast adenylate cyclase (S58776) [Homo sapiens]		22278995, 29331822, 29331825, 29331827, 264806, 21908754, 264883, 21908788, 21906768, 35896423, 264558	
204	79855188 (407, 408)	Novel Protein sim. GBank gi 2833808 emb CAB13310 - (Z99111) similar to hypothetical proteins [Bacillus subtilis]	UNCLASSIFIED	264809	
205	10090583 (409, 410)	Novel Protein sim. GBank gi 2134381 pir S60678 - polybromo 1 protein - chicken	transport	264809	
206	8758473 (411, 412)	Novel Protein sim. GBank	UNCLASSIFIED	264604	
207	20754522 (413, 414)	Novel Protein sim. GBank gi 2134381 pir S60678 - polybromo 1 protein - chicken	UNCLASSIFIED	264556	
208	20289261 (415, 416)	Novel Protein sim. GBank		264605	
209	80071069 (417, 418)	Novel Protein sim. GBank gi 2501040 sp O05814 SYP_MYCTU - PROLYL-TRNA SYNTHETASE (PROLINE-TRNA LIGASE) (PRORS)		264605, 284689	
210	80168800 (419, 420)			264805, 284907, 284909, 284766, 284687, 264691, 284629, 18108374, 264638	
211	80034539 (421, 422)	Novel Protein sim. GBank		263978	
212	82442474 (423, 424)	Novel Protein sim. GBank gi 5031809 ref NP_005538.1 pISLR - immunoglobulin superfamily containing leucine-rich repeat	UNCLASSIFIED	264508, 264805, 264906, 264907, 284908, 264600, 284762, 284534, 264632, 264634, 284635, 284639, 264488	
213	80248562 (425, 426)	Novel Protein sim. GBank gi 3122358 sp O33123 LEU2_MYCLE - 3- ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI)	Contains protein domain (PF00330) - Aconitase family (aconitate hydratase)	22278998, 264508, 264600, 264602, 264603, 284605, 33857023, 264565, 264486	
214	80079381 (427, 428)	Novel Protein sim. GBank gi 116238 sp P19421 CH60_COXBU - 60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN) (HEAT SHOCK PROTEIN B)	Contains protein domain (PF00118) - TCP-1/cpn60 chaperonin family	284600, 284693	
215	14873283 (429, 430)	Novel Protein sim. GBank gi 3417287 (AC002310) - Unknown gene product [Homo sapiens]	UNCLASSIFIED	264628	
216	80177716 (431, 432)	Novel Protein sim. GBank	Contains protein domain (PF00096) - Zinc finger, C2H2 type	264448	
217	78603634 (433, 434)	Novel Protein sim. GBank gi 2506924 sp P49754 VP41_HUMAN - VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG (S53)		264508	
218	80258475 (435, 436)	Novel Protein sim. GBank gi 1173288 sp P38106 RSEA_ECOLI - SIGMA-E FACTOR NEGATIVE REGULATORY PROTEIN	mapolymerase	264594	
219	20438797 (437, 438)	Novel Protein sim. GBank gi 1781097 emb CAB06231 - (Z83864) gttB [Mycobacterium tuberculosis]	synthase	264604	
220	13499572 (439, 440)	Novel Protein sim. GBank gi 2884703 (AF052427) - unknown [Trypanosoma cruzi]	nucleaseinhib	264689	
221	11287498 (441, 442)	Novel Protein sim. GBank gi 4587313 dbj BAA76709.1 - (AB025248) alpha-1,2-mannosidase [Bacillus sp. M-90]	UNCLASSIFIED	264555	

222	79862802 (443, 444)	Novel Protein sim. GBank gij1877288[emb]CAB07049] - (Z92770) hypothetical protein Rv0143c [Mycobacterium tuberculosis]		UNCLASSIFIED	284605, 284769, 35896423
223	83053868 (445, 446)			UNCLASSIFIED	284906, 284807, 284603
224	79557920 (447, 448)				284684, 284693
225	79558541 (448, 450)	Novel Protein sim. GBank gij2274851[dbj]BAA21515] - (D64159) 3-7 gene product [Homo sapiens]		UNCLASSIFIED	284692
226	79172397 (451, 452)	Novel Protein sim. GBank gij868245 (U29488) - C56C10.7 gene product [Caenorhabditis elegans]		UNCLASSIFIED	22278998, 284112, 33657023, 263981
227	81777186 (453, 454)			UNCLASSIFIED	35685917, 284636, 284907
228	79872285 (455, 456)				284768, 284807, 284908, 284692, 284593, 284639
229	79838288 (457, 458)				284908, 284910
230	11013209 (459, 460)			UNCLASSIFIED	284631
231	20822207 (461, 462)	Novel Protein sim. GBank gij1835114[emb]CAA71733] - (Y10744) homoserine O-acetyltransferase [Leptospira meyeri]			284908, 284600, 284603, 284692
232	80055035 (463, 464)				
233	80063054 (465, 466)	Novel Protein sim. GBank gij2842340 (AF032970) - Imidazolone propionate hydrolase [Pseudomonas putida]	Contains protein domain (PF00449) - Urease	UNCLASSIFIED	284600, 284603, 284605, 284687, 284769
234	7523998 (467, 468)	Novel Protein sim. GBank gij3510505 (AF030881) - polypeptide [Fugu rubripes]		UNCLASSIFIED	284604
235	80203671 (469, 470)				284369
236	78940001 (471, 472)	Novel Protein sim. GBank gij2104608[emb]CAB08805] - (Z95388) PckA [Mycobacterium leprae]		UNCLASSIFIED	284106
237	11755273 (473, 474)			carboxylase	284905
238	78461401 (475, 476)				284681
239	82435190 (477, 478)	Novel Protein sim. GBank gij2495617[sp]Q57252[YDIJ_HAEN - HYPOTHETICAL PROTEIN HI1163]	Contains protein domain (PF00037) - 4Fe-4S ferredoxins and related iron-sulfur cluster binding domains.	UNCLASSIFIED	284639
240	21635575 (479, 480)	Novel Protein sim. GBank gij3183458[sp]P75788[YLIA_ECOLI - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YLIA]		transport	284906, 285010, 284603, 284762, 284682, 284638, 284838, 284486
241	80377307 (481, 482)	Novel Protein sim. GBank gij3875920[emb]CAB04111] - (Z81503) predicted using Genefinder; similar to collagen; cDNA EST EMBL:D65450 comes from this gene; cDNA EST EMBL:D68888 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	284259, 284769
242	82148454 (483, 484)				284908, 284909, 284764, 284639
243	79633207 (485, 486)			UNCLASSIFIED	
244	80248882 (487, 488)	Novel Protein sim. GBank gij2624302[emb]CAA15575] - (AL008967) ald [Mycobacterium tuberculosis]		UNCLASSIFIED	284489, 284907, 284908, 284511, 284760, 284764, 284692, 284635, 284637
245	79863543 (489, 490)	Novel Protein sim. GBank gij2920625 (AF044499) - vgrE protein [Escherichia coli]		UNCLASSIFIED	284908
246	79162829 (491, 492)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF01106) - NiR-like domain	dehydrogenase	284600, 284602, 284605, 284769, 284689
				UNCLASSIFIED	284907, 284758
					284637, 18108381, 18108387, 284565

247	78873185 (493, 494)	Novel Protein sim. GBank gi 1836006 emb CAB06648 - (Z85982) argB [Mycobacterium tuberculosis]		kinase	284809, 284691, 35696423, 18108387
248	80489883 (495, 496)	Novel Protein sim. GBank gi 168574 sp P42464 ATPB_CORGL - ATP SYNTHASE BETA CHAIN		synthase	35698286, 284907, 284511, 284802, 284788, 284688, 285021, 35695855, 18108385
249	78764845 (497, 498)			UNCLASSIFIED	284907, 284910, 285011, 284762, 284636
250	78818980 (499, 500)				21908768, 284692
251	84359489 (501, 502)			UNCLASSIFIED	52845158, 29331822, 29331824, 52644045, 265018, 21906785, 21906788, 285020, 27486261, 27486285, 35695763, 18108376, 284556, 284559, 284565
252	78737756 (503, 504)	Novel Protein sim. GBank gi 3327166 db BAA31651 - (AB014578) KIAA0878 protein [Homo sapiens]			284685, 284687, 284632
253	20443124 (505, 506)	Novel Protein sim. GBank gi 3036880 emb CAA18513 - (AL022374) putative ATP-dependent DNA helicase [Streptomyces coelicolor]		helicase	284604
254	80027421 (507, 508)	Novel Protein sim. GBank gi 3915488 sp P34422 YL31_CAEEL - HYPOTHETICAL SYMPORTER IN COTT-RAPA INTERGENIC REGION		UNCLASSIFIED	284508, 284808, 284602, 284687, 265021, 284488
255	11398315 (509, 510)	Novel Protein sim. GBank gi 1665720 db BAA04134 - (D17312) diarrheal toxin [Bacillus cereus]		UNCLASSIFIED	284593
256	80028158 (511, 512)	Novel Protein sim. GBank gi 465787 sp P34422 YL31_CAEEL - HYPOTHETICAL 86.0 KD PROTEIN F44B9.1 IN CHROMOSOME III	Contains protein domain (PF00326) - Prolyl oligopeptidase family	peptidase	284602, 284692
257	20289282 (513, 514)	Novel Protein sim. GBank gi 172039 sp P42315 SCOA_BACSU - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE SUBUNIT A (SUCCINYL COA:3-OXOACID COA-TRANSFERASE) (OXCT A)	Contains protein domain (PF01144) - Coenzyme A transferase	transferase	284605
258	20459464 (515, 516)	Novel Protein sim. GBank gi 3127836 emb CAA18902 - (AL023498) hypothetical protein [Streptomyces coelicolor]		UNCLASSIFIED	284604
259	78910152 (517, 518)			collagen	284681, 284688, 284692
260	20379437 (519, 520)			UNCLASSIFIED	284692, 284556
261	20285883 (521, 522)	Novel Protein sim. GBank gi 123761 sp P24221 HUTH_STRGR - HISTIDINE AMMONIA-LYASE (HISTIDASE)	Contains protein domain (PF00221) - Phenylalanine and histidine ammonia lyases	UNCLASSIFIED	284600
262	80189317 (523, 524)			UNCLASSIFIED	285017, 284369
263	88095045 (525, 526)	Novel Protein sim. GBank gi 3924708 emb CAA84646 - (Z35597) Weak similarity with sea squirt nidogen precursor protein (blastp score 71); cDNA EST EMBL: T02069 comes from this gene; cDNA EST EMBL: D76135 comes from this gene; cDNA EST EMBL: D73147 comes from this gene; cDNA EST EMB...		UNCLASSIFIED	284488, 284905, 284906, 284907, 284908, 284909, 284512, 284910, 284758, 284596, 284604, 265019, 284805, 284760, 18108351, 284763, 284764, 284288, 284788, 284789, 284769, 284691, 284692, 284693, 284628, 284634, 284635, 284555, 284636, 284638, 284639
264	87370826 (527, 528)	Novel Protein sim. GBank gi 3043734 db BAA25531 - (AB011177) KIAA0605 protein [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	protease	284259, 284808, 21806754, 265018, 265019, 265020

265	95355846 (528, 530)	Novel Protein sim. GBank gi 4589624 dbj BAA76834.1 - (AB023207) KIAA0980 protein [Homo sapiens]		kinase	264488, 35896286, 29331824, 56182181, 35898052, 264508, 264905, 264908, 264907, 66712502, 264808, 264809, 264511, 264512, 264910, 264592, 264595, 264758, 264598, 55811388, 264600, 265017, 264603, 264604, 264605, 264760, 18108351, 264762, 264681, 264764, 264288, 264766, 264768, 264769, 21908765, 21908767, 21908769, 265020, 264891, 33857023, 33857109, 33857182, 264828, 35898423, 35895855, 264630, 264631, 264632, 264634, 264635, 264636, 264555, 264638, 83373044, 56526488, 87168518, 264564, 264566, 264486
266	79588075 (531, 532)				264600
267	11362222 (533, 534)			UNCLASSIFIED	264828
268	79809568 (535, 536)			UNCLASSIFIED	264687, 264769, 264689
269	80025810 (537, 538)			UNCLASSIFIED	264802
270	84361144 (539, 540)	Novel Protein sim. GBank gi 4507367 ref NP_003182.1 pTARS - threonyl-tRNA synthetase		UNCLASSIFIED	264693
271	79552301 (541, 542)			UNCLASSIFIED	264909, 264693
272	8674778 (543, 544)	Novel Protein sim. GBank gi 4980738 gb AAD35331.1 AE00170 - (AE001707) glucose-1-phosphate adenylyltransferase [Thermotoga maritima]		synthase	264908
273	12840694 (545, 546)	Novel Protein sim. GBank gi 1168224 sp P44589 5NTD_HAEIN - PROBABLE 5'-NUCLEOTIDASE PRECURSOR		UNCLASSIFIED	264688
274	39524246 (547, 548)				264564
275	82787041 (549, 550)	Novel Protein sim. GBank gi 3253159 (AF005355) - [translation initiation factor eIF2C [Oryctolagus cuniculus]		UNCLASSIFIED	264807, 264908, 264909, 264766, 264768, 264691, 264632, 264636
276	86671073 (551, 552)	Novel Protein sim. GBank gi 134920 sp P21897 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)			265008, 60432229
277	80079735 (553, 554)	Novel Protein sim. GBank gi 129021 sp P20984 OBG_BACSU - SPOB-ASSOCIATED GTP-BINDING PROTEIN		ribosomalprot	264800, 18108387
278	12966947 (555, 556)			UNCLASSIFIED	264689
279	95292719 (557, 558)	Novel Protein sim. GBank gi 79839 pir J503812 - uvrB protein - Micrococcus luteus		nuclease	264508, 264604, 21908764, 264638, 264557, 264404
280	5603617 (559, 560)				264259
281	80249599 (561, 562)	Novel Protein sim. GBank gi 3123160 sp Q18984 YLN2_CAEEL - HYPOTHETICAL 48.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II			18108392, 264634, 264555, 264556, 264557, 264558
282	18598682 (563, 564)			UNCLASSIFIED	265019
283	20614211 (565, 566)			UNCLASSIFIED	264555

284	91212160 (567, 568)	Novel Protein sim. GBank gjl2429094 (U58632) - acetyl xylan esterase; AxeA [Thermotoga neapolitana]	Contains protein domain (PF00300) - Phosphoglycerate mutase family	UNCLASSIFIED	35696052, 29331828, 264508, 264905, 264600, 264602, 264682, 264764, 56181562, 21908764, 18108376, 264636, 264559, 18108387
285	8757940 (569, 570)			UNCLASSIFIED	264603
286	80503235 (571, 572)	Novel Protein sim. GBank gjl2072674[embjCAB08305] - (Z95120) rhIE [Mycobacterium tuberculosis]	Contains protein domain (PF00270) - ATPase associated DEAD/DEAH box helicase	UNCLASSIFIED	35696052, 264769, 264638
287	12745521 (573, 574)			UNCLASSIFIED	264689
288	20756502 (575, 576)	Novel Protein sim. GBank gjl765323[bsj157676 - (S74439) silk fibroin heavy chain (C-terminal)] [Bombyx mori-silkworms, Peptide Partial, 633 aa] [Bombyx mori]		collagen	264557
289	80043804 (577, 578)	Novel Protein sim. GBank gjl1870009[embjCAB06860] - (Z92539) hypothetical protein Rv1019 [Mycobacterium tuberculosis]	Contains protein domain (PF00440) - ribosomal protein L24 family		264593, 264800
290	80430175 (579, 580)			UNCLASSIFIED	264788
291	20747431 (581, 582)	Novel Protein sim. GBank gjl2506664[spjP40120]YDCG_ECOLI - 59.4 PROTEIN IN TRG-RIML INTERGENIC REGION PRECURSOR		UNCLASSIFIED	264601
292	80052555 (583, 584)	Novel Protein sim. GBank gjl625182 (L39015) - mitochondrial glutamyl-tRNA synthetase [Saccharomyces cerevisiae]		UNCLASSIFIED	264605
293	80062519 (585, 586)	Novel Protein sim. GBank gjl1718085[spjP5328]UVRD_MYCLE - PUTATIVE DNA HELICASE II HOMOLOG	helicase		264909, 264605, 264687, 264689, 264692
294	79830303 (587, 588)	Novel Protein sim. GBank gjl17422[spjP10040]CRB_DROME - CRUMBS PROTEIN PRECURSOR (95F)	Contains protein domain (PF00008) - EGF-like domain	oncogene	35696052, 264906, 265011, 264628, 55811576
295	79444180 (589, 590)	Novel Protein sim. GBank gjl1181619[dbjBAA11565] - (D82364) a variant of TSC-22 [Gallus gallus]			52844507, 29331822, 264592, 265020, 264639
296	79807076 (591, 592)	Novel Protein sim. GBank gjl3649789[dbjBAA33403] - (AB012226) SecA [Vibrio alginolyticus]		synthase	264508
297	79631297 (593, 594)	Novel Protein sim. GBank gjl5689967[embjCAB52004.1] - (AL109683) putative membrane protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	264905, 264687, 264638
298	80418688 (595, 596)			UNCLASSIFIED	264905, 264681, 264639, 264766

299	95283298 (597, 598)	Novel Protein sim. GBank gij220537[jbjBAA01477] - (D10827) zinc finger protein [Mus musculus]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	264488, 263994, 56994075, 22278997, 22278998, 22278999, 20281099, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264905, 264906, 264907, 264908, 52644045, 264909, 264511, 265006, 264910, 264585, 264586, 264758, 33657084, 87168559, 265018, 265019, 264764, 264288, 264766, 264687, 56181562, 264769, 21906765, 21906768, 21906769, 33657023, 264692, 33657109, 27486281, 18108370, 264628, 264629, 55811576, 35895855, 264631, 264634, 264635, 264636, 264639, 83373044, 18108387, 87168518, 22279000, 22279002, 264585, 264586, 264567
300	20711340 (598, 600)	Novel Protein sim. GBank gij145922 (M20981) - Iron dicitrate transport protein precursor [Escherichia coli]	UNCLASSIFIED	264602
301	13511332 (601, 602)	Novel Protein sim. GBank gij174661[spjP44594]TGT_HAEIN - QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)	transport	264687
302	9875260 (603, 604)	Novel Protein sim. GBank gij174661[spjP44594]TGT_HAEIN - QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)		264808
303	79574895 (605, 608)	Novel Protein sim. GBank gij67985[pirj]HJNVAV - helicase (EC 3.6.1.-) - Autographa californica nuclear polyhedrosis virus	helicase	264689
304	20711344 (607, 608)	Novel Protein sim. GBank gij67985[pirj]HJNVAV - helicase (EC 3.6.1.-) - Autographa californica nuclear polyhedrosis virus		264602
305	80412520 (608, 610)	Novel Protein sim. GBank gij728867[spjP40602]APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR		264763
306	8515876 (611, 612)	Novel Protein sim. GBank gij1657554[gbjAAB18082.1] - (U73857) hypothetical protein [Escherichia coli]	UNCLASSIFIED	263978
307	80222801 (613, 614)	Novel Protein sim. GBank gij728867[spjP40602]APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR	UNCLASSIFIED	265010, 21906768, 265020, 18108374, 263977
308	80084305 (615, 616)	Novel Protein sim. GBank gij1710612[spjQ10793]RNH2_MYCTU - PROBABLE RIBONUCLEASE HII (RNASE HII)	Contains protein domain (PF01351) - Ribonuclease HII	264910, 264600, 264605, 264687, 264689, 264636, 18108387
309	80504138 (617, 618)	Novel Protein sim. GBank gij5420387[embjCAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		264769
310	80053616 (619, 620)	Novel Protein sim. GBank gij1144522 (U34957) - phosphoribosylaminimidazolesuccinocarboxamide synthase [Mycobacterium tuberculosis]	synthase	264603
311	11090659 (621, 622)	Novel Protein sim. GBank gij1144522 (U34957) - phosphoribosylaminimidazolesuccinocarboxamide synthase [Mycobacterium tuberculosis]		264602
312	80054347 (623, 624)	Novel Protein sim. GBank gij1144522 (U34957) - phosphoribosylaminimidazolesuccinocarboxamide synthase [Mycobacterium tuberculosis]	UNCLASSIFIED	264586
313	80046168 (625, 626)	Novel Protein sim. GBank gij1144522 (U34957) - phosphoribosylaminimidazolesuccinocarboxamide synthase [Mycobacterium tuberculosis]		264603, 264567

314	87645112 (627, 628)	Novel Protein sim. GBank gi 3861583 (AF092175) - Ikaros [Danto ref10]	Contains protein domain (PF00320) - GATA zinc finger	dna_ma_bind	284259, 60432289, 29331828, 284905, 284908, 284908, 284908, 284910, 60432229, 33657402, 60433438, 33109854, 265011, 265017, 284603, 285018, 284288, 284766, 284692, 35695763, 284828, 284628, 284639, 60170394, 22279002, 284568
315	82358091 (629, 630)	Novel Protein sim. GBank gi 1652620 dbj BAA17540 (D90907) pyridine nucleotide transhydrogenase beta subunit [Synecchocystis sp.]			284508, 284600, 264762, 284687, 284768, 52644229, 284769, 284889, 284835, 284636, 284638, 284488
316	79911071 (631, 632)	Novel Protein sim. GBank		UNCLASSIFIED	284693
317	20466944 (633, 634)	gi 118244 sp P24178 DAPE_ECOLI - SUCCINYL-DIAMINOPIMELATE DESUCCINYLASE (SDAP)		UNCLASSIFIED	284605
318	94141836 (635, 636)	Novel Protein sim. GBank gi 4680228 gb AAD27583.1 AF11827 - (AF118274) DNB-5 [Homo sapiens]	Contains protein domain (PF00528) - Dictyostellium (slime mold) repeats	transport	284908, 284909, 284910, 284593, 284594, 284760, 284288, 284768, 284789, 21908769, 284691, 284693, 284628, 65274791, 284635, 284638, 284638, 83373044, 22279002, 284586
319	17289360 (637, 638)	Novel Protein sim. GBank gi 1149693 emb CAA80220 - (X88499) rbsC [Clostridium perfringens]		transport	265018
320	13527675 (639, 640)	Novel Protein sim. GBank gi 2811033 sp O05314 GLGC_MYCTU - GLUCOSE-1-PHOSPHATE ADENYL-TRANSFERASE (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE)		synthase	264687
321	94134387 (641, 642)	Novel Protein sim. GBank gi 1680716 (U68234) - all-trans-retinoic acid 4-hydroxylase [Danto ref10]		cyto450	284509, 284908, 284907, 284908, 285009, 284596, 284784, 284628, 284634, 284635, 284638, 284639, 83373044, 284587
322	68489053 (643, 644)	Novel Protein sim. GBank gi 1160355 (U33058) - UNC-89 [Caenorhabditis elegans]		UNCLASSIFIED	55811150, 284691, 60431528, 55810764
323	94653725 (645, 646)			UNCLASSIFIED	264488, 265009, 264593, 264628, 284635
324	79174383 (647, 648)				284687
325	79862691 (649, 650)			UNCLASSIFIED	284693
326	28774974 (651, 652)			UNCLASSIFIED	284288, 18108385
327	79776267 (653, 654)	Novel Protein sim. GBank gi 451544 (U04267) - proline-rich cell wall protein [Gossypium barbadense]			284488, 284805, 264509, 264910
328	80253202 (655, 656)			UNCLASSIFIED	264592
329	10173821 (657, 658)			UNCLASSIFIED	284510
330	86597767 (659, 660)	Novel Protein sim. GBank gi 4191358 (AF087825) - claudin-7 [Mus musculus]		UNCLASSIFIED	284259, 284908
331	79754888 (661, 662)	Novel Protein sim. GBank gi 80741 pir IS20912 - regulatory protein whiB - Streptomyces coelicolor		transcriptfactor	264910, 284687, 264689, 284636, 284567
332	80071440 (663, 664)	Novel Protein sim. GBank gi 14049 sp P19480 AHPF_SALTY - ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT F (ALKYL HYDROPEROXIDE REDUCTASE F52A PROTEIN)		reductase	35698423, 284636, 284638, 284565
333	13009555 (665, 666)				284687

334	80230771 (667, 668)	Novel Protein sim. GBank glj3222228[pil][S32227 - glutamate dehydrogenase (NADP+)] (EC 1.4.1.4) - Corynebacterium glutamicum	Contains protein domain (PF00208) - Glutamate/Leucine/Phenylalanine/Va line dehydrogenase	dehydrogenase	264905, 264600, 264604, 264486
335	80057026 (669, 670)	Novel Protein sim. GBank glj2193938[emb][CAB09602] - (Z96800) glpQ2 [Mycobacterium tuberculosis]		esterase	264907, 264603, 264693, 18108374, 264636, 18108387
336	80414319 (671, 672)			UNCLASSIFIED	265009, 264766, 264686
337	11090829 (673, 674)				264602
338	95413134 (675, 676)	Novel Protein sim. GBank glj5454074[ref][NP_008303.1]pSMRT - silencing mediator for retinoid and thyroid hormone receptors	Contains protein domain (PF00249) - Myb-like DNA-binding domain	nuc_recp	264569, 18108397, 22278998, 29331822, 20281099, 29331824, 56182181, 66714117, 29331825, 35896052, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 265006, 265008, 264910, 265009, 264758, 55812038, 65274444, 265011, 87168559, 265017, 265018, 265019, 264760, 55811150, 284681, 284762, 18108351, 264682, 264764, 264766, 264685, 264686, 264768, 52844229, 264689, 55811957, 35895917, 264692, 264693, 264628, 18108370, 18108374, 55811576, 35698423, 35695855, 264635, 264555, 264636, 264556, 264637, 264557, 18106380, 264638, 264558, 264639, 18106381, 83373044, 18108385, 87168516, 60432113
339	11398513 (677, 678)	Novel Protein sim. GBank glj4001713[dbj][BAA35087.1] - (AB015879) DnaK [Porphyromonas gingivalis]		eph	264593
340	80504149 (679, 680)	Novel Protein sim. GBank glj2842699[sp]Q92353[UBPC_SCHPO - PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C6G9.08 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME)]		ubiquitin	264905, 265019, 264769, 18108374
341	11075198 (681, 682)	Novel Protein sim. GBank glj2688580 (AE001166) - conserved hypothetical protein [Borrelia burgdorferi]	Contains protein domain (PF00290) - Tryptophan synthase alpha chain	isomerase	264605
342	80054198 (683, 684)	Novel Protein sim. GBank glj1684738[emb][CAA70601] - (Y09452) Yed J hypothetical protein [Pseudomonas syringae]			264603, 264604
343	20466782 (685, 686)				264605
344	80428870 (687, 688)	Novel Protein sim. GBank glj2117275[emb][CAB09104] - (Z85618) hypothetical protein Rv0807 [Mycobacterium tuberculosis]		UNCLASSIFIED	264600, 264605, 264766, 18108370, 18108374, 35895855
345	80258853 (689, 690)	Novel Protein sim. GBank glj3023317[sp]Q48935[APHA_MYCRA - ACETYL POLYAMINE AMINOHYDROLASE]		histone	264593
346	79831058 (691, 692)	Novel Protein sim. GBank glj4239787[emb][CAA75437] - (Y15166) NADP-glutamate dehydrogenase [Pseudomonas aeruginosa]	Contains protein domain (PF00208) - Glutamate/Leucine/Phenylalanine/Va line dehydrogenase	dehydrogenase	264905

347	78158195 (693, 694)	Novel Protein sim. GBank gi 731675 sp P38795 YH4_YEAST - HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION		UNCLASSIFIED	265006, 265008, 265010, 265018, 263967, 263981
348	80020208 (695, 696)	Novel Protein sim. GBank gi 1073610 pir IS47672 - ugpB protein - Escherichia coli		transport	264602, 18108351, 18108387
349	17282112 (697, 698)				265007
350	80502370 (699, 700)	Novel Protein sim. GBank gi 3261598 emb CAB00917 - (Z77137) hypothetical protein Rv1277 [Mycobacterium tuberculosis]		nuclease	265009, 264769, 264689, 18108370
351	80501805 (701, 702)	Novel Protein sim. GBank gi 2959367 emb CAA17821 - (AL022117) hypothetical protein [Schizosaccharomyces pombe]		glycoprotein	264769, 264805, 264808
352	11611585 (703, 704)	Novel Protein sim. GBank gi 4416302 gb AAD20307 - (AF105716) copia-type pol polyprotein [Zea mays]		protease	264595
353	80061653 (705, 706)	Novel Protein sim. GBank gi 1174887 sp P42873 URE1_STAXY - UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE)	Contains protein domain (PF00449) - Urease	UNCLASSIFIED	264604
354	56626130 (707, 708)			UNCLASSIFIED	264628
355	80046344 (709, 710)			UNCLASSIFIED	264808, 264595, 264683, 22279002
356	80043835 (711, 712)	Novel Protein sim. GBank gi 115157 sp P16574 BVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA	Contains protein domain (PF00072) - Response regulator receiver domain	transcriptfactor	264809, 264591, 264592
357	80070568 (713, 714)	Novel Protein sim. GBank gi 497637 (J03939) - cytochrome oxidase d subunit I [Escherichia coli]		oxidase	264605
358	37032756 (715, 716)	Novel Protein sim. GBank gi 2290990 (AF006000) - Brg1 [Bordetella pertussis]		UNCLASSIFIED	264768
359	80501488 (717, 718)			UNCLASSIFIED	264604, 264769
360	80026748 (719, 720)			UNCLASSIFIED	264594
361	80584075 (721, 722)	Novel Protein sim. GBank gi 3510639 (AF049344) - UDP- GalNAc:polypeptide N-acetylglucosaminyltransferase T5 [Rattus norvegicus]		transferase	22278996, 284259, 29331822, 293331824, 264605, 55811957, 285022
362	13089485 (723, 724)	Novel Protein sim. GBank gi 113764 sp P25718 AMY1_ECOLI - ALPHA-AMYLASE PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)		amylase	264688
363	79750145 (725, 726)				264568
364	82443593 (727, 728)	Novel Protein sim. GBank gi 2829816 sp P85171 NUOK_MYCTU - NADH DEHYDROGENASE I CHAIN K (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 11) (NUO11)	Contains protein domain (PF00420) - NADH-ubiquinone/plastoquinone oxidoreductase chain 4L	dehydrogenase	264769, 264602, 284604, 284508, 264762, 264638, 264486

365	88040288 (728, 730)	Novel Protein sim. GBank gij4929268 gb AAD33924.1 - (AF144237) LOMP protein [Homo sapiens]	Contains protein domain (PF00412) - LIM domain containing proteins	264488, 21908768, 21908767, 55811576, 21908769, 29148829, 22278995, 22278996, 265020, 265022, 264634, 284691, 284593, 33657023, 33657402, 264693, 264639, 264594, 29331824, 264758, 18108385, 29331827, 87168559, 265018, 22279000, 265019, 284482, 264761, 264681, 18108351, 265017, 284757
366	81821838 (731, 732)			
367	85357471 (733, 734)	Novel Protein sim. GBank gij4503843 ref NP_003908.1 pG2AD - UNKNOWN	Contains protein domain (PF01602) - Adaptin N terminal region	60424178, 65274572, 56182575, 22278994, 56994075, 22278998, 264259, 29331822, 29331824, 56182181, 60424269, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 284905, 264828, 56182435, 265008, 264512, 265008, 264591, 55812038, 55811388, 265010, 87168559, 265017, 265018, 284604, 265019, 55811150, 264448, 264369, 264288, 264688, 264768, 56181562, 21908768, 21908769, 55811957, 35695917, 265022, 60170815, 33657023, 65274620, 18108365, 263967, 33657109, 33657349, 35695763, 264628, 18108376, 55811576, 65274791, 35695855, 56182323, 63373044, 60432113, 264563, 264584, 264587, 284509
368	79607265 (735, 736)			
369	95292917 (737, 738)	Novel Protein sim. GBank gij3913029 sp P94967 ALR_MYCSM - ALANINE RACEMASE	UNCLASSIFIED	284508, 284604, 284605, 284636
370	89090866 (739, 740)	Novel Protein sim. GBank gij3249559 (AF018261) - EH domain binding protein Epsin [Rattus norvegicus]		284905, 284592, 284605, 284766, 284691
371	95292599 (741, 742)	Novel Protein sim. GBank gij2995299 emb CAA16328 - (AL022268) putative tRNA delta(2)-isopenielypyrophosphate transferase [Streptomyces coelicolor]	Contains protein domain (PF01715) - IPP transferase	284905, 284908, 284510, 284600, 284601, 284602, 284603, 285018, 284604, 284605, 265021, 284692, 264636, 284564
372	80021107 (743, 744)	Novel Protein sim. GBank gij2506393 sp P31576 FXX_ECOLI - FERREDOXIN LIKE PROTEIN		264564
373	79863786 (745, 746)		UNCLASSIFIED	264909
374	79847568 (747, 748)	Novel Protein sim. GBank gij3341840 emb CAA13164 - (AJ231122) z811 [Vibrio cholerae]	UNCLASSIFIED	264905, 284906
375	91230181 (749, 750)	Novel Protein sim. GBank gij5456934 gb AAD43716.1 - (AF152322) protocadherin gamma A2 [Homo sapiens]	cadherin	65274572, 264259, 29331828, 56182435, 60433356, 60433438, 284757, 55812038, 284758, 55811957, 264690, 33657023
376	80505214 (751, 752)	Novel Protein sim. GBank gij1805408 dbj BAA08970 - (D50453) homologues to nitrile hydratase region 3'-hypothetical protein P47K of P. chlororaptis [Bacillus subtilis]	UNCLASSIFIED	284769
377	10339083 (753, 754)			284906

378	80056153 (755, 756)	Novel Protein sim. GBank gij1076013 pir A49930 - carb protein homolog - Mycobacterium bovis (strain BCG) (fragment)	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)	UNCLASSIFIED	265008, 264555
379	80503437 (757, 758)			synthase	264789
380	80060937 (759, 760)	Novel Protein sim. GBank gij216556 dbj BAA02174 - (D12651) glucose dehydrogenase [Escherichia coli]	Contains protein domain (PF01011) - PQQ enzyme repeat	dehydrogenase	264604
381	11769027 (761, 762)			UNCLASSIFIED	264684
382	80054377 (763, 764)				264592
383	83259025 (765, 766)	Novel Protein sim. GBank gij3327136 dbj BAA31636 - (AB014561) KIAA0861 protein [Homo sapiens]			264595, 265017, 265021, 264638, 87188518, 22279002
384	95314255 (767, 768)			UNCLASSIFIED	264259, 29331822, 60432289, 29331827, 264286, 264766, 263967, 65274791, 35695855, 263981, 83373044, 264567
385	10237678 (769, 770)				264692
386	78633434 (771, 772)	Novel Protein sim. GBank gij1073456 pir S47810 - probable alcohol dehydrogenase (EC 1.1.1.1) - Escherichia coli	Contains protein domain (PF00465) - Iron-containing alcohol dehydrogenases	dehydrogenase	264906
387	17660637 (773, 774)	Novel Protein sim. GBank gij1460074 emb CAB01049 - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis]	Contains protein domain (PF01841) - Transglutaminase-like superfamily	UNCLASSIFIED	264760
388	87741376 (775, 776)	Novel Protein sim. GBank gij4240169 dbj BAA74863.1 - (AB020847) KIAA0840 protein [Homo sapiens]	Contains protein domain (PF00846) - F-box domain.	homeobox	35696286, 264805, 66712502, 60432229, 264593, 60433356, 264688, 264688, 21906765, 264891, 22279000, 264482
389	79316971 (777, 778)			UNCLASSIFIED	18108394, 22278996, 264630, 264556, 22279002
390	80079949 (779, 780)			UNCLASSIFIED	264600
391	7657302 (781, 782)	Novel Protein sim. GBank gij854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]			264482
392	79786056 (783, 784)			UNCLASSIFIED	264908
393	33206031 (785, 786)	Novel Protein sim. GBank gij3378523 emb CAA08867 - (AJ009832) cyclomaltodextrinase glucanotransferase [Thermotoga neapolitana]		synthase	264802, 21906764
394	10104463 (787, 788)				264693
395	80228010 (789, 790)			UNCLASSIFIED	264508, 264563
396	20436224 (791, 792)	Novel Protein sim. GBank gij2677780 (U70327) - unknown [Paretioplus polyactis]	Contains protein domain (PF00047) - Immunoglobulin domain	struct	264556
397	80417014 (793, 794)	Novel Protein sim. GBank gij4507909 ref NP_000388.1 pWAS - Wiskott-Aldrich syndrome (eczema-thrombocytopenia)			265007, 265009, 264508, 264556, 264629, 264766
398	91230517 (795, 796)	Novel Protein sim. GBank gij1518458 (U45998) - mitochondrial solute carrier [Onchocerca volvulus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	18108398, 22278995, 22278996, 56994075, 22278999, 264259, 29331824, 29331826, 264905, 264908, 265007, 265008, 265009, 21906754, 33657084, 265017, 264448, 264288, 264766, 21906765, 21908766, 21908767, 265020, 265021, 33657023, 33657109, 264628, 35896423, 35895855, 264952, 18108380, 264567, 18108391

399	60055278 (797, 798)	Novel Protein sim. GBank gi 3358091 dbj BAA31995 - (AB015974) glycerol kinase [Pseudomonas tolaasii]	Contains protein domain (PF00370) - FGYY family of carbohydrate kinases	kinase	264592, 264595
400	94117490 (799, 800)	Novel Protein sim. GBank gi 728835 sp P39192 ALU5_HUMAN - IIII ALU SUBFAMILY SC WARNING ENTRY IIII	Contains protein domain (PF00560) - Leucine Rich Repeat	cadherin	18108394, 56182575, 22278995, 22278997, 22278998, 264259, 29331824, 265006, 265007, 265009, 60432229, 33657402, 21906754, 265010, 265017, 265018, 265019, 18108351, 18108357, 21906765, 265021, 265022, 264691, 264692, 33657023, 18108370, 65274791, 264634, 264636, 60170394, 56182323
401	11397491 (801, 802)	Novel Protein sim. GBank gi 4828292 gb AAD33527.1 AF13211 - (AF132117) FhuA [Staphylococcus aureus]		transport	264594
402	95420284 (803, 804)	Novel Protein sim. GBank gi 5689487 dbj BAA83027.1 - (AB028998) KIAA1075 protein [Homo sapiens]	Contains protein domain (PF00017) - Src homology domain 2	phosphatase	65274572, 56182575, 35696286, 22278996, 22278998, 264093, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264906, 264907, 264909, 265006, 264511, 265007, 265008, 264910, 264591, 33657402, 60433356, 60433438, 264598, 21906754, 52644298, 265010, 265011, 87168559, 265017, 265018, 265019, 264681, 18108351, 264682, 264448, 264288, 264684, 264766, 264767, 264688, 21906765, 21906766, 21908767, 21908768, 21906769, 55811957, 265020, 265021, 265022, 264690, 264693, 65274620, 35695783, 264628, 18108370, 264629, 18108379, 35698423, 55811578, 264635, 264636, 264557, 264639, 18108385, 22279002, 264563, 264564, 264565, 264566, 264768, 264632, 264639, 264563
403	80439913 (805, 806)			UNCLASSIFIED	264682
404	11809885 (807, 808)			polymerase	265009, 264682
405	79471280 (809, 810)	Novel Protein sim. GBank gi 2661649 amb CAA15755 - (AL009198) dnaE2 [Mycobacterium tuberculosis]			
406	79634172 (811, 812)		Contains protein domain (PF00159) - Pancreatic hormone peptides	UNCLASSIFIED	18108357, 264693
407	80478229 (813, 814)				
408	80079958 (815, 816)			UNCLASSIFIED	264769
409	5840527 (817, 818)	Novel Protein sim. GBank gi 3047117 (AF058918) - similar to ATP-dependent RNA helicases [Arabidopsis thaliana]		UNCLASSIFIED	264600
				helicase	264259

410	95357496 (819, 820)	Novel Protein sim. GBank gi 475016 dbj BAA06184 - (D29801) Unknown [Mus musculus]		UNCLASSIFIED	264489, 52846365, 52846842, 56181686, 35892286, 52845080, 29331822, 29331824, 56182181, 29331825, 60424289, 35896052, 33658970, 264508, 264509, 284905, 284908, 264907, 284908, 52844045, 284909, 284510, 285007, 284512, 285008, 284910, 33657402, 284758, 52846317, 55811388, 285010, 265011, 285017, 284604, 285018, 55811150, 284762, 284764, 284768, 284887, 284768, 284769, 52844229, 21906768, 285020, 285021, 284534, 52844150, 284692, 33857023, 65274620, 33857109, 33857182, 27488261, 35895763, 284828, 284829, 60431528, 18108376, 283978, 35898423, 35895855, 284632, 284634, 284635, 284637, 284638, 284558, 284839, 58182323, 284559, 60432113, 22279002, 284583, 284585, 284486
411	80501870 (821, 822)			UNCLASSIFIED	284769
412	80241662 (823, 824)				284907, 284910, 283973, 22279002
413	11076446 (825, 826)	Novel Protein sim. GBank gi 3261784 emb CAB08997 - (Z95558) htpX [Mycobacterium tuberculosis]		eph	284605
414	82050554 (827, 828)	Novel Protein sim. GBank gi 129038 sp P20707 ODO1_AZOV1 - 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (ALPHA-KETOGLUTARATE DEHYDROGENASE)		dehydrogenase	18108374, 264760, 284769, 284602, 284638, 284603, 284909, 284605
415	84453144 (829, 830)	Novel Protein sim. GBank gi 4888350 gb AAD31273.1 AF13202 - (AF132025) rhophilin [Drosophila melanogaster]		UNCLASSIFIED	264908, 87168518
416	80402775 (831, 832)	Novel Protein sim. GBank gi 2555172 (AF025543) - ArcC; carbamate kinase [Rhizobium etli]		kinase	284488, 284600, 284602, 284764, 284638
417	20153797 (833, 834)	Novel Protein sim. GBank gi 1709171 sp P52311 MTX2_XANOR - MODIFICATION METHYLASE XORII (CYTOSINE-SPECIFIC METHYLTRANSFERASE XORII) [M.XORII]	Contains protein domain (PF00145) - C-5 cytosine-specific DNA methylase		284605
418	84125841 (835, 836)			UNCLASSIFIED	284889, 284693
419	95314273 (837, 838)			collagen	284908, 284910, 264764, 284639
420	37036349 (839, 840)	Novel Protein sim. GBank gi 3261859 emb CAB03751 - (Z81388) hypothetical protein Rv2419c [Mycobacterium tuberculosis]	Contains protein domain (PF00300) - Phosphoglycerate mutase family	phosphatase	284769
421	95292942 (841, 842)	Novel Protein sim. GBank gi 2916942 emb CAA17580 - (AL021999) hypothetical protein Rv0981 [Mycobacterium tuberculosis]	Contains protein domain (PF00072) - Response regulator receiver domain	phosphatase	284908, 284600, 284801, 284603, 284604, 284760, 284769
422	79471293 (843, 844)	Novel Protein sim. GBank gi 231752 sp Q00767 CH81_STRAL - 80 KD CHAPERONIN 1 (PROTEIN CPN60 1) (HSP58)	Contains protein domain (PF00118) - TCP-1/cpn80 chaperonin family	eph	22278996, 284682, 18108376, 18108387
423	79604948 (845, 846)			UNCLASSIFIED	284509

424	78986557 (847, 848)	Novel Protein sim. GBank gi 4826814 ref NP_004977.1 pKTN1 - kinesin 1 (kinesin receptor)		strud	265019	
425	80431450 (848, 850)	Novel Protein sim. GBank gi 1703701 bbs 178462 - KRP5=kinesin-related protein [rats, testes, Peptide Partial, 167 aa]	Contains protein domain (PF00225) - Kinesin motor domain	strud	264909, 265007, 55811386, 264768, 55810764	
426	80064522 (851, 852)				264605, 264559	
427	80057232 (853, 854)	Novel Protein sim. GBank gi 231829 sp P29929 COBN_PSEDE - COBN PROTEIN		UNCLASSIFIED	264603, 264636	
428	79487798 (855, 856)			UNCLASSIFIED	264683	
429	80091252 (857, 858)	Novel Protein sim. GBank gi 81286 p S222697 - extensin - Volvox carterii (fragment)		UNCLASSIFIED	35698423, 35695763, 35695855, 265017, 264584, 264762	
430	80504192 (859, 860)	Novel Protein sim. GBank gi 1806154 emb CAB06451 - (Z84395) hypothetical protein Rv0688 [Mycobacterium tuberculosis]	reductase		264508, 264905, 264509, 264908, 264808, 265008, 264600, 264687, 264769, 264689, 264636, 264638, 18108385, 264486	
431	20624249 (861, 862)				264566	
432	16525372 (863, 864)				265020	
433	81494303 (865, 866)	Novel Protein sim. GBank gi 3123552 emb CAA18608 - (AL022578) dJ393P12.2 (hypothetical Proline-rich protein KIAA0269 LIKE) [Homo sapiens]		UNCLASSIFIED	264807, 264908, 264909, 264910, 264592, 264595, 264758, 264604, 264760, 264762, 264763, 264636, 264637, 22279002	
434	94326323 (867, 868)	Novel Protein sim. GBank gi 2495272 sp Q89826 CDX2_HUMAN - HOMEBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEBOX PROTEIN 2) (CDX-3)	Contains protein domain (PF00169) - PH domain	UNCLASSIFIED	55812038, 56182181, 56181562, 29331828, 35696052, 55810764, 55811576, 65274791, 35695855, 60432113, 55811150, 264636, 264766	
435	80502738 (869, 870)	Novel Protein sim. GBank gi 114105 sp P08532 ARAH_ECOLI - L-ARABINOSE TRANSPORT SYSTEM PERMEASE PROTEIN ARAH	transport		264595, 264769	
436	41085953 (871, 872)			UNCLASSIFIED	265020, 22279002	
437	11399291 (873, 874)			UNCLASSIFIED	264593	
438	11773835 (875, 876)			UNCLASSIFIED	264686	
439	80019495 (877, 878)	Novel Protein sim. GBank gi 3242702 (AC003040) - hypothetical protein [Arabidopsis thaliana]			264905, 264600, 264602, 264604	
440	79841062 (879, 880)	Novel Protein sim. GBank gi 2291232 gb AA085351.1 - (AF016427) Contains similarity to Pfam domain: PF00004 (AAA). Score=268.1, E-value=3.7e-77, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00004) - ATPases associated with various cellular activities (AAA)		35696052, 264905, 264908, 264909, 265011, 35696423	
441	20386935 (881, 882)	Novel Protein sim. GBank gi 5639946 gb AAD45904.1 AF16132 - (AF161328) histidine kinase CstS [Corynebacterium diphtheriae]			264605	
442	85281058 (883, 884)	Novel Protein sim. GBank gi 1184790 (U46068) - von Ebner minor salivary gland protein [Mus musculus]		UNCLASSIFIED	29331830, 264909	
443	82456427 (885, 886)	Novel Protein sim. GBank gi 5689893 emb CAB52056.1 - (AL109732) putative ATP-binding RNA helicase [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	35696052, 264508, 264906, 264512, 264604, 264762, 264769, 264689, 264636	
444	11395897 (887, 888)	Novel Protein sim. GBank gi 1783249 dbj BAA11726 - (D83026) homologous to citrate-sodium symport (citrate transporters); hypothetical [Bacillus subtilis]		UNCLASSIFIED	264591	

445	79552709 (889, 890)	Novel Protein sim. GBank gjl5531272[embjCAB50897.1] - (AJ243800) WSC4 homologue [Kluyveromyces fragilis]			UNCLASSIFIED	264693
446	79810937 (891, 892)	Novel Protein sim. GBank gjl538413 (L36315) - zinc finger protein [Mus musculus]	Contains protein domain (PF00098) - Zinc finger, C2H2 type			264509
447	80438888 (893, 894)	Novel Protein sim. GBank gjl1542914[embjCAB02185] - (Z80108) fmi [Mycobacterium tuberculosis]	Contains protein domain (PF00551) - Formyl transferase		transcript factor	264768, 55811576
448	80238110 (895, 896)	Novel Protein sim. GBank gjl18794[spjP10443]DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN			dehydrogenase	264508, 264600, 264603, 264605, 264682, 264768, 18108362, 264634, 18108387
449	20460634 (897, 898)	Novel Protein sim. GBank gjl18794[spjP10443]DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN			polymerase	264605, 264559
450	94631210 (899, 900)	Novel Protein sim. GBank gjl4589508[dbjBAA76775.1] - (AB023148) KIAA0931 protein [Homo sapiens]	Contains protein domain (PF00481) - Protein phosphatase 2C		phosphatase	65274572, 22278988, 29331824, 29331826, 284906, 284910, 284592, 52848317, 285017, 21906787, 55811957, 56526488, 22279002
451	21433609 (901, 902)				UNCLASSIFIED	264486
452	10267278 (903, 904)					264692
453	52560098 (905, 906)	Novel Protein sim. GBank gjl2650814 (AE001104) - conserved hypothetical protein [Archaeoglobus fulgidus]			UNCLASSIFIED	264907, 264600
454	39523922 (907, 908)	Novel Protein sim. GBank gjl2493000[spjQ09450]SCOT_CAEEL - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (3-OXOACID COA-TRANSFERASE)			transferase	264603
455	13089692 (909, 910)					
456	79563081 (911, 912)				UNCLASSIFIED	264687
457	79831273 (913, 914)	Novel Protein sim. GBank gjl446868[embjCAB38153.1] - (AL035591) putative integral membrane export protein [Streptomyces coelicolor]			UNCLASSIFIED	264691
458	79561227 (915, 916)	Novel Protein sim. GBank gjl3411053 (AF034863) - synaptic scaffolding molecule [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)		kinase	55812038, 265010, 265018, 264681
459	80567359 (917, 918)	Novel Protein sim. GBank gjl4506075[ref]NP_002733.1[pPRKC - protein kinase C, mu]	Contains protein domain (PF00130) - Phorbol esters/diacylglycerol binding domain (C1 domain)		kinase	22278997, 264259, 29331826, 265018, 264448, 284369, 21908785, 35698423
460	79245880 (919, 920)	Novel Protein sim. GBank gjl113158[spjP25516]ACO1_ECOLI - ACONITATE HYDRATASE 1 (CITRATE HYDRO-LYASE 1) (ACONITASE 1)			UNCLASSIFIED	264806
461	95267618 (921, 922)	Novel Protein sim. GBank gjl1168574[spjP42464]ATPB_CORGL - ATP SYNTHASE BETA CHAIN			synthase	264602, 264605, 264768, 284769, 265021, 33857023, 284559

462	78606589 (923, 924)	Novel Protein sim. GBank gil1348891 sp P45597 PTF1_XANCP - MULTIPHOSPHORYL TRANSFER PROTEIN (MTP) (CONTAINS: PHOSPHOENOLPYRUVATE-PROTEIN PHOSPHOTRANSFERASE (PHOSPHOTRANSFERASE SYSTEM, ENZYME I); PHOSPHOCARRIER PROTEIN HPR (PROTEIN H); PTS SYSTEM, FRUCTOSE-SPECIFIC IIA COMPONENT ...	Contains protein domain (PF00391) - PEP-utilizing enzymes	UNCLASSIFIED	284807
463	79786417 (925, 926)	Novel Protein sim. GBank gil854065 emb CAA58337 - (X83413) U88 (Human herpesvirus 6)		UNCLASSIFIED	284805, 284806, 284808, 284809, 284910, 284591, 284595, 285011, 284832, 284835, 284836, 284837, 284838, 284839
464	82340151 (927, 928)			UNCLASSIFIED	284834
465	83005730 (929, 930)	Novel Protein sim. GBank gil5689778 emb CAB52137.1 - (AJ242832) calpain [Homo sapiens]	Contains protein domain (PF00648) - Calpain family cysteine protease	UNCLASSIFIED	285017, 21906764, 285020
466	20460845 (931, 932)	Novel Protein sim. GBank gil1806175 emb CAB06470 - (Z84395) rpsC [Mycobacterium tuberculosis]	Contains protein domain (PF00417) - Ribosomal protein S3, N-terminal domain.	UNCLASSIFIED	284605, 284559
467	80408035 (933, 934)	Novel Protein sim. GBank gil548705 sp P36949 RBSB_BACSU - D-RIBOSE-BINDING PROTEIN PRECURSOR		UNCLASSIFIED	284784
468	52562208 (935, 936)			UNCLASSIFIED	284692
469	19520527 (937, 938)	Novel Protein sim. GBank gil2114024 emb CAB08957 - (Z95558) grcC1 [Mycobacterium tuberculosis]		UNCLASSIFIED	284488
470	80502756 (939, 940)	Novel Protein sim. GBank gil2909459 emb CAA17347 - (AL021929) cobQ [Mycobacterium tuberculosis]	synthase		284602, 284769
471	17937351 (941, 942)	Novel Protein sim. GBank gil114921 sp P17447 BETT_ECOLI - HIGH-AFFINITY CHOLINE TRANSPORT PROTEIN	transport		265019
472	80047458 (943, 944)				
473	20558793 (945, 946)	Novel Protein sim. GBank gil862343 (L10908) - Gcap1 gene product [Mus musculus]		UNCLASSIFIED	284596, 284885, 284557 284369
474	80593365 (947, 948)			UNCLASSIFIED	22278997, 284682, 284288
475	82454685 (949, 950)			UNCLASSIFIED	284907, 284908, 284511, 285009, 284782, 284448, 284636, 284638
476	94143857 (951, 952)	Novel Protein sim. GBank gil5453656 ref NP_006329.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	65274572, 60432049, 284259, 284508, 52844045, 55812038, 284758, 285011, 284288, 284886, 52844229, 85274791, 284638, 284586
477	79175833 (953, 954)			UNCLASSIFIED	284638
478	78633483 (955, 956)			UNCLASSIFIED	284690, 284693
479	80189746 (957, 958)			collagen	284686, 35895855, 285008, 284631, 284910, 284632, 284638, 285018, 284369, 284909
480	79390729 (959, 960)	Novel Protein sim. GBank gil1127551 (U18939) - orf2 [Batrachocottus baikalensis]		mapolymerase	284389
481	78624578 (961, 962)			UNCLASSIFIED	284693
482	83050611 (963, 964)	Novel Protein sim. GBank gil4083042 (AF088085) - GP900; (mudn-like glycoprotein [Cryptosporidium parvum])		UNCLASSIFIED	284909, 284686, 284768, 284693, 55811576, 56182323, 18108385

483	20293306 (965, 966)	Novel Protein sim. GBank gij2104303[emb]CAB08632] - (Z95387) hypothetical protein Rv2610c [Mycobacterium tuberculosis]	Contains protein domain (PF00534) - Glycosyl transferases group 1		284600
484	11618046 (987, 988)	Novel Protein sim. GBank gij3450883 (AF083334) - fibronin [Antheraea pernyi]		UNCLASSIFIED	284584
485	60191234 (969, 970)	Novel Protein sim. GBank gij5042272[emb]CAB44526.1] - (AL078616) nuoF, NADH dehydrogenase subunit [Streptomyces coelicolor]		UNCLASSIFIED	284368, 21908765, 22279000, 22279002
486	80059042 (971, 972)			dehydrogenase	284604
487	11613339 (973, 974)				284638
488	91222383 (975, 976)	Novel Protein sim. GBank gij5724778[gb]AAC53522.2] - (AF012273) rho-type GTPase-activating protein rhoGAPX-1 [Mus musculus]	Contains protein domain (PF00620) - RhoGAP domain		284686, 66714117, 284768, 18108385, 55811576, 265006, 265008, 265009, 265019, 22279002, 284259, 18108370, 284907, 284764, 58182323, 284288, 284693
489	10867710 (977, 978)	Novel Protein sim. GBank gij3882223[db]BAA34471.1] - (AB018294) KIAA0751 protein [Homo sapiens]		kinase	284639
490	95381124 (979, 980)	Novel Protein sim. GBank gij82091[pir]A25494 - hydroxyproline-rich glycoprotein - tomato (fragment)		collagen	22278996, 29331822, 29331828, 284107, 284908, 284110, 265009, 264592, 264593, 60433358, 264288, 264693, 263974, 263976, 20281071, 60432113
491	80498412 (981, 982)	Novel Protein sim. GBank gij2894206[emb]CAA17072] - (AL021840) hypothetical protein Rv3258c [Mycobacterium tuberculosis]		UNCLASSIFIED	284769
492	87421264 (983, 984)				284600
493	11692942 (985, 986)			UNCLASSIFIED	284638
494	67726804 (987, 988)	Novel Protein sim. GBank gij5262605[emb]CAB45743.1] - (AL080150) hypothetical protein [Homo sapiens]		UNCLASSIFIED	284489, 35696286, 60432289, 29331828, 35696052, 284509, 284905, 284906, 284907, 284908, 284909, 284510, 284511, 265009, 284910, 33657402, 284762, 284764, 284768, 284769, 284888, 21908765, 21908769, 35695917, 265020, 284693, 33657109, 284629, 35696423, 35695895, 284634, 284638
495	80028599 (989, 990)	Novel Protein sim. GBank gij2791517[emb]CAA16054] - (AL021246) hypothetical protein Rv2477c [Mycobacterium tuberculosis]	Contains protein domain (PF00005) - ABC transporter	transport	284602, 284682, 284638
496	78985624 (991, 992)	Novel Protein sim. GBank gij230281[pdb]1R69] - 434 Repressor (Amino-Terminal Domain) (R1-69)	Contains protein domain (PF01381) - Helix-turn-helix		284601, 265021
497	78848661 (993, 994)	Novel Protein sim. GBank gij128736[sp]P28225[PDXH_ECOLI - PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (PNP/PMP OXIDASE)]		oxidase	265006

488	88095488 (995, 998)	Novel Protein sim. GBank gi 1145789 (U41662) - neuroligin 2 [Rattus norvegicus]	Contains protein domain (PF00135) - Carboxylesterases	- esterase	284259, 29331826, 35698052, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 264591, 33657402, 264758, 265010, 265011, 264800, 264601, 264805, 264683, 264764, 264766, 264767, 264768, 264687, 264769, 21906767, 33657023, 264693, 264628, 264629, 35698423, 264630, 264632, 264634, 264635, 264637, 264638, 264558, 264639, 18108385, 264563, 264564, 264565, 264566, 264567
489	20438222 (997, 998)	Novel Protein sim. GBank gi 97480 pir J519739 - Integral membrane protein - Rhodobacter capsulatus		UNCLASSIFIED	284605
500	11076810 (999, 1000)				284605
501	13418034 (1001, 1002)	Novel Protein sim. GBank gi 5708250 emb CAB52363.1 - (AL108747) putative integral membrane protein		UNCLASSIFIED	264688
502	80021176 (1003, 1004)	[Sireptomycetes coelicolor A3(2)]	Contains protein domain (PF00342) - Phosphoglucose isomerase	isomerase	22278986, 265011, 264602, 264605, 264635
503	20264483 (1005, 1006)	Novel Protein sim. GBank gi 4468678 emb CAB38132.1 - (AL035591) glucose-6-phosphate isomerase [Sireptomycetes coelicolor]		UNCLASSIFIED	264584
504	10887321 (1007, 1008)			UNCLASSIFIED	264687
505	95003068 (1009, 1010)			UNCLASSIFIED	264369
506	16454292 (1011, 1012)	Novel Protein sim. GBank gi 4033509 sp P02598 CALM_TETPY - CALMODULIN	Contains protein domain (PF00038) - EF hand	- struct	265010
507	20451598 (1013, 1014)	Novel Protein sim. GBank gi 2501089 sp Q46127 SYW_CLOLO - TRYPTOPHANYL-TRNA SYNTHETASE (TRYPTOPHAN-TRNA LIGASE) (TRPRS)		UNCLASSIFIED	264604
508	79841424 (1015, 1016)	Novel Protein sim. GBank gi 468068 sp P34618 YO82_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN ZK1236.2 IN CHROMOSOME III		UNCLASSIFIED	264908
509	11776388 (1017, 1018)				264638
510	83373465 (1019, 1020)			UNCLASSIFIED	264687, 264639
511	16525578 (1021, 1022)				265007
512	20398484 (1023, 1024)	Novel Protein sim. GBank gi 2497419 sp P55635 Y4RB_RHISN - PUTATIVE INTEGRASE/RECOMBINASE Y4RB		UNCLASSIFIED	264565
513	79457404 (1025, 1026)	Novel Protein sim. GBank gi 1276897 (U41809) - cyclin J [Drosophila melanogaster]	Contains protein domain (PF00134) - Cyclin	- cyclin	264683, 264689, 35698423, 264639
514	79813805 (1027, 1028)	Novel Protein sim. GBank gi 184790 (U46068) - von Ebner minor salivary gland protein [Mus musculus]		UNCLASSIFIED	29331830, 264909
515	79462591 (1029, 1030)				22278999, 264690
516	9862020 (1031, 1032)	Novel Protein sim. GBank gi 2127400 pir S65770 - maltotrioglycosyltrehalose trehalohydrolase - Arthrobacter sp. (strain Q38)		amylase	264910

517	95292894 (1033, 1034)	Novel Protein sim. GBank gi 2883605 (AE000725) - ribose 5 phosphate isomerase B [Aquifex aeolicus]		isomerase	265018, 264605, 284764, 284766, 284687, 284691, 264585
518	8491831 (1035, 1036)	Novel Protein sim. GBank gi 954065[emb]CAA58337] - (X83413) U88 [Human herpesvirus 8]		UNCLASSIFIED	264487
519	91677888 (1037, 1038)	Novel Protein sim. GBank gi 5689365[dbj]BAA83073.1] - (AB024075) B120 [Homo sapiens]	Contains protein domain (PF01388) - ARID DNA binding domain	dna_ma_bind	52644507, 22278997, 22278998, 60432049, 284259, 52645080, 29331824, 86714117, 80424269, 29331826, 35696052, 264905, 29331830, 86712502, 264511, 265007, 284591, 60432229, 33657402, 60433438, 21908754, 33109854, 52644296, 87168474, 87188559, 265017, 265018, 264604, 265019, 284681, 264448, 284369, 284288, 284685, 21908765, 21908768, 21908767, 21908769, 265021, 60170815, 33657023, 264692, 52845129, 33657109, 27486262, 27486264, 35895763, 18108370, 264629, 52644332, 56182323, 264639, 83373044, 18108385, 58526488, 60432113
520	79869188 (1039, 1040)				284769
521	11076821 (1041, 1042)	Novel Protein sim. GBank gi 1169128[sp]P46839[CTPA_MYCLE - CATION-TRANSPORTING P-TYPE ATPASE A		transport	264605
522	80435080 (1043, 1044)	Novel Protein sim. GBank gi 1172869[sp]P44331[RBSK_HAEIN - RIBOKINASE	Contains protein domain (PF00284) - pfkB family carbohydrate kinase	kinase	264505, 284768
523	18358013 (1045, 1046)	Novel Protein sim. GBank gi 2132243[pir]S81028 - hypothetical protein YPL236c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	284629
524	80261805 (1047, 1048)	Novel Protein sim. GBank gi 4033608[dbj]BAA35136] - (AB012308) B2HC [Anthracidaris crassispina]		ATPase_associated	264092, 264596, 265011
525	78810046 (1049, 1050)				264907
526	36827630 (1051, 1052)	Novel Protein sim. GBank gi 4108610[emb]CAA21365] - (AL031866) ORF42, len=388 aa, similarity to an aminotransferase, in P95957 Sulfolobus solfataricus, (401 aa), 33.1% identity in 393 aa overlap. Fasta scores: opt:468, E(): 8.5e-24, in Q64602 R. norvegicus, (425 aa), 28.6% ident...		UNCLASSIFIED	264758
527	80504728 (1053, 1054)			UNCLASSIFIED	264769
528	85484134 (1055, 1056)			UNCLASSIFIED	56182575, 265017, 265018
529	17936610 (1057, 1058)	Novel Protein sim. GBank gi 731088[sp]P24215[UXUA_ECOLI - MANNONATE DEHYDRATASE (D-MANNONATE HYDROLASE)		hydrolase	265019
530	10887336 (1059, 1060)	Novel Protein sim. GBank gi 42144[emb]CAA25200] - (X00513) NusA protein (nusA) [Escherichia coli]		UNCLASSIFIED	284687
531	80226576 (1061, 1062)			UNCLASSIFIED	
532	90933444 (1063, 1064)	Novel Protein sim. GBank gi 5262640[emb]CAB45758.1] - (AL080170) hypothetical protein [Homo sapiens]	Contains protein domain (PF00622) - SPRY domain	UNCLASSIFIED	284555, 264556, 264557, 264558, 18108385, 284488, 264490, 264259, 264592, 264760, 265021, 264690, 263976, 264558

533	87761531 (1065, 1066)	Novel Protein sim. GBank gi 4883636 gb AAD31593.1 AF11229 - (AF112299) Integral inner nuclear membrane protein MAN1 [Homo sapiens]			264807, 264809, 264788, 35695917, 264630, 264555
534	82388264 (1067, 1068)	Novel Protein sim. GBank gi 2995352 emb CAA04608.1 - (AJ001206) pep1 [Streptomyces coelicolor]	UNCLASSIFIED		264805, 265011, 264601, 264602, 264605, 264782, 264788, 265020, 264693, 264636
535	79841850 (1069, 1070)	Novel Protein sim. GBank gi 3878636 emb CAA88953 - (Z49128) similar to cAMP-dependent protein kinase; cDNA EST EMBL: T00719 comes from this gene; cDNA EST yk465d8.3 comes from this gene; cDNA EST yk465d8.5 comes from this gene; cDNA EST yk492f4.3 comes from this gene; cDNA EST y...	ATPase associated	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	264908
536	79907207 (1071, 1072)	Novel Protein sim. GBank gi 2495828 sp P55757 YOHL_SERMA - HYPOTHETICAL 10.1 KD PROTEIN IN BIOA 5 REGION	reductase		18108376, 264805, 264806, 264807, 264909
537	94147448 (1073, 1074)	Novel Protein sim. GBank			265008, 264605, 65274791
538	87821863 (1075, 1076)	Novel Protein sim. GBank gi 134920 sp P21997 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)	collagen	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	29331822, 29331824, 29331825, 29331826, 29331827, 264808, 52844045, 33657402, 265017, 264762, 264683, 264288, 264685, 21906765, 35695763, 264558, 60170394, 264559, 22279002
539	28386269 (1077, 1078)	Novel Protein sim. GBank gi 2498433 sp Q12341 HAT1_YEAST - HISTONE ACETYLTRANSFERASE	histone		264602, 265019
540	79637077 (1079, 1080)	Novel Protein sim. GBank			264693
541	87762268 (1081, 1082)	Novel Protein sim. GBank gi 3882241 dbj BAA34480.1 - (AB018303) KIAA0760 protein [Homo sapiens]	transcriptfactor	Contains protein domain (PF00096) - Zinc finger, C2H2 type	18108394, 22278997, 22278998, 264259, 264112, 265009, 33657402, 55812038, 52846317, 265017, 21906765, 264693, 55811576, 264635, 56528486, 264568
542	95285638 (1083, 1084)	Novel Protein sim. GBank gi 5042272 emb CAB44526.1 - (AL078618) nuoF, NADH dehydrogenase subunit [Streptomyces coelicolor]	dehydrogenase		264910, 265018, 264689, 264638, 264486
543	79788290 (1085, 1086)	Novel Protein sim. GBank gi 2791398 emb CAA15984 - (AL021184) hypothetical protein Rv1464 [Mycobacterium tuberculosis]	UNCLASSIFIED		264602, 264908
544	20437191 (1087, 1088)	Novel Protein sim. GBank	UNCLASSIFIED		264605
545	80434504 (1089, 1090)	Novel Protein sim. GBank			264768, 264634, 264907, 264592, 264909
546	80248016 (1091, 1092)	Novel Protein sim. GBank gi 4887211 gb AAD32237.1 AF14744 - (AF147449) penicillin binding protein 1B [Pseudomonas aeruginosa]			264600, 264602, 21908765
547	11077563 (1093, 1094)	Novel Protein sim. GBank gi 1350855 sp P19176 RPOC_PSEPU - DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (TRANSCRIPTASE BETA' CHAIN) (RNA POLYMERASE BETA' SUBUNIT)	mapolymerase		264604
548	82114936 (1095, 1096)	Novel Protein sim. GBank gi 2330021 (AF019250) - kinesin- related protein; KRP; Costal2 [Drosophila melanogaster]	UNCLASSIFIED		264488, 264905, 264910, 264760, 264693, 264639, 264583, 264584

549	95421904 (1097, 1098)	Novel Protein sim. GBank gi 4337460 gb AAD18133 - (AF056195) neuroblastoma-amplified protein [Homo sapiens]		UNCLASSIFIED	264488, 65274572, 18108388, 22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331824, 66714117, 29331825, 29331826, 35696052, 265007, 265008, 264910, 264592, 33657402, 33109954, 265017, 265018, 265019, 18108351, 264448, 264784, 264369, 264288, 264786, 264688, 264688, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 264691, 33657023, 264692, 264693, 65274620, 52645129, 33657109, 27486261, 27486262, 27486264, 33657349, 55811576, 18108387, 60432113, 22279002
550	10888816 (1089, 1100)				264688
551	80439990 (1101, 1102)	Novel Protein sim. GBank gi 3122893 sp P94985 SYFB_MYCTU - PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (PHENYLALANINE--TRNA LIGASE BETA CHAIN) (PHERS)		UNCLASSIFIED	284908, 284909, 284768
552	94672870 (1103, 1104)				
553	80106002 (1105, 1106)	Novel Protein sim. GBank gi 552087 (M33753) - crumbs protein [Drosophila melanogaster]	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	264689, 264639, 264563
554	78618378 (1107, 1108)	Novel Protein sim. GBank gi 5019771 gb AAD37857.1 AF13326 - (AF133263) histidine protein kinase-response regulator hybrid protein CvgSY [Pseudomonas syringae pv. syringae]		kinase	264906
555	78866347 (1109, 1110)	Novel Protein sim. GBank gi 131515 sp P02908 PTGA_SALTY - PTS SYSTEM, GLUCOSE-SPECIFIC IIA COMPONENT (EIIA-GLC) (GLUCOSE-PERMEASE IIA COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A COMPONENT) (EIIA-GLC)	Contains protein domain (PF00358) - phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 1	transport	284762
556	20457127 (1111, 1112)	Novel Protein sim. GBank gi 3914014 sp P86380 MFD_MYCTU - TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)		transcriptfactor	264508, 264605, 264559
557	19523405 (1113, 1114)	Novel Protein sim. GBank gi 5042273 emb CAB44527.1 - (AL078618) nuoE, NADH dehydrogenase subunit [Streptomyces coelicolor]		dehydrogenase	264488
558	20724428 (1115, 1116)	Novel Protein sim. GBank gi 170933 sp P45331 METE_HAEIN - 5-METHYL TETRAHYDROPTEROYL TRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (METHIONINE SYNTHASE, VITAMIN-B12 INDEPENDENT ISOZYME) (COBALAMIN-INDEPENDENT METHIONINE SYNTHASE)		UNCLASSIFIED	264602
559	80084353 (1117, 1118)	Novel Protein sim. GBank gi 4980567 gb AAD35173.1 AE00169 - (AE001694) iron(III) ABC transporter, permease protein [Thermotoga maritima]		UNCLASSIFIED	264634

560	80066533 (1119, 1120)	Novel Protein sim. GBank gil2492595[sp]Q53183Y4TR_RHISN - PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TR	Contains protein domain (PF00005) - ABC transporter	transport	18108386, 284908, 284602, 284604, 18108374
561	20293187 (1121, 1122)			UNCLASSIFIED	284600
562	11698161 (1123, 1124)			UNCLASSIFIED	284689
563	79761420 (1125, 1126)	Novel Protein sim. GBank gil4104925 (AF042276) - poly(hydroxyalcanoate) granule associated protein GA2 [Pseudomonas putida]		UNCLASSIFIED	284910, 284691
564	56716390 (1127, 1128)	Novel Protein sim. GBank gil2792310 (AF040570) - unknown [Amycolatopsis mediterranei]		dehydrogenase	284592
565	56465618 (1129, 1130)	Novel Protein sim. GBank gil3449294[dbj]BAA32462] - (AB011532) MEGF8 [Rattus norvegicus]	Contains protein domain (PF00008) - EGF-like domain	synthase	265010
566	94323888 (1131, 1132)	Novel Protein sim. GBank gil4539568[emb]CAB38487.1] - (AL035636) putative helicase [Streptomyces coelicolor]		helicase	264909, 264510, 265008, 284910, 264758, 284600, 284602, 284604, 284605, 284768, 284687, 284689, 35695917, 264693, 65274620, 264486
567	79560955 (1133, 1134)			UNCLASSIFIED	284681, 284691, 284593
568	94681793 (1135, 1136)	Novel Protein sim. GBank gil100506[pir]IS17455 - Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) - Flaveria trinervia (fragment)	Contains protein domain (PF00390) - Malic enzyme	dehydrogenase	284689
569	39508897 (1137, 1138)	Novel Protein sim. GBank gil3915843[sp]O31212[RS2_STRCO - 30S RIBOSOMAL PROTEIN S2	Contains protein domain (PF00318) - Ribosomal protein S2	ribosomalprot	284565
570	78375927 (1139, 1140)			UNCLASSIFIED	18108376, 18108387, 284565
571	79793961 (1141, 1142)	Novel Protein sim. GBank gil115122[sp]P21627[BRAD_PSEAE - HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PROTEIN BRAD		transport	284907, 284909
572	36988838 (1143, 1144)			UNCLASSIFIED	284762
573	20715521 (1145, 1146)	Novel Protein sim. GBank gil4539223[emb]CAB39881.1] - (AL049497) putative integral membrane protein [Streptomyces coelicolor]		UNCLASSIFIED	265007, 284601
574	13521592 (1147, 1148)				284636
575	13076416 (1149, 1150)	Novel Protein sim. GBank gil118794[sp]P10443[DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN		polymerase	284687
576	20482246 (1151, 1152)	Novel Protein sim. GBank gil5457825[emb]CAB49116.1] - (AJ248283) PAB2227 [Pyrococcus abyssi]			264605
577	66727102 (1153, 1154)	Novel Protein sim. GBank gil5042274[emb]CAB44528.1] - (AL076618) nuoD, NADH dehydrogenase subunit [Streptomyces coelicolor]	Contains protein domain (PF00346) - Respiratory-chain NADH dehydrogenase, 49 Kd subunit	dehydrogenase	35696052, 284636
578	11804477 (1155, 1156)				264636
579	11784723 (1157, 1158)	Novel Protein sim. GBank gil1723081[sp]Q11046[Y089_MYCTU - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CY50.09		transport	264682, 264556

580	80059417 (1159, 1160)					22278998, 35696052, 264555, 264556, 264558
581	79230833 (1161, 1162)				UNCLASSIFIED	265008, 264584
582	80049617 (1163, 1164)	Novel Protein sim. GBank gi 3243131 (AF045777) - titin	Contains protein domain (PF00047) -		struct	265021, 264555, 264557
583	79321392 (1165, 1166)	[Drosophila melanogaster] Novel Protein sim. GBank gi 2501182 sp P7728 YAJR_ECOLI - HYPOTHETICAL 49.0 KD PROTEIN IN ABPA-CYOE INTERGENIC REGION			transport	264594
584	79845024 (1167, 1168)				UNCLASSIFIED	264488, 264808, 264766, 264687, 35688423
585	79581454 (1169, 1170)	Novel Protein sim. GBank gi 3882221 dbj BAA34470.1 - (AB018293) KIAA0750 protein [Homo sapiens]			UNCLASSIFIED	265018, 264684, 21908769
586	38277486 (1171, 1172)				UNCLASSIFIED	264908, 265007
587	80497359 (1173, 1174)	Novel Protein sim. GBank gi 4467250 emb CAB37575 - (AL035569) probable Glu-tRNA Gln amidotransferase subunit [Streptomyces coelicolor]			hydrolase	264800, 264802, 264605, 264769, 264690, 264557
588	79557239 (1175, 1176)	Novel Protein sim. GBank gi 5689519 dbj BAA83043.1 - (AB028014) KIAA1091 protein [Homo sapiens]			UNCLASSIFIED	265020, 264692
589	79805828 (1177, 1178)				UNCLASSIFIED	22278998, 264907, 264809, 264510, 265009, 265010, 264807, 264769, 35695917, 18108376, 264634, 264638, 264638
590	79815629 (1179, 1180)				UNCLASSIFIED	264906, 264909
591	10313540 (1181, 1182)	Novel Protein sim. GBank gi 2143293 emb CAB09390 - (Z95972) poB [Mycobacterium tuberculosis]			mapolymerase	264691
592	13889767 (1183, 1184)				MHC	263872
593	82348699 (1185, 1186)	Novel Protein sim. GBank gi 4511983 gb AAD21543.1 - (AF088886) electrotransfer ubiquinone oxidoreductase [Zymomonas mobilis]			dehydrogenase	264511, 264762, 264769, 264488
594	20212392 (1187, 1188)	Novel Protein sim. GBank gi 1272368 (U51896) - LfGE [Vibrio parahaemolyticus]			UNCLASSIFIED	264605
595	10064064 (1189, 1190)	Novel Protein sim. GBank gi 131490 sp P20966 PTFB_ECOLI - PTS SYSTEM, FRUCTOSE-SPECIFIC IIBC COMPONENT (EIIBC-FRU) (FRUCTOSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EII-FRU)				264769
596	13085170 (1191, 1192)				UNCLASSIFIED	264636
597	80259003 (1193, 1194)				UNCLASSIFIED	264592
598	94140216 (1195, 1196)				UNCLASSIFIED	264758, 55810784, 264555, 264558, 264837, 83373044
599	20385137 (1197, 1198)	Novel Protein sim. GBank gi 125328 sp P04951 KDSB_ECOLI - 3-DEOXY-MANNO- OCTULONATE CYTIDYL TRANSFERASE (CMP-KDO SYNTHETASE) (CMP-2-KETO-3-DEOXYOCTULONIC ACID SYNTHETASE) (CKS)			UNCLASSIFIED	264803
600	10357663 (1199, 1200)					
601	79610404 (1201, 1202)	Novel Protein sim. GBank gi 2127414 pir S60064 - hypothetical protein 2 - Corynebacterium glutamicum			UNCLASSIFIED	264908 264510

602	78250602 (1203, 1204)	Novel Protein sim. GBank gij3522861gbjAAC34243.1 - (AC004411) putative pto kinase [Arabidopsis thaliana]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	265007
603	11466067 (1205, 1208)			UNCLASSIFIED	264595
604	81675420 (1207, 1208)				264756
605	20436657 (1208, 1210)	Novel Protein sim. GBank gij1175322 sp P44917 Y883_HAEIN - HYPOTHETICAL PROTEIN HI0883		UNCLASSIFIED	264605
606	80334582 (1211, 1212)	Novel Protein sim. GBank gij5020284 gb AAD38043.1 AF15136 - (AF151363) Cdc42 GTPase-activating protein [Mus musculus]		UNCLASSIFIED	264764
607	95361506 (1213, 1214)	Novel Protein sim. GBank gij188864 (M74027) - mucin [Homo sapiens]		UNCLASSIFIED	264508, 264908, 85658542, 264682, 264687, 264689, 264534, 18108376, 35698423, 264636, 264555, 264638
608	11810888 (1215, 1216)			UNCLASSIFIED	264682
609	80064775 (1217, 1218)	Novel Protein sim. GBank gij2496701 sp P55552 Y4LL_RHISN - HYPOTHETICAL 91.8 KD PROTEIN Y4LL	Contains protein domain (PF00989) - PAS domain	UNCLASSIFIED	264605
610	78629413 (1219, 1220)				264692
611	87586205 (1221, 1222)				264508, 264905, 264807, 264908, 264909, 264511, 264910, 264758, 264604, 264684, 264766, 264689, 264692, 264628, 264635, 264636, 264637, 264558
612	85287851 (1223, 1224)	Novel Protein sim. GBank gij1877386 emb CAB07118 - (Z92772) recD [Mycobacterium tuberculosis]	Contains protein domain (PF01443) - Viral (Superfamily 1) RNA helicase	nuclease	264600, 264801, 264804, 264769, 264558, 264565
613	7523475 (1225, 1226)			UNCLASSIFIED	264369
614	79989348 (1227, 1228)	Novel Protein sim. GBank gij5114231 gb AAD40238.1 AF13670 - (AF136709) histidine kinase YycG [Staphylococcus aureus]		kinase	18108372, 264563
615	39586698 (1229, 1230)	Novel Protein sim. GBank gij1339950 dbj BAA12741 - (D85230) large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]		synthase	264600, 264602, 264629
616	20465331 (1231, 1232)	Novel Protein sim. GBank gij544387 sp P35873 GALE_ERWAM - UDP-GLUCOSE 4-EPIMERASE (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE)		isomerase	264605
617	91227222 (1233, 1234)	Novel Protein sim. GBank gij2498097 sp Q60769 TNP3_MOUSE - TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20)	Contains protein domain (PF00641) - Zn-finger in Ran binding protein and others.	Inf	52645156, 21906765, 35698423, 21906768, 21906769, 22278994, 35698286, 22278998, 265020, 265021, 265007, 265008, 264636, 52644150, 33657023, 264692, 264693, 29331822, 29331824, 55612038, 83373044, 56182181, 60424268, 66714117, 29331825, 33657109, 29331826, 33657182, 29331827, 35698052, 29331828, 27486262, 33657349, 56526486, 265018, 265019, 22278002, 264482, 264448, 29331830, 66712502, 264809

618	20632843 (1235, 1238)	Novel Protein sim. GBank gi 5459388 emb CAB50746.1 - (AL096838) putative aminotransferase [Streptomyces coelicolor]		isomerase	284603
619	91227224 (1237, 1238)				56994075, 29331828, 33856970, 285008, 33857402, 33109954, 87168559, 284448, 18108374, 83373044
620	81183143 (1239, 1240)	Novel Protein sim. GBank gi 484335 sp Q05922 DUS2_MOUSE - DUAL SPECIFICITY PROTEIN PHOSPHATASE 2 (DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1)		phosphatase	29148498, 284758, 284369, 29148627
621	80239251 (1241, 1242)			UNCLASSIFIED	284558, 284558, 284639
622	20456427 (1243, 1244)	Novel Protein sim. GBank gi 2633557 emb CAB13060 - (Z99110) yldF [Bacillus subtilis]		UNCLASSIFIED	284805
623	10131798 (1245, 1246)	Novel Protein sim. GBank gi 1857710 gb AAB48482 - (U87224) contactin associated protein [Rattus norvegicus]	Contains protein domain (PF00054) - Laminin G domain	laminin	284906
624	19534127 (1247, 1248)	Novel Protein sim. GBank gi 1705703 sp P52225 CCMF_PSEFL - CYTOCHROME C-TYPE BIOGENESIS PROTEIN CYCK		cytochrome	284596
625	13084819 (1249, 1250)	Novel Protein sim. GBank gi 2894252 emb CAA17114.1 - (AL021841) hypothetical protein Rv3342 [Mycobacterium tuberculosis]		UNCLASSIFIED	284688
626	88062803 (1251, 1252)	Novel Protein sim. GBank gi 416592 sp P32323 AGA1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR		UNCLASSIFIED	29331822, 284905, 284908, 33857023, 33857109, 284558
627	80255457 (1253, 1254)	Novel Protein sim. GBank gi 3098418 (AF040944) - P140 [Mus musculus]		UNCLASSIFIED	18108394, 284112, 284583, 285022, 284635
628	80077096 (1255, 1256)	Novel Protein sim. GBank gi 1711543 sp P50526 SSP1_SCHPO - SERINE/THREONINE-PROTEIN KINASE SSP1	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	284800
629	78851602 (1257, 1258)	Novel Protein sim. GBank gi 143204 (U34305) - ORF2; Method: conceptual translation supplied by author. [Shigella sonnei]		isomerase	284906, 284907
630	39565156 (1259, 1260)	Novel Protein sim. GBank gi 3236368 (AF064748) - S3-12 [Mus musculus]		UNCLASSIFIED	284490
631	20598718 (1261, 1262)	Novel Protein sim. GBank gi 140687 sp P11888 YGG8_ECOLI - HYPOTHETICAL 30.9 KD PROTEIN IN SBM-FBA INTERGENIC REGION (ORF 4) (F288)			283978
632	27843890 (1263, 1284)			UNCLASSIFIED	284906, 284800, 284605, 284769, 284689, 284488
633	80477772 (1265, 1266)			UNCLASSIFIED	284769
634	17938808 (1267, 1288)				285018
635	79574508 (1269, 1270)			UNCLASSIFIED	284689
636	79910981 (1271, 1272)			UNCLASSIFIED	284596, 284762, 284693

637	82455788 (1273, 1274)	Novel Protein sim. GBank gi 2326739 emb CAB10953 - (Z98268) recN [Mycobacterium tuberculosis]		nuclease	264908, 264907, 264510, 264511, 264601, 264602, 264603, 264604, 264605, 18108351, 264762, 264766, 264687, 264768, 264689, 35685917, 264683, 264634, 264638, 264639, 264559, 18108385
638	14997457 (1275, 1276)	Novel Protein sim. GBank gi 4678662 emb CAB41074.1 - (AL049645) putative large ATP-binding protein [Streptomyces coelicolor]			264638
639	80204210 (1277, 1278)	Novel Protein sim. GBank gi 4589629 dbj BAA76838.1 - (AB023209) KIAA0892 protein [Homo sapiens]	struct		264112, 263974
640	17929579 (1279, 1280)	Novel Protein sim. GBank gi 1432083 (U60981) - homolog to Skp1p, an evolutionarily conserved kinetochore protein in budding yeast [Arabidopsis thaliana]	Contains protein domain (PF01466) - Inapolymerase Skp1 family		265009, 265010
641	79636398 (1281, 1282)			UNCLASSIFIED	264693
642	19998737 (1283, 1284)			UNCLASSIFIED	264565
643	81516220 (1285, 1286)			UNCLASSIFIED	264906, 264908, 264758, 264288, 264632, 264635, 264639, 264584
644	11751367 (1287, 1288)			UNCLASSIFIED	264684
645	95010907 (1289, 1290)			UNCLASSIFIED	264906, 264762, 264693, 264639, 264559
646	80069083 (1291, 1292)				264595, 264586
647	80257085 (1293, 1294)	Novel Protein sim. GBank gi 4507613 ref NP_003738.1 pTNKS - TANKYRASE	Contains protein domain (PF00023) - Ank repeat		264909, 264591
648	80077428 (1295, 1296)	Novel Protein sim. GBank gi 1044983 pfs 169646 - protamine [Monodonta turbinata, gonads, Peptide, 106 aa]		UNCLASSIFIED	264600
649	80247447 (1297, 1298)			UNCLASSIFIED	263978
650	11798316 (1299, 1300)			UNCLASSIFIED	264686
651	11776932 (1301, 1302)	Novel Protein sim. GBank gi 1346918 sp P1283 PURA_ECOLI - ADENYLOSUCCINATE SYNTHETASE (IMP-ASPARTATE LIGASE)			264602, 264638
652	85516704 (1303, 1304)			UNCLASSIFIED	264905, 264907, 264909, 263978, 264637
653	82124947 (1305, 1306)	Novel Protein sim. GBank gi 1722977 sp Q10638 Y03C_MYCTU - HYPOTHETICAL 82.8 KD PROTEIN CY130.12C		UNCLASSIFIED	22278998, 264510, 264511, 264512, 264593, 21906754, 264603, 264760, 18108376, 264556
654	95010589 (1307, 1308)			UNCLASSIFIED	264908, 264595, 264632
655	79320692 (1309, 1310)	Novel Protein sim. GBank gi 130327 sp P26647 PLSC_ECOLI - 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (1-AGP ACYLTRANSFERASE) (1-AGPAT) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE) (LPAAT)	Contains protein domain (PF01553) - Acyltransferase		264592
656	80416739 (1311, 1312)			UNCLASSIFIED	264602, 264605, 264766, 264691
657	20811010 (1313, 1314)			UNCLASSIFIED	264557, 264558

658	87761815 (1315, 1316)	Novel Protein sim. GBank gij5689493[dbj BAA83030.1] - (AB029001) KIAA1078 protein [Homo sapiens]		UNCLASSIFIED	22278996, 60432049, 29331822, 29331824, 29331828, 265007, 265008, 33857402, 33857084, 285017, 284448, 21906785, 21906766, 283987, 20281149, 18108370, 18108374, 284482
659	87718663 (1317, 1318)	Novel Protein sim. GBank gij2137872[pir J48724 - zinc finger protein PZF - mouse	Contains protein domain (PF00086) - Zinc finger, C2H2 type	transcriptfactor	22278999, 60432049, 66714117, 29331827, 265007, 284786, 58181562, 18108359, 18108385, 18108370, 18108381
660	81897822 (1319, 1320)			UNCLASSIFIED	284757
661	80028023 (1321, 1322)	Novel Protein sim. GBank gij134180[sp P15401 SACY_BACSU - LEVANSUCRASE AND SUCRASE SYNTHESIS OPERON ANTITERMINATOR	Contains protein domain (PF00874) - Transcriptional antiterminator bglG family	UNCLASSIFIED	284510, 265009, 264600, 264602, 264603, 264604, 264605, 32833988, 18108376, 264636, 18108387, 22278000
662	20463731 (1323, 1324)	Novel Protein sim. GBank gij4545229[gb AAD22450.1 AF11618 - (AF116183) SecA homolog [Actinobacillus actinomycetemcomitans]		UNCLASSIFIED	264605
663	20528080 (1325, 1326)	Novel Protein sim. GBank gij5689250[dbj BAA82881.1] - (AB024335) similar to orf5 [Comamonas testosteroni]		dehydrogenase	264605
664	80508512 (1327, 1328)	Novel Protein sim. GBank gij1652848[dbj BAA17766] - (D90809) DNA photolyase [Synecocystis sp.]		UNCLASSIFIED	264768
665	80079053 (1329, 1330)	Novel Protein sim. GBank gij116841[sp P21640 COBJ_PSEDE - PRECORRIN-3B C17 METHYLTRANSFERASE (PRECORRIN-3 METHYLTRANSFERASE)		isomerase	264600
666	78603142 (1331, 1332)	Novel Protein sim. GBank gij3261829[emb CAB10927] - (Z98280) hypothetical protein Rv1230c [Mycobacterium tuberculosis]		glycoprotein	264807, 265007
667	94631802 (1333, 1334)	Novel Protein sim. GBank gij5688851[dbj BAA82702.1] - (AB017438) Orf5 [Streptomyces coelicolor]		UNCLASSIFIED	264689, 264602, 264593
668	82051891 (1335, 1336)	Novel Protein sim. GBank gij3581853[emb CAA20809] - (AL031541) 50S ribosomal protein L20 [Streptomyces coelicolor]	Contains protein domain (PF00453) - Ribosomal protein L20	ribosomalprot	264905, 264906, 264908, 264600, 264601, 264603, 264605, 264760, 264689, 264636, 264638, 284639
669	12967154 (1337, 1338)			UNCLASSIFIED	264637
670	80236549 (1339, 1340)	Novel Protein sim. GBank gij2582531 (AF026444) - 2-Isopropylmalate synthase [Streptomyces coelicolor]		synthase	264905, 264906, 264908, 264601, 264762, 264766, 264689, 264638, 18108385, 264488
671	79601388 (1341, 1342)		Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	264690, 264692, 264693, 264636, 18108387
672	79834371 (1343, 1344)	Novel Protein sim. GBank gij2114430 (U92703) - Orf-1/EBF-like-3 transcription factor [Mus musculus]		transcriptfactor	264810, 265017
673	82285788 (1345, 1346)	Novel Protein sim. GBank gij4589285[gb AAD26430.1 AF13515 - (AF135154) ferric alkaligin siderophore receptor [Bordetella pertussis]			264759
674	79189258 (1347, 1348)			UNCLASSIFIED	264629

675	87895870 (1349, 1350)	Novel Protein sim. GBank gi 4980755 gb AAD35347.1 AE00170 - (AE001708) D- alanine-D-alanine ligase [Thermotoga maritima]	Contains protein domain (PF01820) - D-ala D-ala ligase	UNCLASSIFIED	284488, 22278999, 66714117, 284508, 284511, 285008, 60433438, 284800, 284801, 284802, 284803, 284804, 284805, 284782, 284887, 284789, 60431802, 18108374, 284638, 284838
676	78899807 (1351, 1352)	Novel Protein sim. GBank gi 1723588 sp Q10479 YDF7_SCHPO - PUTATIVE GLUCOSYLTRANSFERASE C17C9.07			285010
677	21644312 (1353, 1354)	Novel Protein sim. GBank gi 887208 (U03976) - dynein heavy chain isotype 5C [Tripneustes gratilla]		ATPase-associated	284591, 284832
678	84225200 (1355, 1356)	Novel Protein sim. GBank gi 1586274 pr 2203365A - laminin alpha5 [Mus musculus]	Contains protein domain (PF00053) - Laminin EGF-like (Domains III and V)	laminin	284758, 284882, 284557
679	78868855 (1357, 1358)	Novel Protein sim. GBank gi 3928723 emb CAA22219 - (AL034355) putative ABC transporter [Streptomyces coelicolor]		UNCLASSIFIED	22278998, 284693
680	20726424 (1359, 1360)				284600, 284602
681	94322017 (1361, 1362)	Novel Protein sim. GBank gi 5174493 ref NP_006050.1 pLAMC - laminin, gamma 3	Contains protein domain (PF00053) - Laminin EGF-like (Domains III and V)	laminin	284102, 284907, 284908, 285008, 284693, 263972, 83373044, 284568
682	11392476 (1363, 1364)			UNCLASSIFIED	284595
683	80083880 (1365, 1366)	Novel Protein sim. GBank gi 4758208 ref NP_004081.1 pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase Vh1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	phosphatase	284834
684	20465367 (1367, 1368)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]			284605
685	80246735 (1369, 1370)				284909, 283967, 283981
686	79208608 (1371, 1372)				284631
687	80085829 (1373, 1374)				284693, 284635
688	79853412 (1375, 1376)	Novel Protein sim. GBank gi 2688962 (AF027768) - LspA [Serratia marcescens]		peptidase	284907, 284638
689	88064256 (1377, 1378)	Novel Protein sim. GBank gi 3046931 (AF049330) - PPAR gamma coactivator [Mus musculus]	Contains protein domain (PF00078) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	284908, 284907, 285007, 285009, 60433438, 21908754, 284780, 18108358, 21908768, 21908769, 285021, 18108381, 283974, 18108379, 284557, 18108385, 22279002
690	80389750 (1379, 1380)	Novel Protein sim. GBank gi 2498941 sp Q15428 SP62_HUMAN - SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A68)		UNCLASSIFIED	284510, 284511, 284764, 284769
691	81854392 (1381, 1382)			UNCLASSIFIED	284757
692	83608938 (1383, 1384)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	55812038, 55811957, 285018, 55811150, 18108351, 284908, 60431528, 284594
693	79586116 (1385, 1386)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 8]		UNCLASSIFIED	284635
694	82455983 (1387, 1388)	Novel Protein sim. GBank gi 267327 sp Q01033 VG48_HSVSA - HYPOTHETICAL GENE 48 PROTEIN			22278998, 284510, 284602, 284803, 284762, 284887, 284769, 284693

695	94147849 (1389, 1390)	Novel Protein sim. GBank gij4468339[embjCAB38059.1] - (AJ010901) MUC4 [Homo sapiens]	Contains protein domain (PF00084) - von Willebrand factor type D domain	UNCLASSIFIED	58182575, 284509, 284905, 284907, 29331830, 284908, 284909, 284511, 285007, 284910, 284758, 284784, 284288, 85274791, 284905, 284595
696	79830982 (1391, 1392)	Novel Protein sim. GBank gij2649950 (AE001058) - glutamine ABC transporter, ATP-binding protein (glnQ) [Archaeoglobus fulgidus]	Contains protein domain (PF00005) - ABC transporter	transport	
697	11767889 (1393, 1394)	Novel Protein sim. GBank gij1731343[spjQ10894]YY25_MYCTU - HYPOTHETICAL 24.4 KD PROTEIN CY49.25	Contains protein domain (PF01836) - Transposase	UNCLASSIFIED	284692
698	8695862 (1395, 1396)			UNCLASSIFIED	264888, 3565917
699	79582558 (1397, 1398)			UNCLASSIFIED	264882
700	79839098 (1399, 1400)				264893
701	80230242 (1401, 1402)	Novel Protein sim. GBank gij1001236[dbjBAA10477] - (D84003) hypothetical protein [Synecocystis sp.]		UNCLASSIFIED	264488, 284510, 284511, 284602, 284605, 284689
702	79814789 (1403, 1404)	Novel Protein sim. GBank gij2488935[spjQ48338]SOXG_CORSP - SARCOSINE OXIDASE GAMMA SUBUNIT		UNCLASSIFIED	284809
703	20446820 (1405, 1406)			oxidase	284604
704	94312224 (1407, 1408)	Novel Protein sim. GBank gij3150513 (AF087219) - contains similarity to the kelch/MIPP family [Caenorhabditis elegans]	Contains protein domain (PF01344) - Kelch motif	UNCLASSIFIED	284288, 58181562, 33657109, 284629, 55811576
705	17932141 (1409, 1410)	Novel Protein sim. GBank gij421091[pirjS30730] - hypothetical protein o208 - Escherichia coli		UNCLASSIFIED	265006
706	20288062 (1411, 1412)	Novel Protein sim. GBank gij3024872[spjQ55780]Y074_SYNY3 - HYPOTHETICAL 52.8 KD PROTEIN SLR0074			284600
707	20638065 (1413, 1414)	Novel Protein sim. GBank gij3420608[gbjAAC31907.1] - (AF075709) ABC transporter ATP-binding subunit [Pseudomonas putida]		transport	264603
708	20708282 (1415, 1416)				284801, 284892
709	88001439 (1417, 1418)	Novel Protein sim. GBank gij3849741[embjCAA03985] - (AJ000281) mucin [Homo sapiens]		stuct	18108388, 284637, 284908, 284909
710	11356683 (1419, 1420)	Novel Protein sim. GBank gij3080425[embjCAA18744.1] - (AL022604) putative protein [Arabidopsis thaliana]			264369
711	17931418 (1421, 1422)				265019
712	80258164 (1423, 1424)	Novel Protein sim. GBank gij4758886[refjNP_002323.1]pLRP1 - low density lipoprotein related protein 1 (alpha-2-macroglobulin receptor)	Contains protein domain (PF00058) - Low-density lipoprotein receptor repeat class B	apolipoprotein	284591
713	79263126 (1425, 1426)	Novel Protein sim. GBank gij1703288[spjQ11056]AM12_MYCTU - PUTATIVE AMIDASE CY50.19C		hydrolase	264906, 284907
714	27847651 (1427, 1428)	Novel Protein sim. GBank gij4502351[refjNP_001692.1]pBAAT - bile acid Coenzyme A: amino acid N-acyltransferase; glycine N-choleyltransferase			284508, 284555

715	78639423 (1429, 1430)	Novel Protein sim. GBank gi 1789035 (AE000352) - orf. hypothetical protein [Escherichia coli]		UNCLASSIFIED	264907	
716	78559072 (1431, 1432)				264692	
717	79491842 (1433, 1434)	Novel Protein sim. GBank gi 2494074 sp P55653 GABD_RHISN - PROBABLE SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (SSDH)		dehydrogenase	264636	
718	94319658 (1435, 1436)	Novel Protein sim. GBank gi 3873679 emb CAA94886 - (Z71178) similar to pro-collagen domains: cDNA EST EMBL:D27978 comes from this gene; cDNA EST EMBL:D27977 comes from this gene; cDNA EST EMBL:D34199 comes from this gene; cDNA EST EMBL:D84392 comes from this gene; cDNA EST EMBL:...	Contains protein domain (PF00093) - von Willebrand factor type C domain	kinase	18108392, 22278994, 22278998, 265008, 265016, 264681, 18108354, 264684, 264685, 264686, 264687, 264689, 21906769, 18108361, 264691, 264692, 55910764, 264635, 18108381, 18108382, 83373044, 18108388	
719	17679564 (1437, 1438)	Novel Protein sim. GBank gi 2104302 emb CA80863 - (Z95387) hypothetical protein Rv2611c [Mycobacterium tuberculosis]		UNCLASSIFIED	265011	
720	79841684 (1439, 1440)				264908	
721	15020180 (1441, 1442)	Novel Protein sim. GBank gi 123530 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	264629	
722	9862603 (1443, 1444)	Novel Protein sim. GBank gi 498253 (U02372) - integrase [Vibrio cholerae]			264910	
723	19755599 (1445, 1446)	Novel Protein sim. GBank gi 2253054 emb CAB10705 - (Z97559) hypothetical protein Rv2114 [Mycobacterium tuberculosis]		UNCLASSIFIED	264691	
724	10126494 (1447, 1448)	Novel Protein sim. GBank gi 4063015 (AF083081) - protease PrtA [Pseudomonas fluorescens]	Contains protein domain (PF00353) - Hemolysin-type calcium-binding proteins	protease	264809	
725	7878679 (1449, 1450)			UNCLASSIFIED	264905, 264907	
726	13088282 (1451, 1452)			UNCLASSIFIED	264636	
727	13522872 (1453, 1454)				264634	
728	20268471 (1455, 1456)	Novel Protein sim. GBank gi 2633910 emb CAB1341 - (Z99112) similar to hypothetical proteins [Bacillus subtilis]			264567	
729	11293753 (1457, 1458)			UNCLASSIFIED	264490	
730	18900373 (1459, 1460)	Novel Protein sim. GBank gi 2494660 sp Q45291 GALE_BRELA - UDP-GLUCOSE 4-EPIMERASE (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE)		isomerase	264564	
731	80058750 (1461, 1462)	Novel Protein sim. GBank gi 1146192 (L47838) - putative [Bacillus subtilis]		UNCLASSIFIED	264605	
732	80258175 (1463, 1464)	Novel Protein sim. GBank gi 1168396 sp P48661 AIP2_YEAST - ACTIN INTERACTING PROTEIN 2		struct	264591, 264594, 264595	
733	20446839 (1465, 1466)			UNCLASSIFIED	264604	
734	20435987 (1467, 1468)	Novel Protein sim. GBank gi 3184080 emb CAA19338 - (AL023781) hypothetical protein [Schizosaccharomyces pombe]		ubiquitin	264604	

735	11607958 (1469, 1470)	Novel Protein sim. GBank gi 401582 sp P27432 YICE_ECOLI - HYPOTHETICAL 48.9 KD PROTEIN IN GLTS-SELC INTERGENIC REGION			264594
736	10878734 (1471, 1472)	Novel Protein sim. GBank gi 400831 sp P31135 POTH_ECOLI - PUTRESCINE TRANSPORT SYSTEM PERMEASE PROTEIN POTH	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	transport	264636
737	78945340 (1473, 1474)		Contains protein domain (PF00615) - Regulator of G protein signaling domain	UNCLASSIFIED	265020
738	17895353 (1475, 1476)				265008
739	79833670 (1477, 1478)	Novel Protein sim. GBank gi 2506867 sp P33225 TORA_ECOLI - TRIMETHYLAMINE- N-OXIDE REDUCTASE PRECURSOR (TMAO REDUCTASE) (TRIMETHYLAMINE OXIDASE)		oxidase	264910
740	19881557 (1479, 1480)				264907, 264764, 264634, 264637
741	79827273 (1481, 1482)	Novel Protein sim. GBank gi 3261828 emb CAB10925 - (Z98260) mrp [Mycobacterium tuberculosis]	Contains protein domain (PF01883) - Domain of unknown function	UNCLASSIFIED	264689, 35696286, 264510, 264908, 18108382
742	82393795 (1483, 1484)	Novel Protein sim. GBank gi 3877494 emb CAA88472.1 - (Z48583) ATP binding protein with similarity to the CDC48/PAS1/SEC18 family; cDNA EST EMBL:D65037 comes from this gene; cDNA EST EMBL:D88340 comes from this gene; cDNA EST EMBL:D65048 comes from this gene; cDNA EST EMBL:D6845...		UNCLASSIFIED	29331822, 264910, 264762
743	82300051 (1485, 1486)	Novel Protein sim. GBank gi 127420 sp P19888 MTBA_BACAR - MODIFICATION METHYLASE BANI (CYTOSINE-SPECIFIC METHYLTRANSFERASE BANI) (M.BANI)	Contains protein domain (PF00145) - C-5 cytosine-specific DNA methylase	UNCLASSIFIED	264488, 264259, 264508, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 265008, 265009, 264910, 264591, 264596, 264759, 265010, 265011, 18108351, 264763, 264288, 264766, 264768, 264693, 18108370, 264629, 18108372, 264630, 264631, 264634, 264558, 18108385, 264482, 264564, 264567
744	80230421 (1487, 1488)				18108397, 264511, 264690, 264628, 264638, 264692, 264639, 264768
745	9841963 (1489, 1490)	Novel Protein sim. GBank gi 78921 pir S04848 - UDP-N- acetylmutamoyltalanyl-D-glutamyl-2, 6-diaminopimelate--D- alanine-D-alanine ligase (EC 6.3.2.15) precursor - Escherichia coli		glycoprotein	264906
746	11073229 (1491, 1492)	Novel Protein sim. GBank gi 3386354 (AF074705) - pyochelin synthetase [Pseudomonas aeruginosa]		synthase	264600
747	94322044 (1493, 1494)	Novel Protein sim. GBank gi 2887411 db BAA24848 - (AB007878) KIAA0418 [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	oxidase	6671417, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 264910, 265011, 264681, 264288, 264766, 264687, 264768, 264769, 21908768, 35695917, 264681, 264693, 264628, 264634, 264635, 264639, 56182323, 83373044
748	11617923 (1495, 1496)				264690

749	20469118 (1497, 1498)	Novel Protein sim. GBank			UNCLASSIFIED	264604
750	20296427 (1499, 1500)	gi 1169727 sp P44948 FPG_HAEIN - FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (FAPY- DNA GLYCOSYLASE)				264600
751	21636169 (1501, 1502)	Novel Protein sim. GBank	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase		264605, 264559
752	82450366 (1503, 1504)	gi 5360088 gb AAD42851.1 AF159688 - (AF159688) serine/threonine kinase PKN3 [Myxococcus xanthus] Novel Protein sim. GBank gi 1168682 sp P44426 BIOA_HAEIN - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7.8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)	Contains protein domain (PF00202) - Aminotransferases class-II pyridoxal phosphate	UNCLASSIFIED		264508, 264907, 264510, 265011, 264762, 264689, 35695855, 264638, 18108387
753	80508718 (1505, 1506)	Novel Protein sim. GBank gi 2851530 sp P32399 YHGE_BACSU - HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLTT INTERGENIC REGION (ORFB)		UNCLASSIFIED		264908, 264600, 264602, 264604, 264760, 264769, 264634
754	95083741 (1507, 1508)			UNCLASSIFIED		264508, 264906, 264907, 264908, 264909, 264759, 264602, 264784, 264769, 264628, 264629, 264630, 264632, 264634, 264635, 264637, 264638, 83373044, 18108385
755	80185449 (1509, 1510)	Novel Protein sim. GBank gi 3449276 emb CAA20420 - (AL031317) putative dehydrogenase [Streptomyces coelicolor]		UNCLASSIFIED		264448, 264690
756	94631686 (1511, 1512)					264769, 264689, 264638, 264639
757	79488533 (1513, 1514)			UNCLASSIFIED		264682, 264685
758	78983176 (1515, 1516)	Novel Protein sim. GBank gi 4580331 emb CAB40107.1 - (AJ001206) putative glycogen debranching enzyme [Streptomyces coelicolor]		amylase		265007, 18108387, 265007, 18108387
759	79475667 (1517, 1518)	Novel Protein sim. GBank gi 2911858 (AF047659) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED		264684, 264686
760	87628888 (1519, 1520)	Novel Protein sim. GBank gi 3451312 emb CAA20449 - (AL031324) membrane atpase [Schizosaccharomyces pombe]	Contains protein domain (PF00122) - E1-E2 ATPase	transport		26331822, 264908, 52644045, 56182435, 60170831, 21906754, 265017, 265019, 264681, 264687, 264688, 21906766, 21906768, 265020, 265021, 265022, 264635, 22278000
761	79877968 (1521, 1522)			UNCLASSIFIED		264766
762	80023563 (1523, 1524)	Novel Protein sim. GBank gi 3327158 db BAA31647 - (AB014572) KIAA0672 protein [Homo sapiens]		UNCLASSIFIED		264907, 264593, 265020
763	20294613 (1525, 1526)	Novel Protein sim. GBank gi 4981268 gb AAD35822.1 AE00174 - (AE001744) lipopolysaccharide core biosynthesis protein KdtB [Thermotoga maritima]				264600
764	39515024 (1527, 1528)					264603

765	80025347 (1529, 1530)	Novel Protein sim. GBank gi 3845093 (AE001371) - erythrocyte membrane protein PIEMP3 [Plasmodium falciparum]		struct	284905, 284906, 284594, 284686, 33657023
766	82417404 (1531, 1532)				284605, 284762, 18108374
767	10296742 (1533, 1534)	Novel Protein sim. GBank gi 541121 pir S40827 - hypothetical protein o300 - Escherichia coli		UNCLASSIFIED	284907
768	78416080 (1535, 1536)			UNCLASSIFIED	284592, 284595
769	80086554 (1537, 1538)	Novel Protein sim. GBank gi 2982501 emb CAA06164 - (AJ004832) neuropathy target esterase [Homo sapiens]		esterase	55810764, 284559
770	80417847 (1539, 1540)	Novel Protein sim. GBank gi 283437 pir S27850 - hypothetical protein - Trypanosoma cruzi (fragment)		UNCLASSIFIED	284905, 284907, 284828, 284909, 285010, 284766, 284628, 284629, 284634, 284638, 284555
771	95329509 (1541, 1542)	Novel Protein sim. GBank gi 4769004 gb AAD29715.1 AF14059 - (AF140598) ring-box protein 1 [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	56182575, 35686286, 264259, 66714117, 264107, 68712502, 56182435, 284112, 55812038, 87168559, 284288, 21906766, 33657023, 65274620, 65274791, 18108381
772	78971362 (1543, 1544)			UNCLASSIFIED	284910
773	78945363 (1545, 1546)			UNCLASSIFIED	265020
774	79856129 (1547, 1548)	Novel Protein sim. GBank gi 5531324 emb CAB51045.1 - (AJ009579) putative alkane 1-monoxygenase [Pseudomonas fluorescens]		UNCLASSIFIED	284909
775	20620141 (1549, 1550)			UNCLASSIFIED	264555
776	78842693 (1551, 1552)		Contains protein domain (PF01006) - Hepatitis C virus non-structural protein NS4a		265019
777	79960378 (1553, 1554)	Novel Protein sim. GBank gi 4505461 ref NP_003624.1 pNRPB - nuclear restricted protein, BTB domain-like (brain)	Contains protein domain (PF01344) - Kelch motif	protease	21906754, 265020, 60170615, 264691
778	20691310 (1555, 1556)			UNCLASSIFIED	264511
779	80054024 (1557, 1558)				264603
780	95288987 (1559, 1560)	Novel Protein sim. GBank gi 1144520 (U34956) - phosphoribosylformylglycinamide synthase [Mycobacterium tuberculosis]		synthase	264907, 284600, 284601, 284602, 264603, 284604, 284605, 264486
781	80250049 (1561, 1562)				264905, 284907, 265010, 284600, 264601, 18108382, 18108374, 284556
782	8758529 (1563, 1564)	Novel Protein sim. GBank gi 4155447 (AE001517) - proline/betaine transporter [Helicobacter pylori J99]		UNCLASSIFIED	284605
783	18410791 (1565, 1566)				265020
784	80051197 (1567, 1568)			UNCLASSIFIED	264635, 33657023, 29331828, 265017, 284585, 284586
785	56073541 (1569, 1570)	Novel Protein sim. GBank gi 3451335 (AC005525) - F22162_1 [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	struct	35696052, 284604
786	20438842 (1571, 1572)	Novel Protein sim. GBank gi 138748 sp P10905 UGPA_ECOLI - SN-GLYCEROL-3-PHOSPHATE TRANSPORT SYSTEM PERMEASE PROTEIN UGPA		transport	264603
787	80258364 (1573, 1574)			UNCLASSIFIED	284593

788	80507844 (1575, 1576)	Novel Protein sim. GBank gi2746079 (AF015310) - BTH1 [Brassica napus]			synthase	264909, 264602, 264603, 264769, 264638
789	17294715 (1577, 1578)	Novel Protein sim. GBank gi2351849 (U93357) - 40 kDa heat shock chaperone protein [Halobacterium cutribrium]			UNCLASSIFIED	265007
790	86284406 (1579, 1580)	Novel Protein sim. GBank gi5706378 [dbj BAA83099.1] - (ABD26118) MALT1 [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain		glycoprotein	22278999, 29331824, 264828, 87168559, 265018, 21908765, 21908767, 21908768, 21908769, 265020, 264692, 22279000, 264563
791	94651627 (1581, 1582)	Novel Protein sim. GBank gi5689948 [emb CA851985.1] - (AL109863) putative isoleucyl-tRNA synthetase [Streptomyces coelicolor A3(2)]				264601, 264605, 264636
792	80058786 (1583, 1584)	Novel Protein sim. GBank gi393194 (L02375) - S-antigen [Plasmodium falciparum]			struct	265021, 264631, 264635, 264556
793	79638730 (1585, 1586)	Novel Protein sim. GBank gi1345408 [dbj BAA05046] - (D26046) AT motif-binding factor [Mus musculus]	Contains protein domain (PF00046) - Homeobox domain		homeobox	264693
794	81839294 (1587, 1588)	Novel Protein sim. GBank gi105884 [pir S24023] - dopamine receptor D4 - human (fragment)			UNCLASSIFIED	264603, 264604, 264910, 264762, 264908, 264639, 264909, 264757
795	80074988 (1589, 1590)	Novel Protein sim. GBank gi1877334 [emb CAB07082] - (Z92771) bta [Mycobacterium tuberculosis]			carboxylase	264488, 35686052, 264905, 264907, 265010, 35698423, 264636
796	86669451 (1591, 1592)					60432229, 55811150, 264630, 264637, 264565
797	87771781 (1593, 1594)	Novel Protein sim. GBank gi2995447 [emb CAA71519] - (Y10495) CDV-IR protein [Mus musculus]			struct	22278998, 264093, 264094, 66714117, 21906767, 21908769, 265020, 265022
798	79865209 (1595, 1596)				transcript factor	264667, 264768, 264693
799	79557816 (1597, 1598)	Novel Protein sim. GBank gi4467250 [emb CAB37575] - (AL035569) probable Glu-tRNA Gln amidotransferase subunit [Streptomyces coelicolor]			hydrolase	264909, 264910, 264636, 264638
800	79970189 (1599, 1600)				UNCLASSIFIED	264488
801	80499399 (1601, 1602)	Novel Protein sim. GBank gi2791517 [emb CAA16054] - (AL021246) hypothetical protein RV2477c [Mycobacterium tuberculosis]			transport	264508, 264511, 265008, 265009, 264769, 264567, 264486
802	79834598 (1603, 1604)	Novel Protein sim. GBank gi4887211 [gb AAD32237.1] AF14744 - (AF147449) penicillin binding protein 1B [Pseudomonas aeruginosa]				264905, 264693
803	20467520 (1605, 1606)				struct	264605
804	10174239 (1607, 1608)	Novel Protein sim. GBank gi1176152 [sp P44507] YHAD_HAEIN - HYPOTHETICAL PROTEIN H10091			kinase	264510
805	79599993 (1609, 1610)					264508
806	80484113 (1611, 1612)	Novel Protein sim. GBank gi2764612 [emb CAA04683] - (AJ001330) ornithine transcarbamoylase [Lactobacillus sakei]	Contains protein domain (PF00185) - Aspartate/ornithine carbamoyltransferase		transferase	264769
807	80381812 (1613, 1614)	Novel Protein sim. GBank gi2833311 [sp Q21828] YNFD_CAEEL - HYPOTHETICAL 18.9 KD PROTEIN R07E5.13 IN CHROMOSOME III				264764

808	35106817 (1615, 1616)	Novel Protein sim. GBank gi 3913092 sp Q46170 ARCD_CLOPE - ARGININE/ORNITHINE ANTIporter		transport	264909, 264602, 21906764, 18108374
809	81454254 (1617, 1618)	Novel Protein sim. GBank gi 3913016 sp P74309 ALF1_SYNY3 - FRUCTOSE- BISPHOSPHATE ALDOLASE CLASS I (FBP ALDOLASE)	Contains protein domain (PF00274) - Fructose-bisphosphate aldolase class-I	UNCLASSIFIED	264508, 264806, 264909, 265007, 264910, 264758, 264600, 264802, 264803, 264605, 264687, 264769, 264689, 264636, 264486
810	80182761 (1619, 1620)	Novel Protein sim. GBank gi 401472 sp P30863 YAFB_ECOLI - HYPOTHETICAL OXIDOREDUCTASE IN ASPU-MLTD INTERGENIC REGION	Contains protein domain (PF00248) - Aldo/keto reductase family	reductase	264369
811	80079280 (1621, 1622)			UNCLASSIFIED	264558
812	10297654 (1623, 1624)			UNCLASSIFIED	264692
813	79612280 (1625, 1626)			UNCLASSIFIED	264906
814	80473427 (1627, 1628)	Novel Protein sim. GBank gi 146168 (J01617) - glutaminyl- tRNA synthetase [Escherichia coli]		synthase	264905, 264602, 264605, 264682, 264687, 264769, 264636
815	95419513 (1629, 1630)	Novel Protein sim. GBank gi 4589652 dbj BAA76848.1 - (AB023221) KIAA1004 protein [Homo sapiens]		UNCLASSIFIED	264488, 22278998, 22278999, 29331822, 29331824, 29331825, 29331827, 29331828, 29146489, 264905, 264908, 265007, 33657402, 60433356, 60433438, 264758, 265011, 265017, 265018, 265019, 264369, 264288, 264685, 21906765, 21906767, 265020, 265021, 264692, 65274620, 33657109, 264629, 18108376, 264635, 264638, 60170394, 56182323, 264584
816	19881910 (1631, 1632)				264600
817	95293316 (1633, 1634)	Novel Protein sim. GBank gi 1761144 emb CAB06254 - (Z83866) hypothetical protein Rv3069 [Mycobacterium tuberculosis]		UNCLASSIFIED	264595
818	80938190 (1635, 1636)	Novel Protein sim. GBank gi 1477468 (U35244) - vacuolar protein sorting homolog r-vps33a [Rattus norvegicus]			65274572, 22278998, 60424269, 35696052, 55812038, 21906768, 55811957, 35695917, 33657023, 18108370, 18108374, 55810764, 35696423, 55811576, 264636
819	80254977 (1637, 1638)	Novel Protein sim. GBank gi 1001352 dbj BAA10839 - (D64006) ABC transporter [Synecocystis sp.]		transport	264565
820	80059688 (1639, 1640)	Novel Protein sim. GBank gi 586814 sp P37484 YYBT_BACSU - HYPOTHETICAL 74.3 KD PROTEIN IN RPLI-COTF INTERGENIC REGION		UNCLASSIFIED	264600, 264602, 264604
821	79762590 (1641, 1642)			UNCLASSIFIED	264910
822	80215310 (1643, 1644)			UNCLASSIFIED	264510, 264594, 264637
823	94892299 (1645, 1646)	Novel Protein sim. GBank gi 3878400 emb CAA95828 - (Z71284) predicted using Genefinder; Weak similarity to Mouse T-complex-associated-testes-expressed-1 protein (PIR Acc. No. A45841); cDNA EST EMBL:D32742 comes from this gene; cDNA EST EMBL:D33617 comes from this gene; cDNA EST...		struc	264509, 264687, 264691
824	80411171 (1647, 1648)	Novel Protein sim. GBank gi 1370076 emb CAA66887 - (X98235) type I [Drosophila melanogaster]	Contains protein domain (PF01429) - Methyl-CpG binding domain		264910, 264763, 264769, 264693

825	20638600 (1649, 1650)	Novel Protein sim. GBank gi 3025132 sp P77391 YEAG_ECOLI - HYPOTHETICAL 74.5 KD PROTEIN IN GAPA-RND INTERGENIC REGION		UNCLASSIFIED	264592
826	11075047 (1651, 1652)	Novel Protein sim. GBank gi 3242281 emb CAA16889 - (AL021848) hypothetical protein Rv3202c [Mycobacterium tuberculosis]			264605
827	80054207 (1653, 1654)	Novel Protein sim. GBank gi 3417424 emb CAA20312 - (AL031261) putative transport protein [Schizosaccharomyces pombe]			264603
828	95106322 (1655, 1656)	Novel Protein sim. GBank gi 4336892 gb AAD17897 - (AF101381) Abnormal X segregation [Drosophila melanogaster]		UNCLASSIFIED	52645080, 264508, 264905, 264509, 264908, 264907, 264908, 264909, 264512, 264910, 264591, 264758, 264800, 264766, 264768, 21808768, 35895917, 264691, 264628, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264556, 264639, 83373044, 18108385, 264583, 264566, 264486
828	81742215 (1657, 1658)			UNCLASSIFIED	264758, 264634
830	20396091 (1659, 1660)	Novel Protein sim. GBank gi 3820539 (AF080002) - UDP-N- acetyl(muramyl) tripeptide synthetase MurC [Helicobacillus mobilis]		UNCLASSIFIED	264603
831	87112435 (1661, 1662)			UNCLASSIFIED	58714117, 264910, 264639
832	19536322 (1663, 1664)	Novel Protein sim. GBank gi 1670004 emb CAB06855 - (Z92539) hypothetical protein Rv1024 [Mycobacterium tuberculosis]		UNCLASSIFIED	264908
833	20726654 (1665, 1666)	Novel Protein sim. GBank gi 2500058 sp Q46267 PFLA_CLOPA - PYRUVATE FORMATE-LYASE ACTIVATING ENZYME		UNCLASSIFIED	264602
834	21428762 (1667, 1668)	Novel Protein sim. GBank gi 2497531 sp Q46078 KPYK_CORGL - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) - Pyruvate kinase	kinase	264600, 264602, 264769, 264689, 264636
835	94140482 (1669, 1670)				264768, 263994, 21908767, 284910, 284632, 264635, 264259, 264639, 264693, 83373044, 264758, 35896052, 22279002, 264508, 264905, 264908, 264448, 263972, 264908, 264909
836	66126552 (1671, 1672)	Novel Protein sim. GBank gi 599315 (U15184) - phosphate transport protein PSTC [Mycobacterium leprae]		transport	35895917, 264557
837	78450450 (1673, 1674)			UNCLASSIFIED	264595
838	79184203 (1675, 1676)	Novel Protein sim. GBank gi 728867 sp P40602 APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR		UNCLASSIFIED	264687
839	78641125 (1677, 1678)	Novel Protein sim. GBank gi 2486533 sp Q50598 Y0D8_MYCTU - HYPOTHETICAL 69.9 KD PROTEIN CY1A11.08		UNCLASSIFIED	264806
840	80059851 (1679, 1680)	Novel Protein sim. GBank gi 4557753 re NP_000372.1 pMID1 - midline 1 protein	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	Interleukin receptor	264762, 264556

841	80376318 (1681, 1682)	Novel Protein sim. GBank gij139805 sp P08045 XFIN_XENLA - XFIN PROTEIN	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	264764
842	80076724 (1683, 1684)	Novel Protein sim. GBank gij211432 dbj BAA20037 - (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00369) - Zinc finger present in dystrophin, CBP/p300	UNCLASSIFIED	264905, 264908, 265008, 265009, 18108374, 56182323, 284558
843	87002847 (1685, 1686)	Novel Protein sim. GBank gij3882325 dbj BAA34522.1 - (AB018345) KIAA0802 protein [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	struct	264091, 29331825, 264906, 264768, 264563
844	17941438 (1687, 1688)	Novel Protein sim. GBank gij2224721 dbj BAA20844 - (AB002388) KIAA0390 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	265011
845	18346844 (1689, 1690)				264629
846	79863441 (1691, 1692)	Novel Protein sim. GBank gij625679 pir A36929 - virulence regulatory protein VsrB - Pseudomonas solanacearum		kinase	264907
847	78695348 (1693, 1694)				264909
848	78489365 (1695, 1696)			UNCLASSIFIED	265020
849	78756387 (1697, 1698)			UNCLASSIFIED	264566
850	78817849 (1699, 1700)	Novel Protein sim. GBank gij3183245 sp P78081 YC_K_ECOLI - PUTATIVE GLUTAMINE SYNTHETASE (GLUTAMATE-AMMONIA LIGASE)	Contains protein domain (PF00120) - Glutamine synthetase	UNCLASSIFIED	264909
851	95320333 (1701, 1702)	Novel Protein sim. GBank gij5454130 ref NP_008280.1 p TLN - talin	Contains protein domain (PF01608) - I/LWEQ domain		264488, 52644507, 264489, 18108398, 65274572, 56182575, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 20281171, 264490, 264259, 52845080, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 29146498, 29146499, 264107, 264905, 264906, 264907, 264908, 52844045, 56182435, 265008, 265007, 265008, 265009, 264910, 60432229, 60431735, 60433358, 33657402, 60433438, 264595, 264758, 264759, 21908754, 33109854, 52644288, 265010, 265011, 87188559, 265017, 265018, 265019, 264760, 264761, 264762, 264681, 18108351, 264763, 264448, 264682, 264764, 264683, 18108354, 264288, 264369, 264685, 264766, 264687, 264768, 264769, 21908765, 21908766, 21908767, 21908768, 29148627, 21908769, 29148629, 55811957, 35695917, 265020, 265021, 265022, 60170815, 52844150, 264691, 264692, 33657023, 264693, 263966, 33657109, 27486281, 27486282, 27486284, 27486285, 35695763, 60431802, 18108370, 20281068, 264629, 18108374, 18108376, 55811576, 35696423, 35695855, 264634, 264635, 264636, 264555, 60431850, 264556, 264691
852	10147366 (1703, 1704)				

853	13032587 (1705, 1706)					264836	
854	80052438 (1707, 1708)	Novel Protein sim. GBank gi 3402836 emb CAA76082 - (Y16138) 2-enoate reductase [Moorilla thermoacifica]			reductase	264566	
855	79641130 (1709, 1710)					264692	
856	11594238 (1711, 1712)				UNCLASSIFIED	264591	
857	79210165 (1713, 1714)				UNCLASSIFIED	264630, 264634	
858	80248910 (1715, 1716)					265008, 265009, 264601, 264602, 264603, 18108351	
859	20296634 (1717, 1718)					264559	
860	80041749 (1719, 1720)				UNCLASSIFIED	264489	
861	85857045 (1721, 1722)				UNCLASSIFIED	33657023, 264630	
862	80078467 (1723, 1724)					264600	
863	80578931 (1725, 1726)	Novel Protein sim. GBank gi 2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]			UNCLASSIFIED	264488, 18108398, 35696286, 264259, 18108351, 264288, 265021	
864	94939904 (1727, 1728)				UNCLASSIFIED	264259, 264112, 263974	
865	80045310 (1729, 1730)	Novel Protein sim. GBank gi 5689894 emb CAB52047.1 - (AL108732) hypothetical protein [Streptomyces coelicolor A3(2)]	Contains protein domain (PF01478) - S4 domain			264635, 264600, 264636, 264591, 264602, 264693	
866	80162031 (1731, 1732)	Novel Protein sim. GBank gi 4557876 ref NP_000341.1 pABCR - ATP binding cassette transporter			transport	264288, 264557, 264558	
867	80082402 (1733, 1734)					264605	
868	10075384 (1735, 1736)				UNCLASSIFIED	264909	
869	80062406 (1737, 1738)					264805, 264687, 18108374	
870	80248651 (1739, 1740)	Novel Protein sim. GBank gi 628660 pir S37755 - Adenylyl-transferase - Escherichia coli			transferase	264601, 264636	
871	20378285 (1741, 1742)	Novel Protein sim. GBank gi 1708180 sp Q10602 HEMK_MYCTU - HEMK PROTEIN HOMOLOG			UNCLASSIFIED	264603	
872	95197114 (1743, 1744)	Novel Protein sim. GBank gi 1545959 emb CAA67763 - (X99384) paladin [Mus musculus]			UNCLASSIFIED	35698286, 22278998, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264509, 264805, 264908, 264907, 264908, 264909, 264510, 265006, 264511, 264512, 265007, 265008, 265009, 264910, 264591, 60433358, 264596, 52646317, 67168474, 265010, 264802, 264803, 265017, 265018, 264605, 18108351, 264764, 264766, 264768, 52644229, 264769, 21906765, 265021, 264534, 264691, 52645128, 264628, 264629, 35696423, 65274791, 264631, 264632, 264635, 264636, 264556, 264637, 264638, 264639, 60432113, 22279000, 22279002, 264564	
873	20189728 (1745, 1746)	Novel Protein sim. GBank gi 4156104 (AE001569) - putative Outer membrane protein [Helicobacter pylori J99]	Contains protein domain (PF00098) - Zinc finger, C2H2 type		UNCLASSIFIED	264595	

874	80077692 (1747, 1748)	Novel Protein sim. GBank gi 134319 sp P07819 SCRB_BACSU - SUCROSE-8- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)		UNCLASSIFIED	284600
875	86808446 (1749, 1750)	Novel Protein sim. GBank gi 481000 pir S37594 - mucin - human (fragment)			284259, 284448, 284288, 284557, 87168518
876	88465157 (1751, 1752)	Novel Protein sim. GBank gi 3128283 (AF010496) - iron(iii) diclrate transport ATP-binding protein [Rhodobacter capsulatus]	Contains protein domain (PF00005) - ABC transporter	transport	264907, 264601, 264602, 284605, 265020, 60431602
877	87802548 (1753, 1754)	Novel Protein sim. GBank gi 731074 sp P40349 URB1_USTMA - SIDEROPHORE BIOSYNTHESIS REGULATORY PROTEIN URBS1	Contains protein domain (PF00320) - GATA zinc finger	transcriptfactor	22278998, 284908, 284369
878	80187289 (1755, 1756)	Novel Protein sim. GBank gi 1351614 sp Q09853 YAE_D_SCHPO - HYPOTHETICAL 181.5 KD PROTEIN C23D3.13C IN CHROMOSOME I		ATPase_associated	284369, 284555
879	94328862 (1757, 1758)	Novel Protein sim. GBank gi 3875304 emb CAA98434 - (Z74030) predicted using Genefinder; cDNA EST EMBL: C07808 comes from this gene; cDNA EST EMBL: C09023 comes from this gene; cDNA EST yk505e9.3 comes from this gene; cDNA EST yk489h9.3 comes from this gene; cDNA EST yk489h9.5 com...			56182575, 28331824, 264508, 264906, 285018, 18108351, 284448, 284883, 21908768, 21908768, 60170815, 33857023, 65274620, 33857109, 18108374, 35895855, 264563
880	8491135 (1759, 1760)	Novel Protein sim. GBank gi 137120 sp P11214 UROT_MOUSE - TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (TPA) (T- PLASMINOGEN ACTIVATOR)	Contains protein domain (PF00051) - Kringle domain	cathepsin	284508
881	11290122 (1761, 1762)			UNCLASSIFIED	264508
882	11077011 (1763, 1764)	Novel Protein sim. GBank gi 2632098 emb CAA75687 - (Y15513) Prodos protein [Drosophila melanogaster]		UNCLASSIFIED	284558
883	79582989 (1765, 1766)			UNCLASSIFIED	264688
884	13517921 (1767, 1768)	Novel Protein sim. GBank gi 115068 emb CAA84425 - (X94978) cell wall-plasma membrane linker protein [Brassica napus]		UNCLASSIFIED	264638
885	80052457 (1769, 1770)	Novel Protein sim. GBank gi 2078027 emb CAB08467 - (Z95208) hypothetical protein Rv2372c [Mycobacterium tuberculosis]		UNCLASSIFIED	264605, 18108382
886	11685138 (1771, 1772)				284690
887	94315307 (1773, 1774)	Novel Protein sim. GBank gi 2695834 emb CAA15904 - (AL021006) suCA [Mycobacterium tuberculosis]		dehydrogenase	35686052, 284908, 284600, 264603, 35695917, 35695855, 284638
888	10083389 (1775, 1776)	Novel Protein sim. GBank gi 5689395 dbj BAA82981.1 - (AB028952) KIAA1029 protein [Homo sapiens]		UNCLASSIFIED	284908
889	20385917 (1777, 1778)	Novel Protein sim. GBank gi 1881338 dbj BAA19365 - (AB001488) PROBABLE INTEGRAL MEMBRANE PROTEIN, SIMILAR TO CHLORAMPHENICOL RESISTANCE PROTEIN OF STREPTOMYCES VENEZUELAE. [Bacillus subtilis]			264603
890	19504337 (1779, 1780)	Novel Protein sim. GBank gi 854085 emb CAA58337 - (X83413) U88 [human herpesvirus 6]			284629

891	13516879 (1781, 1782)	Novel Protein sim. GBank gi 4959396 gb AAD34331.1 AF11248 - (AF112481) RAD54B protein [Homo sapiens]		UNCLASSIFIED	264636
892	87634157 (1783, 1784)	Novel Protein sim. GBank gi 545526 bbs 143833 - LBP. 1b=transcription factor binding to initiation site of HIV-1 (alternatively spliced) [human, Namakwa cells, Peptide, 541 aa]		transcriptfactor	22278986, 22278988, 29331828, 35686052, 264808, 264809, 265009, 265011, 264602, 265019, 264786, 21908765, 21908768, 21908769, 265020, 265021, 56526488 264689, 263967
893	79168037 (1785, 1786)	Novel Protein sim. GBank gi 2829888 sp P80608 CYSK_MAIZE - CYSTEINE SYNTHASE (O-ACETYL SERINE SULFHYDRYLASE) (O- ACETYL SERINE (THIOL)-LYASE) (CSASE)		synthase	
894	11102240 (1787, 1788)				263978
895	80239868 (1789, 1790)			UNCLASSIFIED	264508, 264600, 264555, 264559
896	79747803 (1791, 1792)				264632
897	94991823 (1793, 1794)		Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	264688, 29331828, 264511
898	87895109 (1795, 1796)				56182575, 60432289, 56182435, 60432229, 55811957, 22279000, 264488 264601
899	11100463 (1797, 1798)	Novel Protein sim. GBank gi 1750127 (U66480) - YncC [Bacillus subtilis]		transport	264769, 264691, 264563
900	80499788 (1799, 1800)				
901	80502410 (1801, 1802)	Novel Protein sim. GBank gi 312879 sp O07438 SYA_MYCTU - ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS)	Contains protein domain (PF01411) - tRNA synthetases class II (A)	synthase	264907, 264802, 264805, 264769, 35695917, 18108376, 264563
902	80503301 (1803, 1804)	Novel Protein sim. GBank gi 335570 emb CAA20001 - (AL031124) 3-Isopropylmalate dehydratase large subunit [Streptomyces coelicolor]	Contains protein domain (PF00330) - Aconitase family (aconitate hydratase)	isomerase	264909, 265008, 264602, 264604, 264769, 264689, 264693
903	82060206 (1805, 1806)	Novel Protein sim. GBank gi 2960120 emb CAA18018.1 - (AL022121) gipK [Mycobacterium tuberculosis]	Contains protein domain (PF00370) - FGY family of carbohydrate kinases	kinase	35696052, 264805, 264510, 264511, 264512, 264805, 264760, 18108351, 264762, 264687, 264768, 264769, 264688, 21908764, 35695917, 27466262, 35695855, 264634, 264638, 264486 264604
904	20451078 (1807, 1808)	Novel Protein sim. GBank gi 728887 sp P40906 ARGI_COCIM - ARGINASE	Contains protein domain (PF00491) - Arginase family	hydrolase	
905	9398483 (1809, 1810)	Novel Protein sim. GBank gi 4567200 gb AAD23616.1 AC00716 - (AC007169) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	264909
906	80052628 (1811, 1812)	Novel Protein sim. GBank gi 3738200 emb CAA21292 - (AL031855) putative vacuolar membrane protein [Schizosaccharomyces pombe]			264595, 264605
907	87913201 (1813, 1814)			UNCLASSIFIED	60432288, 264601, 264690
908	11754482 (1815, 1816)			UNCLASSIFIED	264638
909	20727907 (1817, 1818)	Novel Protein sim. GBank gi 3868940 db BAA34296 - (AB015054) Alg2 [Rhizomucor pusillus]		UNCLASSIFIED	264602
910	16775206 (1819, 1820)	Novel Protein sim. GBank gi 4589726 db BAA76883.1 - (AB003137) DnaJ homolog protein [Salix glauca]	Contains protein domain (PF00684) - DnaJ central domain (4 repeats)	eph	265009

911	87454340 (1821, 1822)	Novel Protein sim. GBank gil548774 sp P35885 RL7A_ORYSA - 80S RIBOSOMAL PROTEIN L7A		ribosomalprot	265010, 264604, 80432113
912	20448863 (1823, 1824)	Novel Protein sim. GBank gil2314008 gb AAD07921.1 - (AE00597) CDP-diglyceride hydrolase (cdh) [Helicobacter pylori 26895]		hydrolase	264559
913	20469357 (1825, 1826)				
914	79183351 (1827, 1828)	Novel Protein sim. GBank gil417657 sp Q03604 RIR1_CAEEL - PROBABLE RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CHAIN (RIBONUCLEOTIDE REDUCTASE)	Contains protein domain (PF00317) - Ribonucleotide reductase	UNCLASSIFIED reductase	264604 264636
915	87606703 (1829, 1830)	Novel Protein sim. GBank gil5689571 dbj BAA83069.1 - (AB029040) KIAA1117 protein [Homo sapiens]			18108398, 22278998, 66714117, 264908, 264591, 21906768, 265020, 55811576, 264638
916	79444091 (1831, 1832)	Novel Protein sim. GBank gil4188110 emb CAA71790 - (Y10831) putative integrase [Ralstonia eutropha]		UNCLASSIFIED	264595
917	20195985 (1833, 1834)				
918	91226795 (1835, 1836)	Novel Protein sim. GBank gil1655699 emb CAA69032 - (Y07752) pherophorin-S [Volvox carter]		UNCLASSIFIED synthase	264605 264259, 28331826, 264808, 265019, 264448, 265020, 264635, 83373044
919	80436785 (1837, 1838)	Novel Protein sim. GBank gil5689968 emb CAB52005.1 - (AL109663) putative membrane protein [Streptomyces coelicolor A3(2)]			265006, 264512, 264600, 264602, 264604, 264768, 18108370, 264563
920	79808095 (1839, 1840)	Novel Protein sim. GBank gil1168448 sp Q05813 AMP1_STRL1 - XAA-PRO AMINOPEPTIDASE I (X-PRO AMINOPEPTIDASE I) (AMINOPEPTIDASE P I) (APP) (PEPP I) (AMINOACYLPROLINE AMINOPEPTIDASE I)		peptidase	264508
921	19858634 (1841, 1842)	Novel Protein sim. GBank gil3850084 emb CAA21811.1 - (AL033388) alcohol dehydrogenase [Schizosaccharomyces pombe]		UNCLASSIFIED	264600
922	7982605 (1843, 1844)				265019, 22279002
923	86695830 (1845, 1846)	Novel Protein sim. GBank gil287079 sp P29514 TB86_ARATH - TUBULIN BETA-6 CHAIN		tubulin	264907, 265008, 265009, 265010, 18108351, 264689, 265021, 18108370, 18108374, 18108385
924	21431341 (1847, 1848)				264510
925	20630332 (1848, 1850)	Novel Protein sim. GBank gil2497688 sp Q60863 PAFA_MOUSE - PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (PAF ACETYLHYDROLASE) (PAF 2- ACYLHYDROLASE) (LDL-ASSOCIATED PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1- ALKYLGLYCEROPHOSPHOCHOLINE ESTERASE) (1- ALKYL-2-ACETYLGLYCEROPHO...		esterase	264603
926	79397657 (1851, 1852)	Novel Protein sim. GBank gil3882325 dbj BAA34522.1 - (AB018345) KIAA0802 protein [Homo sapiens]			55811957, 263972, 264639
927	37036201 (1853, 1854)			UNCLASSIFIED	264769

928	80070610 (1855, 1856)	Novel Protein sim. GBank gij156146 (M30316) - xanthine dehydrogenase (AA at 2538) [Calliphora vicina]		dehydrogenase	264605
929	20630336 (1857, 1858)			UNCLASSIFIED	264603
930	5496348 (1859, 1860)	Novel Protein sim. GBank gij4115936[gbjAAD03446.1] - (AF118223) No definition line found [Arabidopsis thaliana]			264258
931	10245731 (1861, 1862)	Novel Protein sim. GBank gij4490809[embjCAB38642.1] - (AJ133495) ribonucleotide reductase major subunit [Staphylococcus aureus]	Contains protein domain (PF00317) - Ribonucleotide reductase	reductase	264486
932	80420613 (1863, 1864)	Novel Protein sim. GBank gij5459398[embjCAB50754.1] - (AL086839) putative integral membrane transport protein [Streptomyces coelicolor]		transport	264508, 264905, 264906, 264909, 264600, 264602, 264603, 264605, 264766, 264558, 18108387, 264486
933	94326010 (1865, 1866)	Novel Protein sim. GBank gij5689523[dbjBAA83045.1] - (AB028016) KIAA1093 protein [Homo sapiens]	Contains protein domain (PF00827) - UBA domain	UNCLASSIFIED	264508, 264688, 264693, 27486261, 18108370, 65274791, 264636, 264559, 22279002
934	80039105 (1867, 1868)	Novel Protein sim. GBank gij119111[spjP12978]EBN2_EBV - EBNA-2 NUCLEAR PROTEIN			264369, 22279002
935	80063162 (1869, 1870)			UNCLASSIFIED	264604, 264605, 264693, 18108370, 18108374
936	80026632 (1871, 1872)	Novel Protein sim. GBank gij845686 (M32103) - ORF-27 [Staphylococcus aureus]		UNCLASSIFIED	22278995, 22278996, 264602, 264687, 32833986, 18108387
937	80250273 (1873, 1874)	Novel Protein sim. GBank gij1360669[pirjCGHU1V - collagen alpha 1(V) chain precursor - human]		synthase	263978
938	80026633 (1875, 1876)	Novel Protein sim. GBank gij2226243[embjCAA74531.1] - (Y14083) hypothetical protein [Bacillus subtilis]		UNCLASSIFIED	264602
939	11071694 (1877, 1878)				264600
940	94144252 (1879, 1880)	Novel Protein sim. GBank gij3560166[embjCAA20678] - (AL031525) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	264905, 264908, 264907, 264908, 264909, 264511, 264910, 264592, 33657402, 264596, 264758, 264760, 264683, 264768, 264768, 264769, 33657023, 33657109, 264628, 264629, 264630, 264635, 264636, 264555, 264637, 264556, 264638, 264639, 83373044, 18108385, 264565, 18108391
941	11398414 (1881, 1882)				264593
942	19484122 (1883, 1884)			UNCLASSIFIED	264760
943	80080258 (1885, 1886)	Novel Protein sim. GBank gij4033729 (AF038595) - apolipoprotein N-acyltransferase [Pseudomonas aeruginosa]		UNCLASSIFIED	264600, 264687, 264689, 264563
944	80218096 (1887, 1888)	Novel Protein sim. GBank gij2494764[spjQ50729]GUAA_MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)		synthase	264511, 264603
945	80052477 (1889, 1890)	Novel Protein sim. GBank gij732353[spjP39606]YWCH_BACSU - HYPOTHETICAL 36.6 KD PROTEIN IN QOXD-VPR INTERGENIC REGION	Contains protein domain (PF00818) - Ica nucleation protein repeat	UNCLASSIFIED	264906, 264604, 264605, 265020, 18108387
946	79248402 (1891, 1892)				265017

947	81802699 (1893, 1894)	Novel Protein sim. GBank gjl2896770[embjCAA17247] - (AL021898) hypothetical protein Rv2033c [Mycobacterium tuberculosis]	Contains protein domain (PF00459) - Inositol monophosphatase family	- phosphatase	18108394, 22278996, 264907, 264909, 265008, 265009, 264910, 264758, 264600, 264802, 265018, 264605, 264769, 264689, 264693
948	88165538 (1895, 1896)	Novel Protein sim. GBank gjl2827284 (AF041037) - novel antagonist of FGF signaling [Homo sapiens]		lgl	18108398, 56182575, 22278997, 22278999, 60432049, 29331822, 29331826, 264907, 56182435, 55811386, 265011, 264600, 265017, 265018, 265019, 18108351, 265020, 265021, 265022, 27486265, 263972, 55811576, 264638, 60170394, 264566
949	88081786 (1897, 1898)	Novel Protein sim. GBank gjl4507985[refjNP_003427.1]pZNF1 - zinc finger protein 135 (clone pHZ-17)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	29331825, 21906764, 27486261, 21908766, 52644286, 33657349, 87168518, 56994075, 265020, 265021, 87168559, 52644150, 264637
950	78485872 (1899, 1900)	Novel Protein sim. GBank gjl1079461[pirjS43865 - cytochrome b, type II - potaroo (fragment)]	Contains protein domain (PF00038) - Intermediate filament proteins	- struct	264683, 18108361
951	20451411 (1901, 1902)	Novel Protein sim. GBank gjl5420387[embjCAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264604
952	79566954 (1903, 1904)	Novel Protein sim. GBank gjl5305702[gbjAAD41779.1]AF12686 - (AF126867) calpain-like protease [Mus musculus]		cathepsin	264910, 264691
953	10186003 (1905, 1906)	Novel Protein sim. GBank gjl2495842[spjQ47142]YFHS_ECOLI - HYPOTHETICAL 41.8 KD PROTEIN IN CSIE-GLYA INTERGENIC REGION		transport	264510
954	9893326 (1907, 1908)	Novel Protein sim. GBank gjl2360985 (AF016253) - D-amino acid dehydrogenase [Klebsiella aerogenes]		dehydrogenase	264508
955	95313410 (1909, 1910)	Novel Protein sim. GBank gjl5454064[refjNP_008319.1]pSIP1 - SYT interacting protein	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	55994075, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264910, 264758, 264759, 265010, 264601, 264760, 18108351, 264762, 264763, 264764, 264766, 264686, 264767, 264687, 264768, 264769, 264689, 264628, 264629, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 56182323, 264639, 18108388, 264563, 264564
956	80064224 (1911, 1912)	Novel Protein sim. GBank gjl2052128[embjCAB08155] - (Z94752) rtmJ [Mycobacterium tuberculosis]			264605
957	80056208 (1913, 1914)			UNCLASSIFIED	264603, 18108362
958	80036446 (1915, 1916)	Novel Protein sim. GBank gjl1709767[spjQ00451]PRF1_LYCES - 38.4 KD PROLINE-RICH PROTEIN		UNCLASSIFIED	264908, 264910, 264762, 263978, 264637
959	80026647 (1917, 1918)	Novel Protein sim. GBank gjl2131050[embjCAB09260] - (Z95844) opca [Mycobacterium tuberculosis]		UNCLASSIFIED	264602, 264692
960	37815408 (1919, 1920)	Novel Protein sim. GBank gjl2129478[pirjS51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	264259
961	20567383 (1921, 1922)				263978
962	11399318 (1923, 1924)				264593

963	80590374 (1925, 1926)				UNCLASSIFIED	284510, 284288, 284555, 284556, 284559, 284488
964	78832019 (1927, 1928)	Novel Protein sim. GBank gi 4588622 dbj BAA76833.1 - (AB023206) KIAA0989 protein [Homo sapiens]			UNCLASSIFIED	284112, 284010, 284689
965	91228485 (1929, 1930)	Novel Protein sim. GBank gi 5420387 emb CAB46678.1 - (AJ243459) proteophosphoglycan [Leishmania major]			UNCLASSIFIED	284488, 285017, 284448, 284634, 284558, 83373044
966	95292815 (1931, 1932)				UNCLASSIFIED	284908, 284592, 284598, 284604, 284768, 21908764, 284892, 284893, 284628, 284638, 284638
967	79255708 (1933, 1934)	Novel Protein sim. GBank gi 1731207 sp Q11158 RGX3_MYCTU - SENSORY TRANSDUCTION PROTEIN REGX3	Contains protein domain (PF00072) - Response regulator receiver domain		phosphatase	284780
968	78560268 (1935, 1936)	Novel Protein sim. GBank gi 2661836 emb CAA75187 - (Y14864) putative transport protein [Methylophilus methylotrophus]			transport	284693
969	79919470 (1937, 1938)	Novel Protein sim. GBank gi 5418878 emb CAB46422.1 - (AL096747) hypothetical protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, C2H2 type		dna_ma_bind	35698286, 284885, 284886, 35695917, 284892, 18108374, 284835
970	95085947 (1939, 1940)				UNCLASSIFIED	18108382, 18108384, 18108388, 22278995, 22278996, 22278998, 22278999, 29147620, 284828, 285006, 265007, 265008, 285009, 18108348, 33109954, 265010, 285011, 18108351, 284288, 21908767, 21908768, 18108370, 18108374, 18108377, 284630, 284635, 18108380, 83373044, 18108387, 18108388
971	78919770 (1941, 1942)				UNCLASSIFIED	265007, 285020, 22279002
972	20710704 (1943, 1944)					284557
973	20370183 (1945, 1946)	Novel Protein sim. GBank gi 1723118 sp P53990 Y174_HUMAN - HYPOTHETICAL PROTEIN KIAA0174				284804
974	80057103 (1947, 1948)				UNCLASSIFIED	284565
975	10198018 (1949, 1950)				UNCLASSIFIED	284510
976	80205742 (1951, 1952)	Novel Protein sim. GBank gi 3881459 emb CAA92988.1 - (Z88753) predicted using GeneFinder; Similarly to Yeast hypothetical protein YIK9 (SW:YIK9_YEAST); cDNA EST EMBL:D27880 comes from this gene; cDNA EST EMBL:D27879 comes from this gene; cDNA EST EMBL:D84477 comes from this ge...			UNCLASSIFIED	284508, 284808, 284758, 284632, 284639, 284563
977	10355349 (1953, 1954)	Novel Protein sim. GBank gi 549458 sp Q05335 XYS3_PSEPU - XYLDLEGF OPERON TRANSCRIPTIONAL ACTIVATOR 3			UNCLASSIFIED	284906
978	80025927 (1955, 1956)				UNCLASSIFIED	284600, 284602, 284603, 284604
979	80447820 (1957, 1958)	Novel Protein sim. GBank gi 3171804 emb CAA75869 - (Y15908) DIA-12C protein [Homo sapiens]			UNCLASSIFIED	284767, 284768, 285008, 285007, 284808
980	80025928 (1958, 1960)				UNCLASSIFIED	284600, 284602, 284605
981	80098350 (1961, 1962)	Novel Protein sim. GBank gi 3599940 AF017388 - factogenital dysplasia protein 2 [Mus musculus]			UNCLASSIFIED	284692, 284555, 284556, 284557, 284558

982	80195670 (1963, 1964)	Novel Protein sim. GBank gj 2850220 emb CAA71575 - (Y10545) fused-ccdB [Escherichia coli]		UNCLASSIFIED	264404
983	90895041 (1965, 1966)	Novel Protein sim. GBank gj 476389 pir B43402 - myosin heavy chain-B, neuronal - chicken		struct	65274572, 56182575, 284908, 284908, 285007, 285008, 284758, 285010, 55811150, 33657023, 284634, 284557, 284558
984	20468676 (1967, 1968)			UNCLASSIFIED	284605
985	65461368 (1969, 1970)	Novel Protein sim. GBank gj 3451504 emb CAA07660.1 - (AJ007747) hypothetical protein BBLPS1.21 [Bordetella bronchiseptica]	Contains protein domain (PF00534) - Glycosyl transferases group 1	transferase	56182435, 284600
986	87102888 (1971, 1972)			UNCLASSIFIED	264108, 284110, 265020, 60170615
987	79867231 (1973, 1974)				284909
988	19858861 (1975, 1976)			UNCLASSIFIED	284600
989	88095329 (1977, 1978)			UNCLASSIFIED	284508, 265017, 284534, 284584
990	88057746 (1979, 1980)	Novel Protein sim. GBank gj 5725506 gb AAD48080.1 AF06015 - (AF060152) METH1 protein [Homo sapiens]	Contains protein domain (PF01421) - Reprolysin (M12B) family zinc metalloprotease	oxidase	264259, 284908, 265009, 284910, 284598, 264369, 284288, 284786, 284628, 284635, 284588
991	10106140 (1981, 1982)			UNCLASSIFIED	284909
992	79845694 (1983, 1984)	Novel Protein sim. GBank gj 2105049 emb CAB08835 - (Z95436) hypothetical protein Rv3845 [Mycobacterium tuberculosis]	Contains protein domain (PF00211) - Adenylate and Guanylate cyclase catalytic domain	UNCLASSIFIED	284508, 284593
993	10814053 (1985, 1986)				284907
994	11090590 (1987, 1988)	Novel Protein sim. GBank gj 3329297 (AE001355) - Ribonucleoside Reductase, Large Chain [Chlamydia trachomatis]		reductase	284602
995	94321911 (1989, 1990)	Novel Protein sim. GBank gj 5106572 gb AAD39760.1 AF14394 - (AF143946) transcriptional activator SRCAP [Homo sapiens]	Contains protein domain (PF00176) - SNF2 and others N-terminal domain	helicase	18108398, 65274572, 22278996, 264490, 60432049, 29331827, 29146498, 284508, 284905, 264907, 284908, 56182435, 265008, 284591, 284592, 60432229, 60431735, 33657402, 264585, 264758, 21806754, 265010, 265017, 265018, 264605, 284760, 284448, 284763, 284768, 21906765, 21906768, 21906769, 55811957, 284692, 284893, 284629, 35896423, 55811576, 35895855, 284638, 284555, 284556, 284558, 83373044, 22279002, 284583
996	91013745 (1991, 1992)	Novel Protein sim. GBank gj 2911719 (AC004227) - KIA001LB [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)	phosphatase	83373044, 29331824, 283978, 55811957, 56528486, 87168518, 284910, 284908, 284585, 264586, 284693, 284768
997	80503347 (1993, 1994)	Novel Protein sim. GBank gj 2649101 (AE001001) - ABC transporter, ATP-binding protein [Archaeoglobus fulgidus]	Contains protein domain (PF00005) - ABC transporter	transport	35696286, 22278997, 22278999, 284508, 284905, 284908, 265010, 284600, 284602, 284605, 284688, 284769, 265021, 284565, 18108391
998	11397390 (1995, 1996)	Novel Protein sim. GBank gj 123530 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR			284595

999	11768047 (1997, 1998)	Novel Protein sim. GBank gij2508897 sp P46490 YFCA_HAEIN - HYPOTHETICAL PROTEIN HI0198		UNCLASSIFIED	264682
1000	20727844 (1998, 2000)			UNCLASSIFIED	264602
1001	86673131 (2001, 2002)	Novel Protein sim. GBank gij2224689 dbj BAA20833 - (AB002377) KIAA0379 [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	kinase	60432048, 264907, 264908, 264511, 264603, 264683, 264684, 264687, 264689, 29146627, 21906769, 264692, 18108385, 22279000 265008, 264369, 265020
1002	80189603 (2003, 2004)	Novel Protein sim. GBank gij588121 sp P37709 TRHY_RABIT - TRICHOHYALIN		struc	
1003	17933491 (2005, 2006)				265019
1004	16314987 (2007, 2008)	Novel Protein sim. GBank gij854085 emb CAA58337 - (X83413) U88 [Human herpesvirus 8]			264635
1005	79617144 (2009, 2010)	Novel Protein sim. GBank gij114073 sp P07672 APT_ECOLI - ADENINE PHOSPHORIBOSYLTRANSFERASE (APRT)		UNCLASSIFIED	264508
1006	37815429 (2011, 2012)			UNCLASSIFIED	264259
1007	78620871 (2013, 2014)	Novel Protein sim. GBank gij4062979 dbj BAA36210.1 - (AB017138) epsilon subunit of malonate decarboxylase [Pseudomonas putida]		synthase	264905
1008	88094444 (2015, 2016)	Novel Protein sim. GBank gij2808807 emb CAA04607.1 - (AJ001206) putative trehalose synthase [Streptomyces coelicolor]		synthase	265007, 264802, 264605, 264760, 264636
1009	57451289 (2017, 2018)	Novel Protein sim. GBank gij3639077 (AF090113) - AMPA receptor binding protein [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	kinase	264102, 264288
1010	94872537 (2019, 2020)	Novel Protein sim. GBank gij3746332 (AF016307) - possible NADH-dependent oxidase, may function as a demethylase [Sinorhizobium meliloti]		dehydrogenase	264592
1011	85546916 (2021, 2022)	Novel Protein sim. GBank gij2342847 gb AAB88591.1 - (U90853) DHHC-domain-containing cysteine-rich protein [Homo sapiens]		UNCLASSIFIED	35696052, 264905, 264764, 264788, 35695917, 264628
1012	95294456 (2023, 2024)	Novel Protein sim. GBank gij3413411 emb CAA20272 - (AL031231) guanosine pentaphosphate synthetase/ polynucleotide nucleotidyltransferase [Streptomyces coelicolor]	Contains protein domain (PF00013) - KH domain	phosphorylase	35696052, 264905, 264600, 264501, 264602, 264605, 264762, 264766, 264768, 264689
1013	86085772 (2025, 2026)			UNCLASSIFIED	264591, 21908786
1014	86808028 (2027, 2028)				29331824, 265019, 265020

1015	95418879 (2029, 2030)	Novel Protein sim. GBank gij4159995 (AF063095) - SELIL [Mus musculus]	Contains protein domain (PF00040) - Fibronectin type II domain		22278994, 22278995, 56994075, 22278996, 22278999, 264259, 29331825, 29331828, 264907, 56182435, 264510, 264591, 264593, 80433358, 264594, 55812038, 264758, 21908754, 33657084, 265010, 264600, 265017, 265018, 265019, 18108351, 21908765, 21908766, 21908767, 21908768, 55811957, 265022, 33657023, 65274620, 33657182, 32833986, 18108370, 18108377, 55811576, 35698423, 264630, 22279000, 264565
1016	78559694 (2031, 2032)	Novel Protein sim. GBank gij2506969sp P41407 ACPD_ECOLI - ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE)		esterase	264688, 264693
1017	11069213 (2033, 2034)	Novel Protein sim. GBank gij5103943 dbj BAA79259.1 - (AP000059) 802aa long hypothetical oligopeptide-binding protein oppA [Aeropyrum pernix]	Contains protein domain (PF00498) - Bacterial extracellular solute-binding proteins, family 5	transport	264600
1018	80072430 (2035, 2036)	Novel Protein sim. GBank gij4493973 emb CAB39032.1 - (AL034559) predicted using hexExon; MAL3P7.14 (PFC0925w), Hypothetical protein, len: 489 aa [Plasmodium falciparum]			22278996, 28148627, 264563
1019	11703607 (2037, 2038)			UNCLASSIFIED	264686
1020	80234432 (2039, 2040)				264508, 264509, 264512, 264600, 264762, 264769, 264688, 18108370, 264636, 264638, 264486
1021	37036243 (2041, 2042)	Novel Protein sim. GBank gij4633807 gb AAD26859.1 AF12779 - (AF127795) trehalose biosynthetic enzyme TreY [Rhizobium leguminosarum bv. viciae]		synthase	264769
1022	80502627 (2043, 2044)	Novel Protein sim. GBank gij1781230 emb CAB06277 - (Z83867) hypothetical protein Rv3137 [Mycobacterium tuberculosis]	Contains protein domain (PF00459) - Inositol monophosphatase family	phosphatase	35696052, 264508, 265008, 265009, 264769, 18108387, 264563
1023	11399341 (2045, 2046)	Novel Protein sim. GBank gij3777495 (U92083) - calcium transporting ATPase [Pichia angusta]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase_associated	264593
1024	80057129 (2047, 2048)			UNCLASSIFIED	52846942, 33657402, 33657023, 18108379, 55811576, 264631, 264558, 264557, 264559, 18108388, 264566
1025	78644200 (2049, 2050)	Novel Protein sim. GBank gij3483045 emb CAA20556 - (AL031371) putative transport system permease protein [Streptomyces coelicolor]		transport	264693
1026	80025946 (2051, 2052)	Novel Protein sim. GBank gij1174922 sp Q02322 UVRD_HAEIN - DNA HELICASE II		helicase	264602
1027	17659234 (2053, 2054)	Novel Protein sim. GBank gij4757728 ref NP_004886.1 PAGTA - angiotensin vasopressin receptor AII/AVP-like		UNCLASSIFIED	265017

1028	20287828 (2055, 2056)	Novel Protein sim. GBank gi 2791409 emb CAA16003 - (AL021184) acn [Mycobacterium tuberculosis]	Contains protein domain (PF00330) - Aconitase family (aconitate hydratase)	UNCLASSIFIED	284600
1028	94665090 (2057, 2058)			UNCLASSIFIED	284595
1030	88095343 (2059, 2060)			UNCLASSIFIED	284907, 284908, 284510, 284512, 285009, 285010, 285011, 284600, 284602, 284603, 284605, 284769, 18108372, 18108374
1031	95289117 (2061, 2062)			UNCLASSIFIED	284805, 284808, 284909, 284595, 284692, 284630, 284634, 284638
1032	94673275 (2063, 2064)	Novel Protein sim. GBank gi 4503895 ref NP_000145.1 pGALK - galactokinase 1		UNCLASSIFIED	284689
1033	86464818 (2065, 2066)	Novel Protein sim. GBank gi 2982990 (AE000682) - hypothetical protein [Aquifex aeolicus]		UNCLASSIFIED	35896052, 264908, 264510, 18108354, 284687, 284769, 284689, 60431802, 18108385, 284486
1034	79245937 (2067, 2068)	Novel Protein sim. GBank gi 405895 (U00007) - methionyl-tRNA synthetase [Escherichia coli]		UNCLASSIFIED	284906
1035	79956355 (2069, 2070)			UNCLASSIFIED	284692
1036	85804998 (2071, 2072)				284905, 66712502, 284908, 284768
1037	87896058 (2073, 2074)			UNCLASSIFIED	28331824, 284909, 60433438, 285019
1038	20481015 (2075, 2076)	Novel Protein sim. GBank gi 790819 (L39891) - polycystic kidney disease-associated protein [Homo sapiens]	Contains protein domain (PF01477) - PLAT/LH2 domain		284604, 284634
1039	87260021 (2077, 2078)	Novel Protein sim. GBank gi 2605967 (AF030027) - 24 [Equine herpesvirus 4]		UNCLASSIFIED	264092, 264093, 264094, 264683, 264689, 263967
1040	80026840 (2079, 2080)	Novel Protein sim. GBank gi 2352095 (U97022) - DNA topoisomerase I [Ferdobacterium islandicum]	Contains protein domain (PF01131) - Prokaryotic DNA topoisomerase	isomerase	264595
1041	10156682 (2081, 2082)	Novel Protein sim. GBank gi 3256535 dbj BAA29218.1 - (AP000001) 301aa long hypothetical 2-phosphoglycerate kinase [Pyrococcus horikoshii]		kinase	284907
1042	11084375 (2083, 2084)	Novel Protein sim. GBank gi 2058299 emb CAA66953 - (X88309) ARI protein [Drosophila melanogaster]			264605
1043	80057138 (2085, 2086)	Novel Protein sim. GBank gi 1870167 emb CAA70125 - (Y08921) msik [Streptomyces reticuli]	Contains protein domain (PF00005) - ABC transporter	transport	264565, 284567
1044	80025952 (2087, 2088)			UNCLASSIFIED	265006, 284602, 265017
1045	52415482 (2089, 2090)	Novel Protein sim. GBank gi 5689890 emb CAB52053.1 - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)]			29331825, 284637
1046	11754862 (2091, 2092)	Novel Protein sim. GBank gi 954065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		helicase	264686
1047	37036258 (2093, 2094)	Novel Protein sim. GBank gi 421047 dbj BAA74535.1 - (AB019033) orfSA [Pseudomonas sp.]		UNCLASSIFIED	264769
1048	79186400 (2095, 2096)	Novel Protein sim. GBank gi 3413419 emb CAA20279 - (AL031232) hypothetical protein SC10H5.07 [Streptomyces coelicolor]	Contains protein domain (PF00220) - Neurohypophysial hormones, N-terminal Domain	UNCLASSIFIED	264687
1049	81755108 (2097, 2098)	Novel Protein sim. GBank gi 5051636 gb AAD38326.1 AF07372 - (AF073727) EH domain-binding mitotic phosphoprotein [Homo sapiens]		UNCLASSIFIED	284905, 284634
1050	79471521 (2099, 2100)			UNCLASSIFIED	284696

1051	80475471 (2101, 2102)			UNCLASSIFIED	18108374, 284769, 265010, 265011, 284601, 265009, 284604, 264605, 264636, 18108351, 284692
1052	82442982 (2103, 2104)	Novel Protein sim. GBank gi 3123275 sp P35136 SERA_BACSU - D-3-PHOSPHOGLYCERATE DEHYDROGENASE (PGDH)	Contains protein domain (PF00389) - D-isomer specific 2-hydroxyacid dehydrogenases	dehydrogenase	284508, 284762, 284687, 284486
1053	94851640 (2105, 2106)	Novel Protein sim. GBank gi 5441319 emb CAB46717.1 - (AL034386) dJ1158B12.1 (zinc finger, X-linked, duplicated A) [Homo sapiens]			284688, 18108374, 29331824, 83373044, 21908754, 52845156, 56182435, 284689, 29331827, 27488281, 35696052, 21908765, 35696423, 21908768, 56182575, 21908769, 55811957, 87168518, 35696286, 22278997, 285020, 265011, 265021, 265022, 265007, 265018, 22279000, 22279002, 264482, 264906, 52844150, 264909, 264288, 29331822, 52845080, 264786
1054	78580225 (2107, 2108)			UNCLASSIFIED	284688
1055	80594138 (2109, 2110)	Novel Protein sim. GBank gi 5052508 gb AAD38584.1 AF14560 - (AF145609) BcDNA.GH02833 [Drosophila melanogaster]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	284907, 284602, 284681, 264288, 21908768, 33857109, 55610784, 35695855, 284631
1056	17882319 (2111, 2112)	Novel Protein sim. GBank gi 3021676 dbj BAA25358 - (D86033) RNA polymerase sigma-70 factor [Pseudomonas fluorescens]		mapolymerase	264906
1057	85667216 (2113, 2114)	Novel Protein sim. GBank gi 1226281 (U50308) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	284682
1058	80376576 (2115, 2116)				284764
1059	84662754 (2117, 2118)	Novel Protein sim. GBank gi 1170016 sp P46808 GREA_MYCLE - TRANSCRIPTION ELONGATION FACTOR GREA (TRANSCRIPT CLEAVAGE FACTOR GREA)		transcriptfactor	35696052, 35695855, 285009, 284636
1060	79481169 (2119, 2120)	Novel Protein sim. GBank gi 2499087 sp Q09332 UGGG_DROME - UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)		glycoprotein	29146499, 284681, 264683, 264687
1061	11034025 (2121, 2122)	Novel Protein sim. GBank gi 90254 pir A28334 - protein-tyrosine-phosphatase (EC 3.1.3.48) Ly-5 precursor (B-cell variant) - mouse		phosphatase	284634
1062	39567937 (2123, 2124)	Novel Protein sim. GBank gi 3334200 sp Q49954 GCSP_SOLTU - GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN)		dehydrogenase	284593
1063	8490481 (2125, 2126)	Novel Protein sim. GBank gi 2499866 sp Q41226 PSE1_NICSY - PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E A)			264508
1064	78891783 (2127, 2128)	Novel Protein sim. GBank gi 82654 pir JA0086 - 10K zein precursor - maize			265007, 265008, 18108351, 18108385

1065	80021208 (2129, 2130)	Novel Protein sim. GBank gjl2120988[pir]S70682 - glycosyltransferase homolog - Bordetella pertussis		transferase	264600, 264602, 264689
1066	17898879 (2131, 2132)	Novel Protein sim. GBank gjl2506382[sp]P15042[DNLJ_ECOLI - DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (NAD+))		synthase	265009
1067	10132178 (2133, 2134)				264909
1068	82062057 (2135, 2136)	Novel Protein sim. GBank gjl4007689[emb]CAA22355] - (AL034443) putative oxidoreductase [Streptomyces coelicolor]	Contains protein domain (PF00248) - Aldo/keto reductase family	reductase	264688, 18108382, 264558, 264600, 264760
1069	83002954 (2137, 2138)	Novel Protein sim. GBank gjl4589484[dbj]BAA76770.1] - (AB023143) KIAA0928 protein [Homo sapiens]		UNCLASSIFIED	264604
1070	82101992 (2139, 2140)	Novel Protein sim. GBank gjl120304[sp]P15932[FLGK_SALTY - FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 (HAP1)		UNCLASSIFIED	264604, 264760
1071	20710589 (2141, 2142)	Novel Protein sim. GBank gjl1750397 (U81261) - glutamate synthase large subunit [Pseudomonas aeruginosa]		synthase	264602
1072	82356540 (2143, 2144)			UNCLASSIFIED	264687, 264688, 21908784, 35696052, 35695917, 35695855, 264600, 264601, 264602, 265009, 264605, 264508, 264905, 264690, 264906, 264762, 264628, 264768
1073	79814400 (2145, 2146)				264809
1074	80105992 (2147, 2148)	Novel Protein sim. GBank gjl477532[pir]A49175 - Motch B protein - mouse (fragment)	Contains protein domain (PF00008) - EGF-like domain	synthase	264806
1075	81850293 (2149, 2150)	Novel Protein sim. GBank gjl3893109[emb]CAA76940] - (Y17920) CALO protein [Drosophila melanogaster]		UNCLASSIFIED	56994075, 22278998, 264594, 264757, 264596, 265018, 265019, 264681, 264389, 264688, 265020, 18108364, 18108374
1076	80477264 (2151, 2152)	Novel Protein sim. GBank gjl1176203[sp]P46442[YHCM_ECOLI - HYPOTHETICAL 43.1 KD PROTEIN IN RPLM-HHOA INTERGENIC REGION (F375)		ATPase-associated	264769
1077	79831334 (2153, 2154)	Novel Protein sim. GBank gjl4033487[sp]Q44472[TUD4_AGRVI - PUTATIVE HYDROXYPYRUVATE REDUCTASE		kinase	264905
1078	20288874 (2155, 2156)			UNCLASSIFIED	264600
1079	80494518 (2157, 2158)	Novel Protein sim. GBank gjl3413828[emb]CAA20296] - (AL031260) hypothetical protein SC9A10.09 [Streptomyces coelicolor]		UNCLASSIFIED	18108394, 264769, 264634, 264636
1080	11767188 (2159, 2160)			UNCLASSIFIED	264684
1081	94747080 (2161, 2162)				83373044, 265019, 22278002, 264482, 18108351, 264882, 264908, 264693, 264487
1082	81490656 (2163, 2164)			UNCLASSIFIED	264758, 264768, 264769, 21908787, 284511, 284910, 264634, 264635, 264905, 264638, 264906, 264637, 264907, 264908, 264784, 264638, 20281089, 264766, 264595

1083	187446717 (2165, 2166)	Novel Protein sim. GBank gil1722945[sp]Q10523[Y01N_MYCTU - HYPOTHETICAL 44.6 KD PROTEIN CY427.23		UNCLASSIFIED	60424179, 284905, 284908, 284510, 60432229, 284759, 87188474, 284805, 284769, 284689, 18108384, 18108376, 35695855, 284636
1084	37789308 (2167, 2168)	Novel Protein sim. GBank gil18384[sp]P32057[WCAI_ECOLI - PUTATIVE COLANIC ACID BIOSYNTHESIS GLYCOSYL TRANSFERASE WCAI		UNCLASSIFIED	284769
1085	88475368 (2169, 2170)	Novel Protein sim. GBank gil1899190 (U90204) - heat shock protein 60 [Tsukamurella tyrosinosolvens]	Contains protein domain (PF00118) - eph TCP-1/cpn60 chaperonin family		60432229, 284687
1086	79608269 (2171, 2172)	Novel Protein sim. GBank gil172956[sp]P46176[RL14_ACYKS - 50S RIBOSOMAL PROTEIN L14	Contains protein domain (PF00238) - Ribosomal protein L14	ribosomal prot	284486
1087	79603979 (2173, 2174)	Novel Protein sim. GBank gil160198[emb]CAA15431 - (AL008563) dJ327J16.3 (novel CHROMObox family protein) [Homo sapiens]	Contains protein domain (PF00385) - 'chromo' (CHROMatin Organization Modifier) domain	helicase	29331827, 284693
1088	79854963 (2175, 2176)	Novel Protein sim. GBank gil2983155 (AE000693) - phosphoglucosyltransferase/phosphomannomutase [Aquifex aeolicus]		UNCLASSIFIED	284905, 284601, 18108387
1089	80216800 (2177, 2178)	Novel Protein sim. GBank gil4981768[gb]AAD36290.1[AE00177 - (AE001778) NADH dehydrogenase, 30 kDa subunit, putative [Thermotoga maritima]	Contains protein domain (PF00329) - Respiratory-chain NADH dehydrogenase, 30 Kd subunit	UNCLASSIFIED	284488, 284511, 265011, 284682, 284768, 284689, 21808764, 35695917, 265020, 32833986, 18108370, 35695855
1090	11083825 (2179, 2180)	Novel Protein sim. GBank gil4007680[emb]CAA22366 - (AL034443) putative oxidoreductase [Streptomyces coelicolor]			264604
1091	12917471 (2181, 2182)	Novel Protein sim. GBank gil2485562[sp]P77239[YLCD_ECOLI - HYPOTHETICAL 44.3 KD PROTEIN IN NFRB-PHEP INTERGENIC REGION PRECURSOR		UNCLASSIFIED	264637
1092	80252286 (2183, 2184)				264566
1093	80496304 (2185, 2186)	Novel Protein sim. GBank gil2860099[emb]CAA17996.1 - (AL022121) mth [Mycobacterium tuberculosis]	Contains protein domain (PF00730) - Endonuclease III	nuclease	284769, 35695917, 35695855, 284600, 284602, 284803, 284605, 18108351
1094	10880972 (2187, 2188)	Novel Protein sim. GBank gil1001642[dbj]BAA10373 - (D84002) dGTP triphosphohydrolase [Synechocystis sp.]		UNCLASSIFIED	284686
1095	87457250 (2189, 2190)	Novel Protein sim. GBank gil4585587[emb]CAB40855.1 - (AL049828) putative adenine glycosylase [Streptomyces coelicolor]	Contains protein domain (PF00455) - Bacterial regulatory proteins, deoR family	nuclease	284906, 285007, 284595, 284600, 284602, 284603, 284604, 284805, 284762, 284768, 284769, 284636, 284558, 18108387, 60432113, 284482, 284486
1096	80025977 (2191, 2192)	Novel Protein sim. GBank gil115001[sp]P19206[BIOB_BACSH - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)]		synthase	284600, 284602, 284603, 284604, 284605, 35695917, 284692, 284631
1097	79239560 (2193, 2194)			UNCLASSIFIED	265019
1098	79186424 (2195, 2196)	Novel Protein sim. GBank gil114135[sp]P08205[JARGA_ECOLI - AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS)]		synthase	284687

1089	38523838 (2197, 2198)	Novel Protein sim. GBank gi 3915144 sp O33017 TRMD_MYCLE - TRNA (GUANINE- N1)-METHYLTRANSFERASE (M1G- METHYLTRANSFERASE) (TRNA [GM37] METHYLTRANSFERASE)		UNCLASSIFIED	264603
1100	85736571 (2199, 2200)	Novel Protein sim. GBank gi 3023255 sp O84420 ACOD_MESAU - ACYL-COA DESATURASE (STEAROYL-COA DESATURASE) (FATTY ACID DESATURASE) (DELTA(9)-DESATURASE)		desaturase	284259, 284636
1101	80491857 (2201, 2202)	Novel Protein sim. GBank gi 1174735 sp P43012 TOP1_HAEIN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SMIVELASE)	Contains protein domain (PF01398) - Topoisomerase DNA binding C4 zinc finger	isomerase	264769
1102	79777614 (2203, 2204)			UNCLASSIFIED	264910, 264909
1103	81897259 (2205, 2206)	Novel Protein sim. GBank gi 1908598 (U81788) - kinesin-73 [Drosophila melanogaster]		struc	264757
1104	95003115 (2207, 2208)	Novel Protein sim. GBank gi 2835448 (AF048976) - synaptic ras GTPase-activating protein p135 SynGAP [Rattus norvegicus]		UNCLASSIFIED	29331822, 21906754, 264555, 264556, 264558, 22278002
1105	80255121 (2209, 2210)				264566
1106	79314110 (2211, 2212)			UNCLASSIFIED	264555, 284369
1107	80470019 (2213, 2214)				284908, 284769
1108	80440618 (2215, 2216)	Novel Protein sim. GBank gi 1173421 sp P43416 SECY_STRSC - PREPROTEIN TRANSLOCASE SECY SUBUNIT		transport	264807, 284510, 264511, 284600, 284602, 264605, 284768, 284769
1109	80064615 (2217, 2218)	Novel Protein sim. GBank gi 2895310 emb CAA18338 - (AL022288) putative ATP-dependent helicase [Streptomyces coelicolor]		helicase	284602, 284605, 284638
1110	80503554 (2219, 2220)				284908, 284593, 285010, 284601, 284603, 284604, 284605, 284682, 284769, 284693, 284638
1111	80071744 (2221, 2222)	Novel Protein sim. GBank gi 2622039 (AE000868) - type I restriction modification system, subunit S [Methanobacterium thermoautotrophicum]			18108370, 264557
1112	95010088 (2223, 2224)				284908
1113	82458352 (2225, 2226)	Novel Protein sim. GBank gi 3218376 emb CAA19828 - (AL023882) putative oxidoreductase [Streptomyces coelicolor]		UNCLASSIFIED	284600, 284602, 284604, 284605, 284762, 284769, 284565
1114	14988014 (2227, 2228)	Novel Protein sim. GBank gi 1083428 pir J54876 - NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) precursor - mouse		dehydrogenase	264636
1115	11765583 (2229, 2230)				
1116	79841152 (2231, 2232)			UNCLASSIFIED	284686
					264908

1117	95305465 (2233, 2234)	Novel Protein sim. GBank gi 3255965 emb CAA94089 - (Z70200) U5 snRNP-specific 200kD protein [Homo sapiens]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	UNCLASSIFIED	18108392, 264488, 263994, 264489, 18108398, 56182575, 22278995, 22278996, 35698286, 56994075, 22278997, 22278998, 22278999, 264259, 29331822, 56182181, 29331824, 86714117, 29331825, 29331826, 60432288, 29331827, 29331828, 35698052, 33656970, 28146498, 264508, 264905, 264509, 264906, 264907, 264908, 68712502, 264909, 52644045, 56182435, 264510, 264511, 265006, 265007, 264512, 265008, 265009, 264910, 60170831, 264591, 264592, 264593, 60433356, 264594, 60433438, 264595, 55812038, 264596, 264758, 264759, 21906754, 33109954, 33857084, 265011, 87188559, 284800, 264601, 264602, 264603, 265017, 264604, 265018, 264605, 265019, 264760, 55811150, 264681, 264762, 18108351, 264448, 264682, 264784, 264683, 264288, 264369, 264684, 264685, 264766, 264767, 264686, 264687, 264768, 264769, 264688, 18108359, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 29148784, 35695917, 265020, 265021, 265022, 60170615, 264690, 264691, 33657023, 264692, 264693, 65274620, 33657109, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 264691
1118	79563328 (2235, 2236)			UNCLASSIFIED	
1119	79642463 (2237, 2238)			UNCLASSIFIED	
1120	79480463 (2239, 2240)	Novel Protein sim. GBank gi 5420387 emb CAB46678.1 - (AJ243459) proteophosphoglycan [Leishmania major]		collagen	29331827, 265018, 265019, 264681, 265021, 60170615, 18108387
1121	79471716 (2241, 2242)	Novel Protein sim. GBank gi 1644450 (U67864) - MEX-3 [Caenorhabditis elegans]	Contains protein domain (PF00013) - KH domain	UNCLASSIFIED	264683, 264632, 18108388
1122	79456246 (2243, 2244)			UNCLASSIFIED	
1123	79637119 (2245, 2246)	Novel Protein sim. GBank gi 98800 pir S17768 - 3-dehydroquinase synthase (EC 4.8.1.3) - Mycobacterium tuberculosis		synthase	264639, 264563, 264693, 27486265
1124	79811596 (2247, 2248)			UNCLASSIFIED	
1125	79757861 (2249, 2250)			UNCLASSIFIED	
1126	79758914 (2251, 2252)	Novel Protein sim. GBank gi 138154 sp P03843 VGG_BPPHX - MAJOR SPIKE PROTEIN (G PROTEIN) (GPG)		eph	264909, 264910, 264905, 264909, 264910
1127	11800930 (2253, 2254)			UNCLASSIFIED	
1128	8364885 (2255, 2256)	Novel Protein sim. GBank gi 5002704 emb CAB44358.1 - (AJ242630) DNA polymerase I [Methylobacterium sp. DM4]	Contains protein domain (PF00476) - DNA polymerase family A	UNCLASSIFIED	264692, 264511

1129	80422480 (2257, 2258)	Novel Protein sim. GBank gi 5689485 dbj BAA83026.1 - (AB028997) KIAA1074 protein [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	265011, 264766
1130	79420151 (2259, 2260)	Novel Protein sim. GBank gi 4981328 gb AAD35881.1 AE00174 - (AE001747) bioY protein [Thermotoga maritima]		UNCLASSIFIED	264595
1131	80055391 (2261, 2262)	Novel Protein sim. GBank gi 1841552 (U89336) - unknown [Homo sapiens]		UNCLASSIFIED	35998288, 22278998, 29331828, 264603, 264605, 264559
1132	82062248 (2263, 2264)			UNCLASSIFIED	22278998, 264806, 265009, 264600, 264602, 264804, 264605, 264760, 32833986, 18108374
1133	17290437 (2265, 2266)			UNCLASSIFIED	265018
1134	80235376 (2267, 2268)			UNCLASSIFIED	264512, 264534
1135	80029393 (2269, 2270)	Novel Protein sim. GBank gi 4539171 emb CAB39700.1 - (AL048485) conserved hypothetical protein [Streptomyces coelicolor]			264508, 264600, 264602, 264603, 18108376
1136	79842052 (2271, 2272)	Novel Protein sim. GBank gi 4982454 gb AAD36931.1 AE00182 - (AE001823) ATP-dependent protease LA, putative [Thermotoga maritima]		UNCLASSIFIED	264906, 264908
1137	90931557 (2273, 2274)	Novel Protein sim. GBank gi 4972746 gb AAD34768.1 - (AF132180) unknown [Drosophila melanogaster]	Contains protein domain (PF00515) - TPR Domain		22278998, 22278999, 35696052, 264907, 265009, 60433356, 264598, 265010, 264448, 264682, 264767, 264689, 265020, 264692, 55011576, 35695855, 264631, 264632, 22279002
1138	79841163 (2275, 2276)	Novel Protein sim. GBank gi 731807 sp P38739 YHC8_YEAST - HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR	strud		264908
1139	79833561 (2277, 2278)	Novel Protein sim. GBank gi 3650031 (AC005396) - putative proline-rich cell wall protein [Arabidopsis thaliana]	UNCLASSIFIED		264693
1140	39480358 (2279, 2280)		UNCLASSIFIED		264593
1141	79638019 (2281, 2282)		UNCLASSIFIED		265019, 264693
1142	19835848 (2283, 2284)		UNCLASSIFIED		264631
1143	87762158 (2285, 2286)	Novel Protein sim. GBank gi 3928000 emb CAA05880 - (AJ003125) procollagen I N-proteinase [Homo sapiens]	Contains protein domain (PF00090) - Thrombospondin type 1 domain		56182575, 264908, 264600, 264632, 87168518
1144	80088988 (2287, 2288)		UNCLASSIFIED		264635, 264636, 264907, 264593, 264908, 264588, 264909
1145	14610262 (2289, 2290)		UNCLASSIFIED		264112
1146	82062092 (2291, 2292)		UNCLASSIFIED		264769, 264689, 35696286, 264760, 264905, 264488, 264559
1147	80071761 (2293, 2294)				264557
1148	80048433 (2295, 2296)	Novel Protein sim. GBank gi 2499003 sp P76422 THID_ECOLI - PHOSPHOMETHYL-PYRIMIDINE KINASE (HMP-PHOSPHATE KINASE) (HMP-P KINASE)	kinase		264591
1149	11607438 (2297, 2298)	Novel Protein sim. GBank gi 2896734 emb CAA17213.1 - (AL021897) hypothetical protein Rv1097c [Mycobacterium tuberculosis]			264591

1150	81325074 (2289, 2300)	Novel Protein sim. GBank gi 2895095 (AF011337) - putative E1-E2 ATPase [Mus musculus]			ATPase associated	264488, 35698286, 264907, 264908, 264909, 264910, 264593, 264596, 264758, 264764, 264766, 264768, 264693, 264628, 60431850, 264564, 264566, 264567
1151	80070874 (2301, 2302)	Novel Protein sim. GBank gi 4324655 gb AAD16978 - (AF108191) DNA polymerase III alpha subunit [Streptomyces coelicolor]			polymerase	264595
1152	80235547 (2303, 2304)	Novel Protein sim. GBank gi 3874275 emb CAB07311.1 - (Z92825) predicted using GeneFinder; Similarity to Yeast low affinity glucose transporter HXT4 (PS:32467); cDNA EST EMBL: C12555 comes from this gene; cDNA EST yk404c10.3 comes from this gene; cDNA EST yk404c10.5 comes from thi...			glycoprotein	264488, 22278988, 264905, 264629, 264486
1153	80027783 (2305, 2306)					
1154	83002995 (2307, 2308)	Novel Protein sim. GBank gi 4240315 dbj BAA74938.1 - (AB020720) KIAA0913 protein [Homo sapiens]			UNCLASSIFIED	264910, 264555, 264557
1155	79411098 (2309, 2310)					
1156	57147843 (2311, 2312)	Novel Protein sim. GBank gi 586855 sp P37617 ATZN_ECOLI - ZINC-TRANSPORTING ATPASE (ZN(II)-TRANSLOCATING P-TYPE ATPASE)		Contains protein domain (PF00122) - E1-E2 ATPase	UNCLASSIFIED	264690, 264636
1157	95287711 (2313, 2314)	Novel Protein sim. GBank gi 418480 sp P32139 YIHR_ECOLI - HYPOTHETICAL 34.0 KD PROTEIN IN GLNA-RBN INTERGENIC REGION			UNCLASSIFIED	264908, 264907, 264758, 264766, 264769, 264689, 264636, 264566
1158	82454917 (2315, 2316)	Novel Protein sim. GBank gi 248648 sp Q50724 Y08S_MYCTU - HYPOTHETICAL 87.3 KD PROTEIN CY78.27C				264906, 264762, 264687, 264769, 264689, 18108374, 35695855
1159	79188451 (2317, 2318)					264687
1160	91229893 (2319, 2320)	Novel Protein sim. GBank gi 1138408 dbj BAA11490 - (D79995) similar to plg tubulin-tyrosine ligase. [Homo sapiens]				29331822, 29331824, 66714117, 29331826, 60433356, 265018, 265019, 63373044, 18108385, 22279000, 22279002, 264563
1161	7417143 (2321, 2322)					264369
1162	79635357 (2323, 2324)	Novel Protein sim. GBank gi 2443342 dbj BAA22380 - (D88764) alpha 2 type I collagen [Rana catesbeiana]			UNCLASSIFIED	264693
1163	79563186 (2325, 2326)	Novel Protein sim. GBank gi 4503375 ref NP_001376.1 pDPYS - dihydropyrimidinase			UNCLASSIFIED	29331827, 264808
1164	79650829 (2327, 2328)	Novel Protein sim. GBank gi 5052554 gb AAD38607.1 AF14563 - (AF145632) BcDNA.GH06032 [Drosophila melanogaster]			transport	18108398, 29331827, 29331828, 29146498, 29148499, 18108354, 21908768, 29148627, 21908769, 264693, 18108382, 18108385
1165	80491888 (2329, 2330)				UNCLASSIFIED	264802, 264805, 264769, 18108370, 18108374, 264565
1166	88086456 (2331, 2332)	Novel Protein sim. GBank gi 4589476 dbj BAA76766.1 - (AB023139) KIAA0922 protein [Homo sapiens]				264488, 35698286, 22278989, 264259, 66714117, 60432289, 35698052, 264905, 56182435, 265006, 60433438, 264759, 21906754, 33109954, 265017, 265019, 264448, 264288, 264766, 264685, 35698423, 35695855, 264558, 18108385, 60432113

1167	79963862 (2333, 2334)	Novel Protein sim. GBank gj2580433[dbj]BAA23138[(D76414) ppGpp hydrolase [Staphylococcus aureus]		kinase	264488
1168	88094678 (2335, 2336)			UNCLASSIFIED	264259, 29331827, 56182435, 80433438, 265019, 33657023, 35695855, 284586
1169	11805403 (2337, 2338)			UNCLASSIFIED	264681
1170	21832244 (2338, 2340)			UNCLASSIFIED	264602
1171	20434582 (2341, 2342)	Novel Protein sim. GBank gj2772814 (AF028249) - procollagen D [Mytilus edulis]		UNCLASSIFIED	264556
1172	79610113 (2343, 2344)	Novel Protein sim. GBank gj4757846[ref]NP_004317.1[pBCL9 - B-cell CLL/lymphoma 9		UNCLASSIFIED	55810764, 35696052, 264634, 264488
1173	80235713 (2345, 2346)	Novel Protein sim. GBank gj2564053[dbj]BAA22946[- (AB007832) Bm trachealless [Bombyx mori]			264508, 264806, 264907, 264809, 264591, 264632, 264638, 264639
1174	20283077 (2347, 2348)	Novel Protein sim. GBank gj2911027[emb]CAA17520[- (AL021858) mmsA [Mycobacterium tuberculosis]		dehydrogenase	264600
1175	20711847 (2349, 2350)	Novel Protein sim. GBank gj118333[sp]P23234[DCIP_ENTCL - INDOLE-3- PYRUVATE DECARBOXYLASE (INDOLEPYRUVATE DECARBOXYLASE)	Contains protein domain (PF00205) - Thiamine pyrophosphate enzymes	carboxylase	264601
1176	80252845 (2351, 2352)	Novel Protein sim. GBank gj1144520 (U34956) - phosphoribosylformylglycinamide synthase [Mycobacterium tuberculosis]	Contains protein domain (PF00586) - AIR synthase related protein	synthase	264509, 264805, 264593, 264602, 264605
1177	80064647 (2353, 2354)	Novel Protein sim. GBank gj118791[sp]P28643[FABG_CUPLA - 3-OXOACYL-ACYL- CARRIER PROTEIN] REDUCTASE PRECURSOR (3- KETOACYL-ACYL CARRIER PROTEIN REDUCTASE)	Contains protein domain (PF00106) - short chain dehydrogenase	reductase	264605
1178	94128641 (2355, 2356)	Novel Protein sim. GBank gj5031697[ref]NP_005594.1[pFIC1 - familial intrahepatic cholestasis 1, (progressive, Byler disease and benign recurrent)]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase-associated	65274572, 18108398, 22278998, 22278999, 29331826, 264508, 264908, 264828, 33657402, 33108954, 264769, 21906765, 21908766, 21908768, 55811957, 33857023, 264629, 55811576, 35696423, 264636, 264556, 56182323, 60432113, 22279000, 22279002
1179	80055575 (2357, 2358)	Novel Protein sim. GBank gj2980090[emb]CAA17888.1[- (AL022121) dppA [Mycobacterium tuberculosis]	Contains protein domain (PF00496) - Bacterial extracellular solute-binding proteins, family 5	transport	264603
1180	11794446 (2359, 2360)	Novel Protein sim. GBank gj2558814[emb]CAA04787[- (AJ001493) dehydroquinase dehydratase [Streptomyces coelicolor]	Contains protein domain (PF01220) - Dehydroquinase class II	synthase	264638
1181	17946362 (2361, 2362)			UNCLASSIFIED	265017
1182	81494284 (2363, 2364)	Novel Protein sim. GBank gj5420387[emb]CAB46679.1[- (AJ243459) proteophosphoglycan [Leishmania major]			265007, 265009, 264584, 264909, 264693
1183	79574044 (2365, 2366)				264689, 35696423, 264638, 18108385
1184	52559933 (2367, 2368)	Novel Protein sim. GBank gj4091877 (AF061331) - alpha galactosidase precursor [Saccharopolyspora erythraea]	UNCLASSIFIED		264602
1185	79491185 (2369, 2370)	Novel Protein sim. GBank gj2129478[pir]SS1839 - chitinase [EC 3.2.1.14] precursor - beet	glycoprotein		263967

1186	20224012 (2371, 2372)				UNCLASSIFIED	264559	
1187	78248834 (2373, 2374)				UNCLASSIFIED	29331825, 265017, 18108351	
1188	78831387 (2375, 2376)	Novel Protein sim. GBank gi 2996039 (AF054525) - hypothetical protein [Synecococcus PCC7002]			UNCLASSIFIED	264905, 264908	
1189	79609367 (2377, 2378)					264692	
1190	78930589 (2379, 2380)				UNCLASSIFIED	265018	
1191	80310105 (2381, 2382)				UNCLASSIFIED	264600, 264605, 264764, 35695855, 264638, 264486	
1192	13521641 (2383, 2384)			Contains protein domain (PF01581) - FMRamide related peptide family		264636	
1193	11103584 (2385, 2386)				UNCLASSIFIED	263978	
1194	78893947 (2387, 2388)	Novel Protein sim. GBank gi 854085 emb CAA58337 - (X83413) U88 [human herpesvirus 8]			UNCLASSIFIED	265007, 265008	
1195	20445442 (2389, 2390)	Novel Protein sim. GBank gi 1790277 (AE000459) - putative oxidoreductase [Escherichia coli]			UNCLASSIFIED	264605	
1196	13000888 (2391, 2392)					264689	
1197	11392317 (2393, 2394)	Novel Protein sim. GBank gi 2497380 sp Q50715 IMDH_MYCTU - INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (IMP DEHYDROGENASE) (IMPDH) (IMPD)		Contains protein domain (PF00571) - CBS domain		264594	
1198	95280101 (2395, 2396)					264603	
1199	81882011 (2397, 2398)	Novel Protein sim. GBank gi 1709525 sp P54673 P3K1_DICDI - PHOSPHATIDYLINOSITOL 3-KINASE 1 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)				264258, 264757, 33109954, 21908768	
1200	9848880 (2399, 2400)				UNCLASSIFIED	264910	
1201	80503751 (2401, 2402)	Novel Protein sim. GBank gi 2499877 sp P70645 BLMH_RAT - BLEOMYCIN HYDROLASE (BLM HYDROLASE) (BMH)			cathepsin	264766, 264769	
1202	80082633 (2403, 2404)	Novel Protein sim. GBank gi 506342 (U18997) - ORF_0622; reading frame open far upstream of start; possible frameshift, linking to previous ORF [Escherichia coli]			ribosomalprot	264600, 264558	
1203	82123373 (2405, 2406)				UNCLASSIFIED	264768, 264769, 35695917, 284910, 264760, 264908, 264907, 264629, 264908, 264909, 264768	
1204	80503916 (2407, 2408)	Novel Protein sim. GBank gi 2500728 sp Q59912 SECY_STRGB - PREPROTEIN TRANSLOCASE SECY SUBUNIT				264905, 264769, 264636	
1205	80053861 (2409, 2410)				UNCLASSIFIED	264566	
1206	80241865 (2411, 2412)				UNCLASSIFIED	264556, 264557, 264558	
1207	79841192 (2413, 2414)					29331824, 284908, 265021, 18108370	
1208	87755217 (2415, 2416)	Novel Protein sim. GBank gi 2645560 (AF027954) - Bcl-2-related ovarian killer protein [Rattus norvegicus]		Contains protein domain (PF00452) - Apoptosis regulator proteins, Bcl-2 family	apoptosis	29331824, 29331825, 29331827, 265007, 264784, 264683, 264769, 264688, 264689	

1209	79185742 (2417, 2418)	Novel Protein sim. GBank gi 1175033 sp P44398 XYLA_HAEIN - XYLOSE ISOMERASE	Contains protein domain (PF00259) - Xylose isomerase	isomerase	264687, 264688
1210	58426884 (2419, 2420)	Novel Protein sim. GBank gi 421095 pir J30688 - hypothetical protein o248 - Escherichia coli		UNCLASSIFIED	264607, 264693
1211	94665655 (2421, 2422)	Novel Protein sim. GBank gi 3880625 emb CAB07858 - (Z93785) predicted using Genefinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST EMBL: T01682 comes from this gene; cDNA EST EMBL: M75823 comes from this gene; cDNA EST EMBL: D27559 comes from this ge...	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	transferase	264591, 264592, 264585
1212	79167929 (2423, 2424)	Novel Protein sim. GBank gi 3880625 emb CAB07858 - (Z93785) predicted using Genefinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST EMBL: T01682 comes from this gene; cDNA EST EMBL: M75823 comes from this gene; cDNA EST EMBL: D27559 comes from this ge...			264689, 263967
1213	79859633 (2425, 2426)	Novel Protein sim. GBank gi 226292 pir J1505375A - vlr gene [Bordetella pertussis]		kinase	264909
1214	10144306 (2427, 2428)	Novel Protein sim. GBank gi 5726285 gb AA048398.1 AF12616 - (AF126162) HERV-H LTR associating protein 2 [Homo sapiens]		UNCLASSIFIED	264908
1215	80050108 (2429, 2430)	Novel Protein sim. GBank gi 2326739 emb CAB10953 - (Z98266) recN [Mycobacterium tuberculosis]		UNCLASSIFIED	265009, 264801, 264802, 264603, 33857109
1216	20438324 (2431, 2432)	Novel Protein sim. GBank gi 417328 sp P33038 MURA_ENTCL - UDP-N- ACETYLGLUCOSAMINE 1- CARBOXYVINYLTRANSFERASE (ENOYLPIRUVATE TRANSFERASE) (UDP-N-ACETYLGLUCOSAMINE ENOLPYRUVYL TRANSFERASE) (EPT)		transferase	264604
1217	95011344 (2433, 2434)			UNCLASSIFIED	264905, 264907, 264908, 264591, 264766, 264691, 264693, 264629, 264630, 264636, 264584
1218	11093680 (2435, 2436)	Novel Protein sim. GBank gi 1805460 dbj BAA09022 - (D50453) homologue of succinate semialdehyde dehydrogenase GabD of E. coli [Bacillus subtilis]		dehydrogenase	264601
1219	91216252 (2437, 2438)				56181686, 29331822, 80432289, 264601, 264692, 264629
1220	91241524 (2439, 2440)	Novel Protein sim. GBank gi 4240315 dbj BAA74938.1 - (AB020720) KIAA0913 protein [Homo sapiens]		oncogene	52644507, 264905, 264909, 265008, 265019, 265020, 52644150, 33857023, 264693, 33857182, 35895763, 264634, 22279000, 22279002, 264482
1221	83045055 (2441, 2442)	Novel Protein sim. GBank gi 2143886 pir J52523 - nucleoporin p82 homologue - rat (fragment)		UNCLASSIFIED	264768, 265020, 264906
1222	20711865 (2443, 2444)	Novel Protein sim. GBank gi 730805 sp P39663 SPHR_SYNTP7 - ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY PROTEIN SPHR	Contains protein domain (PF00486) - Transcriptional regulatory protein, C terminal	phosphatase	264601
1223	11615647 (2445, 2446)				264593
1224	80432845 (2447, 2448)	Novel Protein sim. GBank gi 1172627 sp P46546 PROB_CORGL - GLUTAMATE 5- KINASE (GAMMA-GLUTAMYL KINASE) (GK)	Contains protein domain (PF01472) - PUA domain	kinase	264593, 264600, 264601, 264603, 264605, 264768, 18108376, 264635, 18108387

1225	80434427 (2449, 2450)	Novel Protein sim. GBank gij2105050[emb]CAB08836] - (Z95436) hypothetical protein RV3844c [Mycobacterium tuberculosis]			264788
1226	80237518 (2451, 2452)			polymerase	264805, 264512, 264889
1227	79422138 (2453, 2454)	Novel Protein sim. GBank gij1708788[sp]P98133[FBN1_BOVIN - FIBRILLIN 1 PRECURSOR (MP340)]		UNCLASSIFIED	264908, 264637, 264639
1228	79209027 (2455, 2456)	Novel Protein sim. GBank gij1653801[dbj]BAA18811] - (D90917) acriflavine resistance protein [Synechocystis sp.]	Contains protein domain (PF00873) - AcrB/AcrD/AcrF family		264805, 264634
1229	94328135 (2457, 2458)			UNCLASSIFIED	87168474, 265011, 87168559, 264681, 264689, 264693, 85274620, 18108374, 264909, 264605, 18108388
1230	80049357 (2459, 2460)	Novel Protein sim. GBank gij116230[sp]P28598[CH60_BACSU - 60 KD CHAPERONIN (PROTEIN CPN60)]	Contains protein domain (PF00118) - TCP-1/cpn60 chaperonin family		
1231	79843141 (2461, 2462)			UNCLASSIFIED	264908
1232	79853104 (2463, 2464)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]		transport	264909
1233	80255179 (2465, 2466)	Novel Protein sim. GBank gij118298[sp]P20730[CHC_BOMMO - CHORION CLASS HIGH-CYSTEINE HCB PROTEIN 13 PRECURSOR (HC-B.13)]		UNCLASSIFIED	265017, 264564
1234	79242158 (2467, 2468)	Novel Protein sim. GBank gij729671[sp]P40280[H2A_MAIZE - HISTONE H2A]	Contains protein domain (PF00125) - Core histone H2A/H2B/H3/H4	histone	265008, 265010, 18108381
1235	79914423 (2469, 2470)				264634, 264762
1236	81927147 (2471, 2472)			UNCLASSIFIED	265018, 55811150, 264585, 264757
1237	83371782 (2473, 2474)	Novel Protein sim. GBank gij3875133[emb]CAA94750] - (Z70750) similar to actin binding domain; cDNA EST EMBL: T00093 comes from this gene; cDNA EST EMBL: D34443 comes from this gene; cDNA EST EMBL: D37508 comes from this gene; cDNA EST EMBL: D84247 comes from this gene; cDNA EST EMBL: ...			264758, 264601, 264766, 264687, 18108372, 264555, 264559
1238	87411577 (2475, 2476)	Novel Protein sim. GBank gij3885470 (AF061443) - G protein-coupled receptor LGR4 [Rattus norvegicus]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264259, 29331822, 29331824, 35696052, 264508, 264908, 52844045, 52846317, 264288, 264769, 264693, 264632, 264634, 264558, 87168518, 264563
1239	82197449 (2477, 2478)	Novel Protein sim. GBank gij4007890[gb]AAC95339] - (AF084383) DOK protein [Mus musculus]		oncogene	264509, 264511, 264759, 264760, 264784, 264557
1240	80497259 (2479, 2480)	Novel Protein sim. GBank gij1176192[sp]P45420[YHCD_ECOLI - HYPOTHETICAL OUTER MEMBRANE USHER PROTEIN IN GLTF-NANT INTERGENIC REGION PRECURSOR]			264769
1241	80020711 (2481, 2482)	Novel Protein sim. GBank gij121383[sp]P18904[GLNA_VIBAL - GLUTAMINE SYNTHETASE (GLUTAMATE-AMMONIA LIGASE)]	Contains protein domain (PF00120) - Glutamine synthetase	UNCLASSIFIED	264601, 264604, 264638
1242	79775890 (2483, 2484)				264908, 264907, 264908, 264634

1243	79779458 (2485, 2486)	Novel Protein sim. GBank gij335567]embjCAA19971] - (AL031124) branched-chain amino acid aminotransferase [Streptomyces coelicolor]		UNCLASSIFIED	18108374, 35695917, 35695855, 265009, 264508, 264909
1244	10284821 (2487, 2488)	Novel Protein sim. GBank gij2970646 (AF051945) - Xin [Mus musculus]		UNCLASSIFIED	264691
1245	80437103 (2489, 2490)	Novel Protein sim. GBank gij4586338]dbj[BAA76357.1] - (AB016787) cytochrome o ubiquinol oxidase B [Pseudomonas putida]	Contains protein domain (PF00115) - Cytochrome C and Quinol oxidase polypeptide I	oxidase	264768
1246	80059321 (2491, 2492)	Novel Protein sim. GBank gij3581849]embjCAA20805] - (AL031541) putative phenylalanyl-tRNA synthetase beta chain [Streptomyces coelicolor]		UNCLASSIFIED	264604, 264636, 264557, 264564
1247	80064831 (2493, 2494)	Novel Protein sim. GBank gij2621684 (AE000842) - adhesion protein [Methanobacterium thermoautotrophicum]			264758, 264605, 264639
1248	88070353 (2495, 2496)	Novel Protein sim. GBank gij1352403]spjP09487]F16P_HUMAN - FRUCTOSE-1,6-BISPHOSPHATASE (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)	Contains protein domain (PF00316) - Fructose-1,6-bisphosphatase	UNCLASSIFIED	18108392, 264259, 26331826, 264106, 264508, 264907, 264828, 265009, 60433356, 264757, 264758, 21908754, 265010, 265011, 265018, 265019, 264760, 18108351, 18108354, 265021, 18108376, 18108377, 264630, 18108385
1249	80056657 (2497, 2498)	Novel Protein sim. GBank gij2791407]embjCAA16001] - (AL021184) hypothetical protein Rv1473 [Mycobacterium tuberculosis]		transport	264908, 265010, 264600, 264603, 264691, 18108376
1250	12694385 (2498, 2500)	Novel Protein sim. GBank gij112785]spjP05100]3MG1_ECOLI - DNA-3-METHYLADENINE GLYCOSIDASE I (3-METHYLADENINE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG I)		UNCLASSIFIED	264689
1251	79850448 (2501, 2502)				264909
1252	79458087 (2503, 2504)			UNCLASSIFIED	264683, 263976
1253	80050121 (2505, 2506)	Novel Protein sim. GBank gij5670176]gbjAAD46816.1]AF16131 - (AF161317) NRAMP manganese transport protein MntA [Salmonella typhimurium]		glycoprotein	264600, 264603, 18108376
1254	87716767 (2507, 2508)	Novel Protein sim. GBank gij103160]ptrj[S22126 - finger protein unkempt - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	35696286, 264910, 264764, 264688, 21906767, 55811957, 264692, 264558, 264639
1255	79169728 (2509, 2510)				264636
1256	87889508 (2511, 2512)	Novel Protein sim. GBank gij2985353]embjCAA04608.1] - (AJ001206) pep2 [Streptomyces coelicolor]		UNCLASSIFIED	60432289, 264600, 264605, 264764, 264687, 264769, 264689, 27486265, 18108374, 18108376
1257	80201435 (2513, 2514)	Novel Protein sim. GBank gij3193306 (AF069300) - contains similarity to Arabidopsis membrane-associated salt inducible-like protein (GB:AL021637) [Arabidopsis thaliana]		UNCLASSIFIED	264094, 265019
1258	20708150 (2515, 2516)			UNCLASSIFIED	264602, 263978
1259	80186012 (2517, 2518)			UNCLASSIFIED	264906, 264446, 264908
1260	80084606 (2519, 2520)			UNCLASSIFIED	264634, 264639

1261	87412802 (2521, 2522)	Novel Protein sim. GBank gi 5889511 dbj BAA83039.1 - (AB028010) KIAA1087 protein [Homo sapiens]	Contains protein domain (PF01699) - Sodium/calcium exchanger protein	cadherin	29331824, 264906, 264909, 264768, 264769, 264689, 264693, 284839, 18108384, 284563
1262	13504589 (2523, 2524)	Novel Protein sim. GBank gi 95100 pir IS21334 - hypothetical protein 4 - Agrobacterium tumefaciens		UNCLASSIFIED	264634
1263	20710997 (2525, 2526)				264602
1264	80083396 (2527, 2528)	Novel Protein sim. GBank gi 3550958 (AF004840) - CDO [Rattus norvegicus]		struct	264634
1265	80253578 (2529, 2530)			UNCLASSIFIED	264563
1266	79914604 (2531, 2532)			UNCLASSIFIED	284786, 264636, 264638, 264567
1267	80558918 (2533, 2534)	Novel Protein sim. GBank gi 1085002 pir IS55056 - mitochondrial carrier protein DIF-1 homolog - Caenorhabditis elegans	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264259, 21806754, 284389
1268	88178473 (2535, 2536)	Novel Protein sim. GBank gi 4886445 emb CAB43370.1 - (AL050269) hypothetical protein [Homo sapiens]	Contains protein domain (PF00583) - Acetyltransferase (GNAT) family	UNCLASSIFIED	18108398, 22278995, 58994075, 60424289, 29331827, 264109, 284512, 265007, 285008, 285009, 264595, 33109954, 33657084, 87188559, 264600, 265018, 285019, 284369, 264688, 21906787, 265020, 52844150, 264691, 33657023, 33657349, 18108374, 264556, 18108365, 60432113, 22279002, 264488
1269	79821846 (2537, 2538)	Novel Protein sim. GBank gi 3334791 emb CAA18939 - (AL031107) hypothetical protein SC5A7.10c [Streptomyces coelicolor]		UNCLASSIFIED	264508, 264905, 264906, 264687, 264693
1270	80031420 (2539, 2540)	Novel Protein sim. GBank gi 2851634 sp Q50591 Y0D1_MYCTU - HYPOTHETICAL 50.0 KD PROTEIN CY1A11.01	Contains protein domain (PF01574) - IMP dehydrogenase / GMP reductase N terminus	dehydrogenase	265010, 264601
1271	79840499 (2541, 2542)			ATPase associated	35698052, 284908
1272	79462878 (2543, 2544)				264686, 264689
1273	80220315 (2545, 2546)	Novel Protein sim. GBank gi 1655665 emb CAB03731 - (Z81368) hypothetical protein Rv2395 [Mycobacterium tuberculosis]		UNCLASSIFIED	264509, 264639
1274	95010802 (2547, 2548)				
1275	20730763 (2549, 2550)	Novel Protein sim. GBank gi 123726 sp P10413 HTPG_EC01 - HEAT SHOCK PROTEIN HTPG (HIGH TEMPERATURE PROTEIN G) (HEAT SHOCK PROTEIN C82.5)	Contains protein domain (PF00183) - Hsp90 protein	UNCLASSIFIED - eph	264905, 264908, 264909, 264769
1276	21148644 (2551, 2552)	Novel Protein sim. GBank gi 2129478 pir IS51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	264389
1277	20438185 (2553, 2554)				
1278	11088385 (2555, 2556)	Novel Protein sim. GBank gi 175473 sp P44555 YAAJ_HAEIN - HYPOTHETICAL PROTEIN HI0183		UNCLASSIFIED	264558
1279	21658756 (2557, 2558)	Novel Protein sim. GBank gi 1929513 (U64318) - ATP synthase subunit beta [Moorelia thermosacchara]		UNCLASSIFIED	264603
1280	79310959 (2559, 2560)	Novel Protein sim. GBank gi 4938504 emb CAB43882.1 - (AL078465) putative protein [Arabidopsis thaliana]		synthase	264605
				struct	263976

1281	94323988 (2561, 2562)	Novel Protein sim. GBank gjl136501 (U39546) - surface protein MCA-32 [Rattus norvegicus]	Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	28331825, 28331828, 284768, 83373044
1282	87537695 (2563, 2564)	Novel Protein sim. GBank gjl3328180 (AF074266) - proto-oncogene AF4 [Mus musculus]		UNCLASSIFIED	265008
1283	20466305 (2565, 2566)	Novel Protein sim. GBank gjl3261721[emb]CAB07057] - (Z92770) hypothetical protein Rv0153c [Mycobacterium tuberculosis]		UNCLASSIFIED	264605
1284	20636325 (2567, 2568)	Novel Protein sim. GBank gjl3929022 (AF057696) - LspB [Haemophilus ducreyi]			264604
1285	80427330 (2569, 2570)	Novel Protein sim. GBank gjl417154[sp]P33126[HS82_ORYSA - HEAT SHOCK PROTEIN 82	Contains protein domain (PF00183) - Hsp90 protein	eph	264766, 264689, 263967
1286	20465254 (2571, 2572)	Novel Protein sim. GBank gjl2078004[emb]CAB08451] - (Z95207) gorA [Mycobacterium tuberculosis]		reductase	264605, 264639
1287	80417530 (2573, 2574)			UNCLASSIFIED	265011, 284602, 284768, 284687, 284769, 284689, 18108370, 284638, 18108385, 284583
1288	95338101 (2575, 2576)	Novel Protein sim. GBank gjl5353510[gb]AAD42161.1[AF08891 - (AF088916) emilin precursor [Homo sapiens]	Contains protein domain (PF00386) - C1q domain	collagen	35696032, 264107, 284508, 284509, 284905, 284908, 284907, 284908, 284909, 284510, 264511, 265007, 284512, 284910, 265009, 33657402, 284595, 284758, 285011, 265019, 264760, 18108351, 284681, 284764, 284288, 264685, 284766, 284687, 284768, 284769, 265020, 285021, 284534, 284692, 18108370, 264628, 18108374, 35896423, 284555, 264556, 284557, 284558, 18108365, 284564, 264566, 284567, 284486, 18108391
1289	11813647 (2577, 2578)			UNCLASSIFIED	264637
1290	19526027 (2579, 2580)	Novel Protein sim. GBank gjl169995[sp]P46023[GPCR_LYMST - G-PROTEIN COUPLED RECEPTOR GRL101 PRECURSOR	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	Im7	264563
1291	80470266 (2581, 2582)	Novel Protein sim. GBank gjl2072674[emb]CAB08305] - (Z95120) rhIE [Mycobacterium tuberculosis]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	265007, 265008, 264769
1292	84723316 (2583, 2584)	Novel Protein sim. GBank gjl1835755 (U86338) - zinc finger protein Png-1 [Mus musculus]	Contains protein domain (PF01530) - Zinc finger, C2HC type	transcriptfactor	264092, 264259, 29331822, 29331824, 264508, 284806, 284809, 284512, 265008, 265009, 284591, 285019, 284369, 284288, 284886, 284768, 284893, 18108374, 264632, 56182323, 284639, 83373044, 22278002, 264482, 284563
1293	80067536 (2585, 2586)			UNCLASSIFIED	265006, 55812038, 264369, 284556
1294	82125808 (2587, 2588)	Novel Protein sim. GBank gjl2129173[pir]F64453 - oxaloacetate decarboxylase (EC 4.1.1.3) alpha subunit - Methanococcus jannaschii		biotindap	264602, 264605, 284760, 18108351, 264689, 33657023, 284559
1295	11688851 (2589, 2590)	Novel Protein sim. GBank gjl5441778[emb]CAB46603.1] - (AL086811) putative alcohol dehydrogenase (zinc-binding) [Streptomyces coelicolor A3(2)]		dehydrogenase	264689

1296	11887904 (2591, 2592)	Novel Protein sim. GBank gi 4882191 gb AAD3686.1 AE00180 - (AE001805) DNA- directed DNA polymerase I [Thermotoga maritima]	Contains protein domain (PF01367) - 5'-3' exonuclease	UNCLASSIFIED	264591, 264639
1297	79639300 (2593, 2594)			polymerase	264693
1298	94239508 (2595, 2596)	Novel Protein sim. GBank gi 1943770 (U97191) - F53F10.1 gene product [Caenorhabditis elegans]		struct	18108348, 265017
1299	80255378 (2597, 2598)				
1300	80064867 (2599, 2600)	Novel Protein sim. GBank gi 3445181 (AC005498) - R31665.2 [Homo sapiens]	Contains protein domain (PF01352) - KRAB box	transcriptfactor	264488, 264906, 264909, 22279002, 264566 264605
1301	17939814 (2601, 2602)	Novel Protein sim. GBank gi 4082973 dbj BAA36204.1 - (AB017138) alpha subunit of malonate decarboxylase [Pseudomonas putida]		UNCLASSIFIED	264906
1302	95416198 (2603, 2604)				
1303	9684121 (2605, 2606)				85658542, 265020
1304	79377196 (2607, 2608)				264908
1305	19805898 (2609, 2610)			UNCLASSIFIED	264508
1306	13059230 (2611, 2612)	Novel Protein sim. GBank gi 3242273 emb CAB07017 - (Z92669) hypothetical protein Rv0238c [Mycobacterium tuberculosis]		UNCLASSIFIED	264566 264636
1307	82201028 (2613, 2614)				
1308	21426814 (2615, 2616)	Novel Protein sim. GBank gi 1502421 (U59433) - 3-ketoacyl acyl carrier protein reductase [Bacillus subtilis]	Contains protein domain (PF00516) - Envelope glycoprotein GP120	UNCLASSIFIED	264907, 264592, 264784 264555
1309	79263011 (2617, 2618)	Novel Protein sim. GBank gi 95819 pir S16298 - ferric enterobactin transport protein fepC - Escherichia coli		transport	264906, 18108354
1310	20466319 (2619, 2620)	Novel Protein sim. GBank gi 5459220 emb CAB48893.1 - (AL098837) putative iron-sulfur protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	264805
1311	87613142 (2621, 2622)				35696286, 29331827, 264908, 265008, 284764, 284786, 264886, 21906767, 21908769, 33695917, 264691, 264693
1312	88061720 (2623, 2624)	Novel Protein sim. GBank gi 4455118 gb AAD21084 - (AF125158) zinc finger DNA binding protein 99 [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	dna_ma_bind	22278995, 22278998, 22278999, 264905, 264908, 265011, 265017, 265019, 264887, 21908768, 265020, 265021, 33657023, 22279002, 264564
1313	91225458 (2625, 2626)	Novel Protein sim. GBank gi 4929733 gb AAD34127.1 AF15189 - (AF151890) CGI-132 protein [Homo sapiens]	Contains protein domain (PF00888) - Ribosomal protein S18	ribosomalprot	22278998, 22278999, 264259, 20281099, 29146498, 264508, 264908, 68712502, 60433356, 60433438, 265011, 265017, 264683, 264288, 21906765, 21906767, 29146827, 21906768, 35695917, 265021, 33657023, 33657109, 18108370, 18108377, 35695855, 60432113, 22279000, 264563, 18108390
1314	56826053 (2627, 2628)				264693
1315	84357192 (2629, 2630)	Novel Protein sim. GBank gi 2589223 (AF026565) - ring finger protein [Mus musculus]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	interleukinrecept	264691

1316	85381609 (2631, 2632)	Novel Protein sim. GBank gij5889407[dbj BAA82987.1] - (AB028958) KIAA1035 protein [Homo sapiens]		kinase	56182575, 56181686, 20281171, 29331822, 29331824, 60424289, 29331825, 35696052, 52844045, 264591, 60432229, 265018, 265019, 55811150, 56181562, 21906765, 21906767, 21906768, 35695917, 60170815, 33857023, 65274620, 33857109, 35695763, 35695855, 18108387, 87188516, 60432113, 22279002, 264564
1317	88055167 (2633, 2634)	Novel Protein sim. GBank gij4836757[gib AAD30541.1 AF13491 - (AF134918) semaphorin subclass 4 member G [Mus musculus]		UNCLASSIFIED	264093, 264806, 264909, 264369, 264684
1318	85322893 (2635, 2636)	Novel Protein sim. GBank gij4680204[gib AAD27567.1 AF11417 - (AF114171) hypothetical protein [Sorghum bicolor]		UNCLASSIFIED	18108392, 18108348, 265011, 265017, 18108359, 18108382, 56182323, 18108385, 22279000
1319	84238546 (2637, 2638)				264908, 264909, 265006, 265008, 264592, 265019, 264766, 56181562, 18108388, 264628, 264629, 18108377, 264638
1320	86603567 (2639, 2640)	Novel Protein sim. GBank gij4240183[dbj BAA74870.1] - (AB020854) KIAA0847 protein [Homo sapiens]		UNCLASSIFIED	35886286, 55812038, 265018, 21906768, 265020, 263978, 22279002
1321	86676351 (2641, 2642)	Novel Protein sim. GBank gij4886505[emb CAB43377.1] - (AL050276) hypothetical protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	transcriptfactor	60432049, 29331828, 264907, 264908, 264909, 264910, 55812038, 264601, 264762, 264764, 264766, 264768, 264769, 264628, 18108374, 264634, 264635, 18108385
1322	87755272 (2643, 2644)	Novel Protein sim. GBank gij5262581[emb CAB45738.1] - (AL080143) hypothetical protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	dna_mn_bind	29331828, 264908, 265020, 33857023, 264693, 264404
1323	84645931 (2645, 2646)	Novel Protein sim. GBank gij5459516[dbj BAA82407.1] - (AB029821) phosphatidylethanolamine N-methyltransferase [Homo sapiens]		synthase	65274572, 56994075, 264259, 29331822, 29331827, 264104, 56182435, 87188474, 18108351, 264288, 21908768, 21906767, 35695917, 265020, 264693, 65274791, 56182323, 18108387
1324	87737614 (2647, 2648)	Novel Protein sim. GBank gij5031717[ref NP_005704.1 pGPBP - goodpasture antigen-binding protein]	Contains protein domain (PF01852) - START domain		22278996, 22278998, 29331828, 264905, 264907, 29331830, 264908, 264510, 265008, 264595, 264759, 21906754, 265018, 264288, 264768, 264769, 21906768, 265022, 18108378, 264631, 264632, 264634, 264636, 264638, 264563, 264564, 264565, 264566
1325	94647471 (2649, 2650)	Novel Protein sim. GBank gij3294501 (U64857) - similar to the DPT/Kunitz family of inhibitors; most similar to tissue factor pathway inhibitor precursor [Caenorhabditis elegans]	Contains protein domain (PF00090) - Thrombospondin type 1 domain	protease	35696286, 264905, 264908, 264907, 264908, 264909, 264910, 264593, 33857402, 264758, 85858542, 264760, 264768, 264769, 264691, 35698423
1326	87316289 (2651, 2652)	Novel Protein sim. GBank gij1397275 (U61947) - C06G3.8 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264259, 66712502, 284682, 284683, 284635

1327	95322897 (2653, 2654)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	Contains protein domain (PF00279) - Plant lipid transfer protein family	UNCLASSIFIED	18108398, 22278986, 22278987, 22278989, 284081, 284259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 284105, 284905, 58182435, 284112, 265008, 265009, 21908754, 265010, 265011, 265017, 265019, 264681, 264448, 264764, 264684, 264288, 264685, 264768, 264688, 21908767, 21908769, 29148829, 265020, 264690, 264691, 264692, 264693, 263987, 33657109, 33657182, 27486282, 33657349, 18108370, 18108374, 55810764, 35885855, 264634, 58182323, 83373044, 87188518, 60432113, 22279000, 22279002, 264563, 264567 284488, 22278997, 29331826, 284595, 18108351, 264786, 22279002, 284482, 284567
1328	87753493 (2655, 2656)			UNCLASSIFIED	22278996, 29331827, 264884, 264692, 33657109
1329	87755276 (2657, 2658)	Novel Protein sim. GBank gi 4678224 gb AAD26969.1 AC00713 - (AC007135) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	
1330	87727737 (2659, 2660)	Novel Protein sim. GBank gi 437310 (L23504) - nodulin [Medicago truncatula]		UNCLASSIFIED	264259, 29331825, 284512, 265019, 265021, 264555, 284558, 56526486
1331	87376764 (2661, 2662)	Novel Protein sim. GBank gi 4589588 dbj BAA78815.1 - (AB023188) KIAA0971 protein [Homo sapiens]		UNCLASSIFIED	264259, 29331826, 29331827, 35696052, 29331828, 60170831, 264448, 264686, 21906765, 55811957, 265020, 33657023, 33657109, 263973, 55811576, 35896423, 35895855, 56182323
1332	84845937 (2663, 2664)	Novel Protein sim. GBank gi 5459516 dbj BAA82407.1 - (AB029821) phosphatidylethanolamine N-methyltransferase [Homo sapiens]		synthase	65274572, 22278986, 56894075, 22278989, 60432049, 284259, 29331822, 29331826, 60432289, 29331827, 35696052, 52844045, 58182435, 284510, 21906754, 87188559, 265018, 265019, 264448, 264288, 264369, 284686, 21906765, 21906766, 21906787, 21906768, 265020, 265021, 52844150, 33657023, 56182323, 18108387, 60432113, 22279002
1333	88098476 (2665, 2666)	Novel Protein sim. GBank gi 5689527 dbj BAA83047.1 - (AB028018) KIAA1095 protein [Homo sapiens]		UNCLASSIFIED	60432289, 66712502, 284591, 60433356, 60433438, 55812038, 265010, 284639, 56526486
1334	87592388 (2667, 2668)	Novel Protein sim. GBank gi 2662536 (AF036685) - Similar to protein-tyrosine phosphatase [Caenorhabditis elegans]		phosphatase	264905
1335	87644798 (2669, 2670)	Novel Protein sim. GBank gi 4240285 dbj BAA74921.1 - (AB020705) KIAA0898 protein [Homo sapiens]	Contains protein domain (PF00843) - B-box zinc finger.	UNCLASSIFIED	22278998, 22278999, 29331827, 264509, 284511, 265007, 265008, 265009, 60433438, 21906754, 87188559, 265017, 284288, 21906765, 21906767, 21906768, 21906769, 265020, 33657109, 27486284, 18108374, 284558, 284638, 284557, 60170394, 264559, 18108385, 284563

1336	87787890 (2671, 2672)	Novel Protein sim. GBank gi 465445 sp P33485 VNUA_PRVKA - PROBABLE NUCLEAR ANTIGEN			264508, 264905, 264512, 264764, 264683, 264635, 264637
1337	94312042 (2673, 2674)	Novel Protein sim. GBank gi 5689471 dbj BAA83019.1 - (AB028890) KIAA1067 protein [Homo sapiens]		UNCLASSIFIED	56182575, 56894075, 22278998, 22278999, 284092, 284259, 60432289, 28331828, 284906, 284908, 284909, 284112, 265008, 285008, 60433358, 55812038, 33657084, 285011, 285017, 285018, 265019, 284682, 284448, 284683, 284369, 284688, 284689, 21908768, 21908769, 285020, 284691, 27488261, 20281069, 18108379, 55811576, 35695855, 56182323, 60432113, 22279002, 264587
1338	80366114 (2675, 2676)			UNCLASSIFIED	29331822, 265010, 264288, 264689, 18108370, 35695855
1339	80249231 (2677, 2678)	Novel Protein sim. GBank gi 1176422 (U43194) - rhophilin [Mus musculus]		UNCLASSIFIED	35696052, 264809, 264688, 264558, 264558
1340	88316311 (2679, 2680)				264905, 264907, 87168559, 264764
1341	88101485 (2681, 2682)				284681, 284685, 284686, 284692
1342	80089017 (2683, 2684)	Novel Protein sim. GBank gi 5019564 emb CAB44507.1 - (AL035542) dJ994E9.5 (hs6M1-17 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) protein)) [Homo sapiens]	Contains protein domain (PF00001) - tm7 7 transmembrane receptor (rhodopsin family)		284628
1343	80082862 (2685, 2686)	Novel Protein sim. GBank gi 4557543 ref NP_001384.1 pECM2 - extracellular matrix protein 2	Contains protein domain (PF00560) - struct Leucine Rich Repeat		284910, 284686, 284534
1344	20562559 (2687, 2688)	Novel Protein sim. GBank gi 2144101 pir I55210 - tricarboxylate carrier - rat (fragment)		glycoprotein	263978
1345	91225546 (2689, 2690)	Novel Protein sim. GBank gi 3881052 emb CAA19523 - (AL023843) predicted using GeneFinder; similar to serine/threonine kinase; cDNA EST yk246a12.3 comes from this gene; cDNA EST yk358c10.5 comes from this gene; cDNA EST EMBL:M89047 comes from this gene; cDNA EST yk246a12.5 comes...	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain		22278998, 264807, 264681, 264685, 264689, 285020, 284693, 22279000, 22279002, 284586
1347	80417393 (2693, 2694)	Novel Protein sim. GBank gi 4504379 ref NP_003058.1 pHG38 - orphan G protein- coupled receptor HG38	Contains protein domain (PF00560) - glycoprotein Leucine Rich Repeat	glycoprotein	284906, 284908, 284909, 285008, 284910, 285011, 285017, 284764, 284766, 284767, 284769, 284631, 284634, 284638, 284567, 284486
1348	87352335 (2695, 2696)	Novel Protein sim. GBank gi 3399720 dbj BAA32100 - (AB010999) peptidylarginine deiminase type IV [Rattus norvegicus]		UNCLASSIFIED	284488, 284489, 284508, 284509, 284510, 284511, 284512, 284591, 284592, 284601, 284684, 284685, 284769, 284532, 284534, 264555, 264556, 264557, 264558, 22279002, 284488

1349	91225548 (2697, 2698)	Novel Protein sim. GBank gij2144101[pir]j55210 - tricarboxylate carrier - rat (fragment)		UNCLASSIFIED	52846842, 35695286, 22278986, 22278988, 22278999, 284259, 29331822, 29331824, 35696052, 284509, 284905, 264906, 264907, 284908, 284909, 264511, 265006, 264512, 284910, 60170831, 284591, 60433438, 284757, 21908754, 265017, 265018, 264605, 264760, 264762, 264288, 264766, 264889, 21908765, 21908768, 21906767, 21906768, 55811957, 35695917, 265020, 264534, 284691, 264692, 33657023, 284693, 33657349, 18108374, 18108376, 35696423, 60170394, 22279000, 22279002, 264563, 264564
1350	87093136 (2699, 2700)			UNCLASSIFIED	52646842, 284259, 29331825, 284908, 264511, 284604, 264288, 21906769, 265020, 33657182, 33657349, 18108374, 35695855, 264555, 264558, 18108385, 22279002, 264486
1351	87361327 (2701, 2702)	Novel Protein sim. GBank gij4887239[gb]AAD32246.1] - (AF084584) BAW protein [Fugu rubripes]		UNCLASSIFIED	284906, 264907, 284638
1352	80076386 (2703, 2704)			UNCLASSIFIED	264693, 263981
1353	95345417 (2705, 2706)	Novel Protein sim. GBank gij2144101[pir]j55210 - tricarboxylate carrier - rat (fragment)			35696286, 60424269, 284805, 264509, 284906, 264907, 284908, 284909, 284511, 264512, 284910, 284758, 284598, 55811386, 265011, 284605, 5581150, 284762, 284764, 284766, 52844229, 56181582, 35695917, 265022, 33657023, 284693, 35695763, 60431528, 264628, 263978, 35696423, 35695855, 264630, 264634, 264635, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 284566
1354	95350845 (2707, 2708)	Novel Protein sim. GBank gij4889108[gb]AAD27763.1[AF07703] - (AF077030) hypothetical 43.2 kDa protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278999, 29331826, 264906, 265008, 33657402, 21906754, 265011, 67168559, 284684, 264369, 264769, 264689, 21908765, 21908768, 52844150, 33657023, 284692, 264693, 18108374, 83373044, 67168518, 22279000
1355	88260186 (2709, 2710)	Novel Protein sim. GBank gij1469199[dbj]BAA09487] - (D50928) The KIAA0138 gene product is novel. [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	22278996, 22278997, 284259, 66714117, 264511, 21908754, 265010, 284769, 264689, 21908765, 21906768, 21906769, 264532, 27486262, 264629, 264638, 264556, 264638, 264639, 264482, 264484

1356	85313981 (2711, 2712)	Novel Protein sim. GBank gi 1113865 (U40342) - ninein [Mus musculus]			sinud	18108397, 22278995, 22278998, 22278998, 284094, 29331826, 284905, 285006, 285007, 285008, 285010, 285017, 285018, 285019, 284764, 18108354, 284889, 21906765, 285022, 18108384, 35696423, 83373044, 18108387
1357	88260268 (2713, 2714)	Novel Protein sim. GBank gi 897693 emb CAA90330 - (Z50026) phosphatidylcholine transfer protein [Bos taurus]	Contains protein domain (PF01852) - START domain			284259, 29331822, 29331825, 264510, 87169559, 285018, 264448, 284288, 21906765, 21908786, 21908788, 285021, 284893, 18108376
1358	38719455 (2715, 2716)	Novel Protein sim. GBank gi 556219 (L36831) - transcription regulator [Mus musculus]				284757
1359	87771843 (2717, 2718)			UNCLASSIFIED		284907, 284909, 284510, 284511, 284512, 18108351, 284764, 284534, 33857023, 18108374, 284634, 284635, 284638, 284639, 18108385, 284486, 284567
1360	87738272 (2719, 2720)	Novel Protein sim. GBank gi 2598282 emb CAA75612 - (Y15417) acetate--CoA ligase [Coprinus cinereus]			synthase	60432289, 284605
1361	87593527 (2721, 2722)	Novel Protein sim. GBank gi 5689443 dbj BAA83005.1 - (AB028976) KIAA1053 protein [Homo sapiens]	Contains protein domain (PF00538) - SAM domain (Sterile alpha motif)	UNCLASSIFIED		35696288, 22278997, 22278999, 284259, 29331826, 284508, 284509, 284905, 284907, 284908, 285007, 285009, 33109954, 21908754, 87168474, 285011, 284761, 284683, 284288, 284788, 284789, 284689, 21908788, 285020, 285021, 33857023, 55811578, 35698423, 284634, 60432113, 22278002, 284482, 284486
1362	95287961 (2723, 2724)	Novel Protein sim. GBank gi 5688411 dbj BAA82889.1 - (AB028960) KIAA1037 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	eph		56182575, 56181686, 60432049, 284259, 29331822, 56182181, 29331827, 35698052, 29331828, 284905, 284908, 284908, 284595, 55812038, 85858542, 55811150, 284681, 284288, 284369, 56181582, 60431528, 55810764, 35698423, 60431850, 284558
1363	85758476 (2725, 2726)	Novel Protein sim. GBank gi 1130494 (U35776) - ADP-ribosylation factor 1-directed GTPase activating protein [Rattus norvegicus]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	UNCLASSIFIED		284488, 29331826, 284907, 284687, 284689, 284693
1364	88178488 (2727, 2728)					60432289, 60433356, 60433438, 87168559, 284603, 18108351, 21908786, 35698423, 60432113
1365	63003108 (2729, 2730)	Novel Protein sim. GBank gi 4589562 dbj BAA76803.1 - (AB023176) KIAA0959 protein [Homo sapiens]		oncogene		284766
1366	87003262 (2731, 2732)	Novel Protein sim. GBank gi 1084944 pir S54495 - hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport		285007

1367	87721210 (2733, 2734)	Novel Protein sim. GBank gi 4884086 emb CAB43240.1 - (AL050019) hypothetical protein [Homo sapiens]	Contains protein domain (PF01342) - SAND domain	UNCLASSIFIED	264488, 52848942, 52846365, 22278995, 56994075, 35898286, 22278996, 22278998, 22278999, 284259, 29331824, 68714117, 29331825, 60432289, 35898052, 284905, 284907, 284908, 284909, 284510, 265006, 265007, 284512, 284910, 265009, 60170831, 33657402, 55812038, 21808754, 285011, 87188559, 285017, 265019, 18108351, 284448, 284882, 284683, 284288, 284388, 284886, 284787, 284889, 21808785, 21808786, 21808788, 21808789, 55811957, 265020, 285021, 285022, 284534, 60170815, 284890, 284891, 18108382, 33857023, 33857108, 33857349, 284628, 18108370, 18108374, 18108376, 55811576, 35898423, 35898555, 284635, 284555, 284637, 284558, 52844332, 60170394, 284558, 18108381, 18108385, 56528486, 22279000, 284563, 284567
1368	94320078 (2735, 2738)	Novel Protein sim. GBank gi 464561 sp P35289 RB15_RAT RAS-RELATED PROTEIN RAB-15	Contains protein domain (PF00071) - Ras family	oncogene	284259, 29331822, 29331826, 60432289, 29331827, 35898052, 284508, 284905, 284908, 284909, 284510, 285007, 284910, 60433438, 284758, 85858542, 87188559, 284600, 284801, 284780, 284784, 284785, 284788, 52844229, 284689, 35895917, 285020, 265021, 284631, 284632, 284634, 284637, 52844332, 284558, 284639, 83373044, 284563, 284588, 284488, 284587, 285008, 60432228, 60433356, 33857084, 21808784, 21808789, 284555, 284638, 284559, 284587
1369	86634033 (2737, 2738)	Novel Protein sim. GBank gi 2092702 (U90550) - butyrophilin [Homo sapiens]		UNCLASSIFIED	
1370	95316910 (2739, 2740)	Novel Protein sim. GBank gi 5031823 ref NP_005823.1 pKCNM - potassium large conductance calcium-activated channel, subfamily M, beta member 2		potassium_channel	22278998, 284259, 29331822, 29331824, 29331826, 29331827, 35898052, 284508, 284509, 284905, 284908, 284907, 284909, 284909, 284510, 284511, 284512, 284758, 285011, 285019, 284784, 284788, 284789, 21808787, 35895917, 18108382, 35898423, 284832, 284835, 284636, 284555, 284638, 284558, 284639, 18108385, 65274727, 284404, 284583, 284588, 284488
1371	95336512 (2741, 2742)	Novel Protein sim. GBank gi 5032203 ref NP_005714.1 pTSPA - tetraspan 5	Contains protein domain (PF00335) - 4 transmembrane segments integral membrane proteins	glycoprotein	22278998, 284259, 29331822, 29331824, 29331825, 29331828, 29331827, 284905, 284509, 29331830, 66712502, 285008, 285009, 284758, 33857084, 85858542, 285010, 285018, 285019, 284782, 284448, 35895917, 33857109, 33857182, 33857349, 35898555, 284558, 22278002, 284563

1372	80248517 (2743, 2744)	Novel Protein sim. GBank gij840708[pbj]BAA093341 - (D50885) trans-sialidase [Trypanosoma cruzi]		collagen	263978
1373	80499421 (2745, 2746)			UNCLASSIFIED	264769, 21906765, 21906767, 22278999, 264691, 264910, 55812038, 265010, 264881, 264684
1374	95087038 (2747, 2748)	Novel Protein sim. GBank gij111878[pir]JC1241 - beta-Interferon-induced protein - rat		Interferon	264907, 264510, 265007, 264512, 265008, 60432229, 264689, 65274791, 264555, 264558, 264557, 63373044, 60432113
1375	94236842 (2749, 2750)	Novel Protein sim. GBank gij5649176[gj]AAD03500.2] - (AF051155) G beta-like protein GBL [Rattus norvegicus]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	52844507, 52845158, 52846842, 52846365, 56182575, 56181686, 22278998, 56994075, 35898286, 22278997, 22278998, 22278999, 264259, 29331822, 52845080, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35898052, 35856970, 264905, 264508, 264808, 264907, 264808, 29331830, 264808, 265006, 264511, 265007, 265008, 265009, 33657402, 60433356, 52646317, 33109954, 33657084, 52644296, 87188474, 87188559, 264800, 265017, 265018, 265019, 55811150, 18108351, 264448, 264784, 264288, 264369, 264786, 52844229, 21908765, 21908766, 21908767, 21906768, 21908769, 55811957, 35895917, 265020, 265021, 52644150, 33657023, 264693, 65274620, 52845129, 33657109, 27486261, 33657349, 27468265, 35895763, 18108376, 55810764, 35898423, 35895855, 264630, 264631, 264634, 264636, 264555, 264638, 18108365, 87188518, 60432113, 22279000, 22279002, 264563, 264564, 264566, 264567, 264768, 264769, 35895917, 22278997, 264691, 264259, 28331622, 264693, 35898052, 264508, 264509, 264905, 264906, 264628, 264908, 264629, 18108372, 264908, 264510, 264511, 264512, 265008, 264630, 264631, 264910, 264632, 264634, 264635, 264636, 264591, 264592, 264637, 264638, 264558, 264639, 33657402, 264595, 18108385, 56526488, 265010, 265011, 264600, 264563, 264762, 264584, 264565, 264764, 264486, 264766
1376	87399050 (2751, 2752)	Novel Protein sim. GBank gij138350[sp]P28988[VGLX_HSVEB - GLYCOPROTEIN X PRECURSOR		UNCLASSIFIED	28331824, 264591, 265018, 264686, 264768, 55811957, 264693, 22278002
1377	86984242 (2753, 2754)	Novel Protein sim. GBank gij1663848 (U75321) - chromaffin granule ATPase II homolog [Mus musculus]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase_associated	

1378	87595071 (2755, 2756)	Novel Protein sim. GBank gi 4107015 dbj BAA36293] - (AB001772) PEM-5 [Clona savignyi]			22278994, 22278998, 284093, 284094, 284259, 29331824, 29331827, 265009, 285018, 265019, 18108351, 264369, 284288, 29148627, 55811957, 284691, 18108368, 33857109, 18108388, 284635, 263881, 18108385
1379	85679344 (2757, 2758)	Novel Protein sim. GBank gi 3252872 (AF035620) - BRCA1-associated protein 2 [Homo sapiens]			265020
1380	87627862 (2759, 2760)	Novel Protein sim. GBank gi 4837737 gb AAD30662.1] - (AF086834) germ cell specific Y-box binding protein [Homo sapiens]		nuc_rept	284510, 284512, 265009, 284288, 284564
1381	86179856 (2761, 2762)	Novel Protein sim. GBank gi 4731580 gb AAD28508.1 AF12538 - (AF125384) L82A [Drosophila melanogaster]		UNCLASSIFIED	87168558, 265017, 284628, 22279002
1382	84847576 (2763, 2764)		Contains protein domain (PF00583) - Acetyltransferase (GNAT) family	UNCLASSIFIED	22278894, 22278997, 22278998, 29331822, 29331824, 29331826, 265007, 60432229, 60433358, 85858542, 265017, 285018, 284685, 284768, 21908788, 35695917, 33857023, 27486261, 27486262, 35695763, 35695855, 87168518, 22279002
1383	87860598 (2765, 2766)			UNCLASSIFIED	18108398, 284692
1384	86915895 (2767, 2768)			UNCLASSIFIED	284488, 284508, 284509, 284905, 284906, 284908, 284909, 284511, 284512, 284910, 284760, 18108351, 284766, 284769, 35695855, 284630, 284638, 284555, 284638, 264483, 284584, 284486
1385	86378788 (2769, 2770)	Novel Protein sim. GBank gi 2384732 (AF015911) - NAC-1 protein [Rattus norvegicus]		UNCLASSIFIED	35696052, 55811386, 284888, 21906765, 265020, 33857023, 18108385
1386	91013049 (2771, 2772)	Novel Protein sim. GBank gi 2384910 (AF022882) - contains similarity to the A-type potassium current class of channel proteins [Caenorhabditis elegans]		Inf	60432288, 29331828, 284906, 284807, 56182435, 285011, 284681, 60170815, 33857023, 83373044, 284586
1387	87797858 (2773, 2774)	Novel Protein sim. GBank gi 4180304 emb CAA10800] - (AJ132192) HS1 binding protein 3 [Mus musculus]		UNCLASSIFIED	284581
1388	95101652 (2775, 2776)	Novel Protein sim. GBank gi 4895184 gb AAD32753.1 AC00723 - (AC007231) putative disease resistance protein [Arabidopsis thaliana]		glycoprotein	65274572, 22278999, 284259, 29331826, 29331827, 35696052, 284509, 284907, 284908, 284909, 265006, 265008, 60170831, 33857402, 80433438, 284598, 21906754, 87168558, 284600, 265017, 284683, 18108354, 52844229, 21906765, 21906766, 21908767, 21908768, 21908769, 285021, 264692, 33857023, 33857109, 35695855, 284558, 60170384, 83373044, 22279000

1389	91256016 (2777, 2778)	Novel Protein sim. GBank gij5689387[dbj BAA82977.1] - (AB028948) KIAA1025 protein [Homo sapiens]	Contains protein domain (PF00641) - Zn-finger in Ran binding protein and others.	UNCLASSIFIED	65274572, 22278999, 284259, 29331822, 29331824, 29331825, 60432289, 29331828, 28146498, 284908, 66712502, 55812038, 265017, 265018, 265019, 18108351, 284369, 21906765, 21906766, 21906767, 21906768, 265020, 265021, 264682, 33657023, 33657349, 18108370, 18108374, 55811576, 264555, 284556, 264557, 60170394, 83373044, 22279000, 264563, 264564, 52645156, 52646365, 284259, 52645080, 29331825, 29331826, 284908, 52644045, 265009, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 284760, 264682, 264288, 284686, 264687, 56181562, 52644229, 21906765, 21906769, 35695917, 265020, 265021, 60170615, 52644150, 33657023, 27486261, 27486284, 65274791, 264631, 264555, 52644332, 87168518, 22279000, 264567
1390	94111916 (2779, 2780)	Novel Protein sim. GBank gij3702295 (AC005783) - R33083_1 [Homo sapiens]	peptidase		52646842, 65274572, 22278994, 22278995, 35696288, 56994075, 22278997, 22278998, 22278999, 60432049, 284259, 52645080, 29331822, 29331824, 60432289, 29331826, 29331827, 35696052, 29331828, 33656970, 264907, 52644045, 265006, 265007, 265008, 60431735, 60433356, 52646317, 55811386, 52644286, 265010, 87168559, 265017, 264604, 265018, 265019, 264448, 264288, 284368, 264766, 21906764, 21906787, 35695917, 265020, 265021, 33657109, 52645129, 27486261, 27486262, 27486265, 33657349, 35695763, 18108370, 18108374, 18108376, 55811576, 35696423, 35695855, 264636, 52644332, 18108382, 18108385, 87168518, 60432113, 22279000, 264484, 264566, 18108391
1391	81227345 (2781, 2782)	Novel Protein sim. GBank gij1346910[sp P28650]PUA1_MOUSE - ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME (IMP-ASPARTATE LIGASE)	Contains protein domain (PF00709) - Adenylosuccinate synthetase		29331826, 29331828, 28331830, 264448, 264288, 33657023, 18108365, 264555, 264556, 83373044
1392	94311097 (2783, 2784)	Novel Protein sim. GBank gij726286 (U22394) - mSin3A [Mus musculus]			52646842, 65274572, 22278994, 22278995, 35696288, 56994075, 22278997, 22278998, 22278999, 60432049, 284259, 52645080, 29331822, 29331824, 60432289, 29331826, 29331827, 35696052, 29331828, 33656970, 264907, 52644045, 265006, 265007, 265008, 60431735, 60433356, 52646317, 55811386, 52644286, 265010, 87168559, 265017, 264604, 265018, 265019, 264448, 264288, 284368, 264766, 21906764, 21906787, 35695917, 265020, 265021, 33657109, 52645129, 27486261, 27486262, 27486265, 33657349, 35695763, 18108370, 18108374, 18108376, 55811576, 35696423, 35695855, 264636, 52644332, 18108382, 18108385, 87168518, 60432113, 22279000, 264484, 264566, 18108391
1393	80409472 (2785, 2786)		Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	284763, 284631
1394	15028819 (2787, 2788)			UNCLASSIFIED	284629
1395	95361471 (2789, 2790)	Novel Protein sim. GBank gij2274845[dbj BAA21534] - (D88461) N-WASP [Rattus rattus]		UNCLASSIFIED	265009, 18108381

1396	95383253 (2791, 2792)	Novel Protein sim. GBank gi 2135904 pir I54810 - pHL E1F1 - human			22278997, 22278999, 284259, 29331825, 60432289, 29331828, 29148498, 29148499, 284907, 284908, 29331830, 284909, 285006, 285007, 285008, 285009, 60433356, 285010, 284802, 285017, 285018, 285019, 18108354, 52844229, 18108358, 21908767, 29148827, 21908768, 21908769, 29148629, 29148784, 285021, 285022, 18108368, 18108374, 58182323, 18108385, 284563, 284567, 35696286, 284907, 66712502, 284510, 35695917, 284892, 284893, 35698423, 284259, 29331822, 29331824, 29331825, 29331827, 35698052, 33656970, 87168474, 285018, 285019, 284882, 284768, 21908767, 285020, 33657023, 27486281, 55811576, 284632, 284639, 83373044, 87168518, 22278002
1397	87631317 (2793, 2794)			UNCLASSIFIED	
1398	91233667 (2795, 2796)	Novel Protein sim. GBank gi 5420389 emb CAB46680.1 - (AJ243480) proteophosphoglycan [Leishmania major]			
1399	87631076 (2797, 2798)	Novel Protein sim. GBank gi 2496887 sp Q09232 YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III		UNCLASSIFIED	
1400	85418064 (2799, 2800)	Novel Protein sim. GBank gi 283920 pir S27939 - tensin - chicken	Contains protein domain (PF00017) - Src homology domain 2	UNCLASSIFIED	56182575, 22278994, 22278997, 284259, 29331822, 29331825, 29331826, 29331827, 29331828, 284908, 56182435, 264112, 285009, 285011, 265017, 265018, 285019, 284760, 284762, 284765, 284288, 284685, 284687, 56181562, 284768, 21908768, 21908767, 55811957, 284691, 284692, 284628, 284629, 55811576, 264634, 284555, 284637, 284557, 284638, 18108381, 284558, 18108384, 60432113, 22278000
1401	91226379 (2801, 2802)	Novel Protein sim. GBank gi 3256185 emb CAA15485 - (AL008635) dJ510H16.1 [Homo sapiens]	Contains protein domain (PF00790) - VHS domain	UNCLASSIFIED	65274572, 60432289, 284909, 284758, 284768, 21908769, 22278002
1402	95361475 (2803, 2804)	Novel Protein sim. GBank gi 1515427 (U57523) - nei homolog [Homo sapiens]	Contains protein domain (PF00008) - Igf EGF-like domain	Igf	284905, 284907, 284908, 284909, 284112, 284693, 33857109, 284634
1403	94147933 (2805, 2806)	Novel Protein sim. GBank gi 5262615 emb CAB45747.1 - (AL080156) hypothetical protein [Homo sapiens]			65274572, 66712502, 285017, 284448, 284288, 21908765, 21908768, 284693, 55811576, 65274791, 60432113
1404	90935393 (2807, 2808)			UNCLASSIFIED	85274572, 22278998, 29331822, 29331828, 66712502, 285008, 60433438, 285017, 284693, 18108385

1405	95095068 (2809, 2810)	Novel Protein sim. GBank gij854065[embjCAA58337] - (X83413) U88 [Human herpesvirus 8]			264488, 56984075, 35696286, 29331822, 29331824, 29331826, 29331828, 35696052, 264508, 264908, 264907, 264908, 264510, 264511, 264910, 33657402, 264594, 264758, 264800, 264604, 264762, 18108351, 264764, 33657023, 33657109, 264628, 264634, 83373044, 22279002, 264583, 264482, 264488, 264587
1406	87612369 (2811, 2812)	Novel Protein sim. GBank gij624076[jb]AAC98425.1[- (U42580) contains Pro-rich Px motifs: SPKPP (20X), PEPPA (9X); similar to soybean pro-rich cell wall protein, corresponds to Swiss-Pro Accession Number P13993 [Paramecium bursaria Chlorella virus 1]	collagen		264907, 264605
1407	94129872 (2813, 2814)	Novel Protein sim. GBank gij2827886 (AF015037) - endooligopeptidase A related protein; EOPA related protein [Oryctolagus cuniculus]	UNCLASSIFIED		35696286, 22278999, 264094, 264259, 66714117, 29331826, 29331827, 29331828, 29146498, 264107, 264908, 265006, 265008, 264910, 60433438, 265011, 265017, 18108351, 264448, 264288, 264686, 21908765, 21906769, 264692, 33657109, 18108370, 264828, 263972, 18108374, 35696423, 55811576, 264631, 264557, 264558, 83373044, 18108365, 87168518, 60432113, 22279002
1408	95361477 (2815, 2816)	Novel Protein sim. GBank gij2564953 (AF030001) - unknown [Mus musculus]	Contains protein domain (PF00008) - oncogene EGF-like domain		264488, 264489, 35696286, 264109, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 265008, 265009, 264910, 33657402, 264757, 264758, 265011, 264601, 265017, 264760, 264762, 264683, 264685, 264766, 264687, 264689, 21906767, 265021, 264690, 264691, 33657023, 264692, 264693, 33657109, 264628, 264629, 35698423, 35695855, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 56182323, 264639, 264583, 264584, 264585, 264586, 264587
1409	66644385 (2817, 2818)	Novel Protein sim. GBank gij2662165[jb]BAA23714[- (AB007902) MH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]			264693
1410	86612587 (2819, 2820)	Novel Protein sim. GBank gij2493790[sp]Q60994[ACR3_MOUSE - 30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADIPOCYTE SPECIFIC PROTEIN ADIPOQ)]	Contains protein domain (PF00386) - complement C1q domain		29331826, 264112, 264512, 265009, 265010, 264601, 264686, 264769, 21906767, 263974, 264631, 264568

1411	87818641 (2821, 2822)	Novel Protein sim. GBank gi 3123155 sp P91343 YM3M_CAEEL - HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	22278995, 22278997, 22278998, 29331822, 60432289, 29331828, 284807, 265017, 265019, 284682, 21908767, 21908768, 21908769, 285020, 284890, 284891, 33857023, 33857109, 27486284, 264628, 263972, 284634, 284558, 18108385
1412	84390819 (2823, 2824)			UNCLASSIFIED	284757
1413	95418559 (2825, 2826)	Novel Protein sim. GBank gi 3879121 emb CAA94370 - (Z70310) predicted using GeneFinder; Similarly to Mouse ankyrin (PIR Acc. No. S3771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA EST E...	Contains protein domain (PF00023) - Ank repeat	homeobox	58994075, 29331822, 35696052, 29331828, 29331830, 284909, 52844045, 284510, 52844298, 85858542, 87168474, 265017, 265018, 284681, 284687, 21908768, 35895917, 285020, 52844150, 284692, 263987, 27488284, 35895783, 284638, 18108387, 284568
1414	94675860 (2827, 2828)	Novel Protein sim. GBank gi 3252981 (AF068921) - Ras- binding protein SUR-8 [Mus musculus]	Contains protein domain (PF00580) - Leucine Rich Repeat	UNCLASSIFIED	284882, 284683, 265022, 284636
1415	94326948 (2829, 2830)	Novel Protein sim. GBank gi 1871187 (U90439) - unknown protein [Arabidopsis thaliana]			52846365, 56182575, 22278994, 22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 284259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 29146498, 88712502, 29331830, 52844045, 264113, 284511, 33657402, 284757, 21908754, 55811388, 285017, 285018, 265019, 284781, 284683, 284369, 284288, 284688, 284689, 21908768, 21908767, 29148827, 21908769, 55811957, 285020, 285021, 284690, 33657023, 65274620, 52845128, 27488262, 27486284, 60431528, 284629, 35895855, 56182323, 284559, 60432113, 264404, 22278002, 284482

1416	94325977 (2831, 2832)	Novel Protein sim. GBank gi 5106557 gb AAD39748.1 AF12305 - (AF123052) MLL septin-like fusion protein [Homo sapiens]	Contains protein domain (PF00735) - struct Cell division protein	18108392, 18108394, 18108397, 18108398, 22278995, 22278996, 35686288, 22278997, 22278998, 22278999, 29331822, 35686052, 29331828, 29146498, 284905, 264907, 264908, 284828, 284909, 284113, 265006, 265007, 265008, 265009, 80170831, 264595, 18108348, 21906754, 87188474, 265010, 265011, 87188559, 265017, 265018, 265019, 264762, 18108351, 264861, 264763, 264882, 264883, 284766, 52644229, 264688, 264689, 21906765, 21906766, 21906767, 29148627, 21906768, 55811957, 29148628, 265020, 52644150, 18108361, 33657023, 18108362, 18108368, 284628, 18108370, 284629, 18108374, 18108379, 55811576, 65274791, 264634, 264636, 56182323, 18108381, 60170394, 18108385, 56526486, 87168518, 22279000
1417	87826663 (2833, 2834)	Novel Protein sim. GBank gi 4958935 dbj BAA78095.1 - (AB027570) suppressor of potassium transport defect 3 [Rattus norvegicus]	ATPase_associated	264107, 264448
1418	87594276 (2835, 2836)		UNCLASSIFIED	264259, 284808, 265010, 52644229, 21906764, 21906768, 284690, 284639, 18108388
1419	87757168 (2837, 2838)	Novel Protein sim. GBank gi 2072284 (U95097) - mitotic phosphoprotein 43 [Xenopus laevis]	struct	264259, 60432289, 265006, 87188474, 264288
1420	87298628 (2839, 2840)	Novel Protein sim. GBank gi 5174421 ref NP_006023.1 pCPNE - copine VI (neuronal)	ATPase_associated	29331824, 265007, 264563
1421	94746986 (2841, 2842)	Novel Protein sim. GBank gi 3876090 emb CAA93459.1 - (Z69635) Similarity to Yeast uridine kinase (SW:URK1_YEAST); cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST EMBL:D67355 comes from this gene; cDNA EST yk209h1.5 comes from this gen...	kinase	18108358, 18108398, 18108397, 21906768, 18108398, 21906767, 58182575, 21906768, 21906769, 56181888, 55811957, 35685917, 35686286, 22278996, 22278997, 22278998, 22278999, 265021, 265022, 80170615, 264259, 33657023, 29331822, 56182181, 29331824, 66714117, 29331825, 33657109, 29331828, 27486261, 29331828, 35686052, 33657349, 264905, 264509, 20281149, 18108370, 284907, 60431528, 68712502, 263972, 55811576, 35688423, 35685855, 264512, 265007, 60431850, 60432228, 60431735, 56182323, 284558, 60170394, 83373044, 55812038, 284758, 18108385, 21906754, 55811388, 87168518, 87168559, 60432113, 265017, 265018, 265019, 22279002, 55811150, 264563, 264682, 264763, 264448, 264566, 264488, 18108391

1422	88178777 (2843, 2844)	Novel Protein sim. GBank gi4505939[ref]NP_000928.1 pPOLR - polymerase (RNA) II (DNA directed) polypeptide A (220kD)		mapolymerase	56994075, 35686286, 87168559, 55811957, 55811576, 284555, 264557, 87168518
1423	86997762 (2845, 2846)			UNCLASSIFIED	264886, 284489, 264692, 264594, 264603, 285018, 284908
1424	95201610 (2847, 2848)	Novel Protein sim. GBank gi437181 (U02289) - GTPase- activating protein [Caenorhabditis elegans]	Contains protein domain (PF00620) - strucd RhoGAP domain		29331822, 29331825, 29331827, 29146498, 264905, 284908, 284908, 284909, 265007, 264910, 265009, 33109954, 285010, 87168559, 285019, 264766, 264687, 21906765, 21906766, 21906767, 21906768, 29146627, 55811957, 29146629, 265021, 264691, 264692, 56526488, 22279002, 264563
1425	21662314 (2849, 2850)	Novel Protein sim. GBank gi100798[ptf]S14959 - proline- rich protein - wheat		UNCLASSIFIED	265007, 284558
1426	94322115 (2851, 2852)	Novel Protein sim. GBank gi2078441 (U56964) - weak similarity to S. cerevisiae intracellular protein transport protein US)1 (SP:P25386) [Caenorhabditis elegans]		UNCLASSIFIED	264488, 60424179, 35698286, 22278997, 22278998, 22278999, 284259, 60432049, 29331822, 29331825, 29331827, 56182435, 284910, 60433358, 60433438, 21906754, 285018, 284288, 21906765, 21906766, 21906767, 21906769, 285020, 265022, 33657109, 18108370, 18108376, 284558, 83373044, 18108385, 56526488, 22279002, 264482
1427	91227510 (2853, 2854)	Novel Protein sim. GBank gi5616074[gb]AAD45616.1 AF06194 - (AF061943) protate- derived STE20-like kinase PSK [Homo sapiens]	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain		22278994, 56994075, 22278997, 29331828, 29331830, 264828, 265006, 265007, 285008, 265009, 284883, 264288, 18108354, 21906765, 21906768, 29146629, 33657023, 18108374, 35695855, 83373044, 22279002, 284584
1428	94323008 (2855, 2856)	Novel Protein sim. GBank gi138350[sp]P28968 VGLX_HSVB - GLYCOPROTEIN X PRECURSOR		glycoprotein	56181686, 264259, 284907, 285007, 285009, 264595, 285010, 284688, 65274620, 264629, 65274791, 22279002, 264586
1429	87888889 (2857, 2858)			UNCLASSIFIED	284112, 284595, 265017, 265019, 21906765, 263977, 284555
1430	94735021 (2859, 2860)	Novel Protein sim. GBank gi1181619[dbj]BAA11565] - (D82364) a variant of TSC-22 [Gallus gallus]			264094, 29331824, 264591, 284593, 285018, 264681, 21906765, 21906767, 65274620, 55811576, 264639, 87168518, 22279002
1431	80429081 (2861, 2862)	Novel Protein sim. GBank gi5420389[emb]CAB46680.1] - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264768, 265020, 284691, 264693, 264638
1432	87463004 (2863, 2864)	Novel Protein sim. GBank gi414797 (L18968) - pyruvate dehydrogenase phosphatase [Bos taurus]		phosphatase	18108394, 28146498, 265007, 60433438, 284763, 29146629, 263969
1433	87605403 (2865, 2866)	Novel Protein sim. GBank gi2460316 (AF022147) - uterus- ovary specific putative transmembrane protein [Rattus norvegicus]	Contains protein domain (PF00100) - Zona pellucida-like domain	UNCLASSIFIED	284259, 284510, 284591, 264603, 264565
1434	85713730 (2867, 2868)			UNCLASSIFIED	284682, 284691

1435	94708213 (2869, 2870)	Novel Protein sim. GBank gi 3970850 dbj BAA34789.1 - (AB015330) HRIHFB2007 [Homo sapiens]		transcript factor	22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 66714117, 29331826, 33656970, 264508, 264905, 66712502, 29331830, 264909, 265007, 265008, 264910, 265009, 60433358, 60433438, 264596, 21906754, 265010, 265017, 265018, 265019, 18108351, 264762, 264448, 264288, 264769, 21906767, 21906768, 21906769, 265020, 265021, 265022, 264890, 264891, 33657109, 264628, 18108374, 18108376, 55811576, 264638, 60170394, 56182323, 264559, 83373044, 87168518, 80432113, 22279000, 22279002, 264563, 284482, 284565
1436	86635024 (2871, 2872)	Novel Protein sim. GBank gi 3183977 emb CAA39515 - (X56044) protein Hf9C [Mus musculus]		UNCLASSIFIED	263978, 284557, 284559
1437	87631082 (2873, 2874)	Novel Protein sim. GBank gi 2496867 sp Q09232 YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III		UNCLASSIFIED	22278997, 66714117, 29331826, 284907, 56182435, 285009, 18108351, 284692, 284693
1438	85544280 (2875, 2876)	Novel Protein sim. GBank gi 1905906 (AD000092) - hypothetical human serine-threonine protein kinase R31240_1 [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	kinase	284488, 264508, 264906, 264909, 264757, 284600, 264601, 264605, 264768, 264769, 264690, 35698423, 264558, 264563, 264568
1439	91231894 (2877, 2878)	Novel Protein sim. GBank gi 3876289 emb CAA94892 - (Z71180) similar to BPTUKUNITZ inhibitor domain; cDNA EST EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene [Caenorhabditis...]	Contains protein domain (PF00450) - Serine carboxypeptidase	cathepsin	284489, 18108394, 65274572, 58182575, 22278994, 22278996, 35698286, 22278997, 22278998, 22278999, 284259, 60432049, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35896052, 33656970, 264107, 264508, 264509, 264907, 66712502, 29331830, 56182435, 284511, 265008, 265007, 265009, 60432229, 60433438, 264595, 55812038, 55811388, 265011, 265017, 265018, 265019, 18108351, 284448, 18108354, 264288, 18108355, 284767, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 33657109, 18108370, 18108374, 55810764, 35695855, 264634, 264638, 56182323, 83373044, 18108387, 87168518, 60432113, 22279000, 264486
1440	87423643 (2879, 2880)	Novel Protein sim. GBank gi 2662165 dbj BAA23714 - (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]		UNCLASSIFIED	264887, 284259, 264908, 264907, 264908, 264909, 265008, 265010, 265017, 265018, 265019, 18108351, 264369, 265020, 33657023, 33657109, 60431528, 55811576, 264635

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1448	87860859 (2897, 2898)				UNCLASSIFIED	66714117, 264908, 264908, 264591, 264601, 264784, 264632
1450	87458686 (2899, 2900)	Novel Protein sim. GBank gi1707074 (U80450) - M01E11.2 [Caenorhabditis elegans]			UNCLASSIFIED	35686286, 35696052, 265008, 265009, 60170831, 33109954, 264883, 264889, 35696423, 35695855, 56528486
1451	87797970 (2801, 2802)	Novel Protein sim. GBank gi1460304[emb]CAA10600] - (AJ132192) HS1 binding protein 3 [Mus musculus]			UNCLASSIFIED	29331826, 264683, 264693, 263978, 264630
1452	85692899 (2803, 2804)	Novel Protein sim. GBank gi12832906[db]BAA24608.1] - (D89340) dipeptidyl peptidase III [Rattus norvegicus]			peptidase	264681, 33657023, 264629
1453	86130434 (2805, 2806)	Novel Protein sim. GBank gi1728831[sp]P39188[ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII]			kinase	264510, 264768
1454	11204896 (2907, 2808)					
1455	87797896 (2809, 2810)				UNCLASSIFIED	264556
1456	86320218 (2811, 2812)	Novel Protein sim. GBank gi1729230[sp]P41004[CUT3_SCHPO - CHROMOSOME SEGREGATION PROTEIN CUT3]			transport	29331822, 66714117, 29331825, 264805, 29331830, 265008, 265008, 265009, 265011, 265019, 18108351, 21908768, 33657109, 18108376, 264632, 56182323, 87168518, 22278995, 22278996, 22278997, 22278998, 22278999, 29331827, 284107, 265017, 21908765, 21908766, 21908767, 21908769, 29148629, 18108370, 22279000
1457	80076900 (2813, 2814)				UNCLASSIFIED	264107, 264568
1458	87800460 (2815, 2816)	Novel Protein sim. GBank gi12246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]			transport	56182575, 22278999, 60432049, 264259, 29331826, 29331827, 29331828, 285017, 265018, 264107, 264110, 265009, 60432229, 265019, 265020, 263972, 263976, 264635, 22279002, 264568
1459	95360920 (2817, 2818)	Novel Protein sim. GBank gi15524667[gb]AAD44333.1[AF15935 - (AF159356) Munc13-4 protein [Rattus norvegicus]	Contains protein domain (PF00168) - C2 domain		kinase	22278997, 264259, 29331824, 29331826, 29331827, 29331828, 285017, 265018, 264760, 264682, 264448, 264288, 264766, 265021, 264692, 33657023, 33657109, 35695855, 264568
1460	95354602 (2819, 2820)				UNCLASSIFIED	29331822, 264591, 55811957, 264691, 264693, 65274620
1461	94741513 (2821, 2822)	Novel Protein sim. GBank gi1707274 (U80931) - strong similarity to class-II of pyridoxal-phosphate-dependent aminotransferases [Caenorhabditis elegans]	Contains protein domain (PF00202) - gaba Aminotransferases class-III pyridoxal phosphate			22278997, 29331822, 35696052, 265009, 264758, 265017, 265018, 265019, 264760, 264369, 264687, 21908765, 21908768, 265022, 33657109, 27486261, 264555, 83373044
1462	87732016 (2823, 2824)				UNCLASSIFIED	264555, 264556
1463	88090605 (2825, 2826)	Novel Protein sim. GBank gi1770466[emb]CAA68912] - (X98259) M-phase phosphoprotein 8 [Homo sapiens]	Contains protein domain (PF00385) - 'chromo' (CHRomain Organization Modifier) domain		struct	60432049, 264259, 29146499, 264906, 264907, 264512, 265017, 264763, 264766, 18108370, 18108374, 264638, 18108385, 18108388

1464	87620482 (2927, 2928)	Novel Protein sim. GBank gij3874447[embjCAB02772] - (Z81039) predicted using GeneFinder; cDNA EST EMBL: T01209 comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk278a11.5 comes from this gene; cDNA EST yk308a9.3 comes from this gene; cDNA EST yk308a9.5 com...		UNCLASSIFIED	284569, 22278995, 22278998, 22278997, 22278998, 29331822, 29331824, 29331825, 35898052, 20281100, 284905, 29331830, 284909, 265007, 33857402, 21908754, 285017, 285018, 284882, 264684, 264369, 284288, 284766, 21908765, 21906766, 21908767, 21906769, 35895917, 284691, 33857023, 284692, 35898423, 35895855, 284630, 284631, 284639, 284565
1465	87425192 (2929, 2930)	Novel Protein sim. GBank gij4589598[dbjBAA76821.1] - (AB023194) KIAA0977 protein [Homo sapiens]		glucoamylase	284488, 22278994, 56894075, 60432049, 284259, 58182181, 60432289, 29331827, 52844045, 264511, 265007, 265008, 284598, 55812038, 55811386, 284800, 284802, 285017, 285018, 284604, 285019, 18108351, 18108354, 58181562, 21908769, 265021, 33857023, 33857182, 55811576, 284557, 18108382, 60432113
1466	87606227 (2931, 2932)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	284512, 285017, 264689, 264558
1467	87614328 (2933, 2934)			struct	264683, 284636
1468	95342862 (2935, 2936)	Novel Protein sim. GBank gij4507241[refNP_003137.1]pSSRP - structure specific recognition protein 1			22278998, 264758, 285018, 285019, 21908769, 265020, 33857109, 22279002
1469	79236174 (2937, 2938)	Novel Protein sim. GBank gij1906596 (U81788) - kinesin-73 [Drosophila melanogaster]		struct	18108394, 18108397, 18108398, 35898052, 29146499, 265007, 265008, 265009, 285010, 285011, 18108354, 18108365, 18108388, 18108374, 18108381, 18108382, 18108384, 18108388
1470	94980482 (2939, 2940)	Novel Protein sim. GBank gij5849170[gb AAD43131.2]AF15909 - (AF159092) syld709613 protein [Homo sapiens]		UNCLASSIFIED	18108394, 18108398, 56182575, 264259, 29331822, 29331824, 29331825, 60432289, 264907, 264909, 265007, 284910, 265009, 264591, 60432229, 60433358, 264595, 60433438, 264758, 33109854, 265010, 285011, 265018, 264760, 284448, 264764, 284288, 284369, 18108357, 284769, 18108358, 21906767, 21908769, 55811957, 285021, 18108381, 284691, 18108382, 18108385, 18108388, 284628, 18108379, 284637, 284557, 18108381, 56182323, 18108382, 83373044, 18108384, 18108388, 87168518, 60432113, 284404, 22279002, 284482, 264567, 264487
1471	87826842 (2941, 2942)	Novel Protein sim. GBank gij3876148[embjCAB01750] - (Z78542) similar to Mitochondrial carrier proteins; cDNA EST EMBL: T01651 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	29331822, 29331824, 29331825, 264828, 264603, 284689, 264693, 18108374, 55811576

1472	87756616 (2943, 2944)	Novel Protein sim. GBank gi 4680707 gb AAD27743.1 AF13296 - (AF132968) CGI-34 protein [Homo sapiens]		UNCLASSIFIED	284905, 18108351, 21906765, 264486
1473	87791608 (2945, 2946)	Novel Protein sim. GBank gi 3688780 (AF042180) - testis-specific Y-encoded-like protein [Mus musculus]	Contains protein domain (PF00956) - Nucleosome assembly protein (NAP)	MHC	18108394, 22278995, 56994075, 22278999, 29331822, 29331824, 86714117, 29331825, 29331828, 35898052, 284908, 284907, 58182435, 265007, 284758, 265018, 265019, 284760, 284764, 284288, 284685, 284686, 284768, 21906768, 55811957, 285021, 284691, 284693, 284629, 55811578, 284634, 284638, 58182323, 22279002, 284566, 284486
1474	85800989 (2947, 2948)	Novel Protein sim. GBank gi 2494880 sp Q92176 CORO_BOVIN - CORONIN-LIKE PROTEIN P57	Contains protein domain (PF00400) - WD domain, G-beta repeat	struct	284488, 35895917, 35898286, 284692, 33857023, 284693, 33657109, 35896052, 284508, 284905, 284908, 284907, 284629, 284908, 284909, 35898423, 35895855, 284511, 284910, 284632, 284634, 284635, 284636, 284637, 284556, 284557, 284639, 284758, 80432113, 284604, 284605, 284565, 284568, 284764, 284486, 284685, 284766, 284681, 284682, 284288, 284566
1475	86871935 (2949, 2950)		Contains protein domain (PF00041) - Fibronectin type III domain	UNCLASSIFIED	
1476	87548655 (2951, 2952)	Novel Protein sim. GBank gi 4757752 ref NP_004684.1 pANGP - angiopoietin 3	Contains protein domain (PF00147) - Fibrinogen beta and gamma chains, C-terminal globular domain	glycoprotein	80424179, 58181688, 29331824, 60424269, 29331828, 35898052, 284508, 284905, 284908, 284907, 284908, 284909, 284512, 285007, 285008, 285009, 284910, 33657402, 284585, 284586, 55812038, 285011, 284601, 284762, 18108351, 264288, 284368, 284685, 284768, 284689, 55811857, 284691, 284692, 284693, 18108370, 60431528, 18108374, 35898423, 284634, 284635, 284636, 60431850, 284555, 284638, 284557, 284639, 18108382, 18108388, 80432113, 22279002
1477	87774279 (2953, 2954)	Novel Protein sim. GBank gi 2498308 sp Q60870 DP1_MOUSE - POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN HOMOLOG) (GP106)		UNCLASSIFIED	284259, 284107, 284905, 285008, 285010, 285011, 284682, 284288, 265020, 265021, 263974
1478	11754412 (2955, 2956)				284686

1479	91640140 (2957, 2958)	Novel Protein sim. GBank gi 5499741 gb AAD43978.1 AF15298 - (AF152981) chromatin-specific transcription elongation factor FACT 140 kDa subunit [Homo sapiens]		peptidase	56182575, 22278995, 22278996, 22278998, 22278999, 29331822, 29331824, 86714117, 284908, 284907, 56182435, 265006, 60170831, 33657402, 264758, 33109954, 21908754, 265017, 265019, 264448, 264288, 264767, 284887, 52644228, 21906764, 284689, 21906765, 21906768, 21906769, 265020, 265021, 60170815, 264691, 33657023, 33657109, 33657182, 27486261, 27486282, 33657349, 18108370, 60431528, 263978, 55811576, 264556, 264557, 60170394, 87188518, 264404, 22279000, 22279002, 264563, 264482
1480	94312412 (2959, 2960)	Novel Protein sim. GBank gi 3550456 emb CAA06328.1 - (AJ005073) Alix [Mus musculus]		UNCLASSIFIED	18108394, 65274572, 56182575, 22278995, 35696286, 58994075, 22278996, 22278997, 22278998, 22278999, 264091, 264259, 35696052, 28148499, 264103, 264105, 264108, 284907, 52844045, 284112, 265007, 265008, 265009, 60433356, 60433438, 264598, 33109954, 33657084, 52844296, 87188474, 265010, 87188559, 265017, 265018, 265019, 264448, 284682, 284683, 264769, 21906765, 21906768, 21906767, 21906768, 21906769, 265020, 265021, 60170815, 52644150, 33657109, 33657182, 263972, 35895855, 264557, 263981, 83373044, 18108385, 87188518, 264566, 264089, 284488
1481	87021442 (2961, 2962)	Novel Protein sim. GBank gi 4836807 gb AAD30568.1 AF14679 - (AF146793) PFT27 [Mus musculus]		MHC	265006, 265007, 265010, 18108374
1482	85320442 (2963, 2964)	Novel Protein sim. GBank gi 4585372 gb AAD25403.1 AF12292 - (AF122923) Whit inhibitory factor-1 [Mus musculus]	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	264908, 284910, 264758
1483	94115503 (2965, 2966)	Novel Protein sim. GBank gi 535428 (U13736) - calmodulin- like protein [Pisum sativum]	Contains protein domain (PF00036) - EF hand	struct	264259, 29331822, 52845080, 29331825, 29331826, 33656970, 29331830, 265007, 55812038, 33109954, 265017, 264288, 21906768, 21906769, 264638, 18108380, 87188518, 22279000
1484	94131544 (2967, 2968)	Novel Protein sim. GBank gi 1911774 bbs 180090 - (S83364) putative Rab5-interacting protein (clone L1-57) [human, HeLa cells, Peptide Partial, 122 aa] [Homo sapiens]		UNCLASSIFIED	264489, 35696288, 284258, 264107, 264908, 265008, 60433356, 33657402, 60433438, 264288, 21906765, 21906768, 29148627, 33657023, 27486262, 18108374, 35698423, 83373044, 60432113
1485	80194441 (2969, 2970)	Novel Protein sim. GBank gi 5360129 gb AAD42883.1 AF15511 - (AF155117) NY-REN 62 antigen [Homo sapiens]	Contains protein domain (PF00225) - Kinesin motor domain	struct	264369, 265020, 18108374

1486	94125086 (2971, 2972)	Novel Protein sim. GBank gij4589516 dbj BAA76780.1 - (AB023153) KIAA0936 protein [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	56182575, 22278999, 264906, 264907, 21906754, 87168474, 265017, 265019, 18108351, 264288, 265020, 264566, 21906754, 264486
1487	86452711 (2973, 2974)	Novel Protein sim. GBank gij5019275 emb CAB44431.1 - (AJ132751) xenobiotic/medium-chain fatty acid:CoA ligase (form XL-III) [Bos taurus]		synthase	
1488	87732026 (2975, 2976)	Novel Protein sim. GBank gij5712131 gb AAD47379.1 AF12049 - (AF120499) DEM1 protein [Homo sapiens]	Contains protein domain (PF01443) - Viral (Superfamily 1) RNA helicase	fgf	264686, 264769, 264689, 264692, 264693, 264509, 264908, 264907, 18108370, 264908, 264629, 264909, 264510, 265008, 264512, 265007, 265008, 265009, 264555, 264556, 264557, 264558, 264762, 264564, 264682, 21906767, 22278999, 265022, 264259, 264893, 29331824, 29331825, 29331826, 29331827, 29331828, 264103, 263972, 66712502, 35698423, 35695855, 265007, 265008, 265009, 63373044, 21906754, 56526486, 265017, 264563, 18108351, 264564, 264566, 264369, 264288
1489	95104277 (2977, 2978)	Novel Protein sim. GBank gij2497303 sp Q82786 FPRP_RAT - PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR (PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN)	Contains protein domain (PF00047) - Immunoglobulin domain	prostaglandin	
1490	87390127 (2979, 2980)			UNCLASSIFIED	56182575, 264259, 29331822, 29331824, 66714117, 29331827, 29331828, 264508, 264905, 66712502, 265007, 265008, 264594, 33657402, 55812038, 87168474, 265018, 18108351, 264369, 264288, 264769, 264689, 21906767, 21906768, 55811957, 60170815, 33657109, 35695855, 264635, 60170394, 56526486, 22279002, 264563, 265007, 264448, 18108372, 264558, 56182323
1491	83594305 (2981, 2982)	Novel Protein sim. GBank gij295671 (L11275) - selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III [Saccharomyces cerevisiae]		UNCLASSIFIED	
1492	85805363 (2983, 2984)	Novel Protein sim. GBank gij1656005 (U71205) - rti [Mus musculus]	Contains protein domain (PF00071) - Ras family	oncogene	22278997, 22278998, 29331822, 264907, 66712502

1493	91677215 (2985, 2986)	Novel Protein sim. GBank gi 5689515 dbj BAA83041.1 - (AB029012) KIAA1089 protein [Homo sapiens]		UNCLASSIFIED	264488, 52646365, 65274572, 56182575, 22278994, 35696286, 56994075, 22278999, 60432049, 29331824, 29331828, 35696052, 264508, 264905, 264906, 52644045, 264909, 56182435, 265006, 265008, 265009, 60170831, 33657402, 55812038, 265010, 265011, 265017, 265018, 265019, 55811150, 264448, 264882, 264885, 264886, 52644229, 21906765, 21906766, 21906768, 21906769, 265020, 265021, 60170615, 52644150, 33657023, 18108364, 18108365, 33657109, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 18108370, 264829, 18108374, 52644332, 56182323, 87168518, 22279002, 264584, 264586, 264587
1494	87605265 (2987, 2988)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - III ALU SUBFAMILY SB WARNING ENTRY III	Contains protein domain (PF01352) - KRAB box	kinase	264907, 265009, 264769, 18108370, 55811576, 264639, 264565, 264488
1495	87605267 (2989, 2990)	Novel Protein sim. GBank gi 4589588 dbj BAA76816.1 - (AB023189) KIAA0972 protein [Homo sapiens]	Contains protein domain (PF01352) - KRAB box	transcriptfactor	22278997, 264259, 264906, 264907, 265008, 264594, 33657084, 265017, 264760, 264448, 33657109, 264630, 264634, 56526486, 264563, 264565, 264566, 264486, 264567
1496	87784322 (2991, 2992)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	35696286, 264908, 265019, 264693
1497	81695428 (2993, 2994)	Novel Protein sim. GBank gi 3874925 emb CAA92591 - (Z68296) Similarly to Mouse A-RAF proto-oncogene serine/threonine-protein kinase (SW:KRAA_MOUSE); cDNA EST EMBL:D27610 comes from this gene; cDNA EST EMBL:T01018 comes from this gene; cDNA EST EMBL:D33256 comes from this gene:...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264910, 264758, 265011, 264784, 264288, 264690, 264634, 264635, 56526486
1498	90934938 (2995, 2996)	Novel Protein sim. GBank gi 728836 sp P39193 ALU6_HUMAN - III ALU SUBFAMILY SP WARNING ENTRY III		oncogene	264488, 65274572, 29331822, 265017, 265018, 21906765, 29148627, 29148629, 18108374, 264637, 264638, 264567
1499	88451589 (2997, 2998)	Novel Protein sim. GBank gi 2570188 (U54556) - microfilament sheath protein SHP3 [Litomosoides sigmodontis]		glucoamylase	263978, 264568
1500	80498386 (2999, 3000)			UNCLASSIFIED	22278998, 264769, 18108379
1501	85795297 (3001, 3002)	Novel Protein sim. GBank gi 2078483 (U43200) - antifreeze glycoprotein precursor [Boreogadus saida]		UNCLASSIFIED	264559
1502	80206141 (3003, 3004)				264508, 264112, 264604, 264684, 52644150, 55811576, 264632, 264556, 264638, 56182323, 264563, 264486
1503	87012701 (3005, 3006)	Novel Protein sim. GBank gi 3900855 (AC004874) - similar to N-acetylgalactosaminyltransferase; similar to Q07537 (PID:q1171989) [Homo sapiens]	Contains protein domain (PF00535) - Glycosyl transferases	transferase	29331822, 265007, 264369

1504	79640051 (3007, 3008)			Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	284693
1505	86102872 (3009, 3010)	Novel Protein sim. GBank gij4753775[emb]CAB41870.1] - (AJ132545) protein kinase [Homo sapiens]		Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	29331826, 35698052, 264509, 264906, 264907, 264908, 264909, 264511, 264910, 55812038, 264759, 264763, 264764, 264689, 35695917, 265022, 33657109, 18108374, 284631, 284635, 264638, 264566
1506	94143219 (3011, 3012)	Novel Protein sim. GBank gij1304201[dbj]BAA06170] - (D29768) alternatively spliced product [Rattus norvegicus]		Contains protein domain (PF00018) - SH3 domain	glycoprotein	65274572, 56182575, 56994075, 22278997, 22278998, 22278999, 264091, 264092, 60432049, 264259, 52645080, 29331822, 29331827, 264108, 29331830, 264908, 56182435, 264110, 264511, 264512, 55812038, 21908754, 87168559, 264600, 265017, 265018, 264681, 18108354, 264369, 264687, 264689, 21908765, 29148627, 21908768, 21908769, 29148629, 52844150, 33657023, 18108376, 65274791, 56182323, 264558, 264559, 18108385, 87168518, 60432113, 22279000, 264565
1507	83738250 (3013, 3014)	Novel Protein sim. GBank gij5689513[dbj]BAA83040.1] - (AB029011) KIAA1088 protein [Homo sapiens]			helicase	264639
1508	11618758 (3015, 3016)	Novel Protein sim. GBank gij5031975[ref]NP_005875.1[pa]K4 - protein kinase related to S. cerevisiae STE20, effector for Cdc42Hs		Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264593
1509	87318451 (3017, 3018)	Novel Protein sim. GBank gij113161[sp]P28614[ACOR_ALCEU - ACETOIN CATABOLISM REGULATORY PROTEIN			UNCLASSIFIED	264259, 29331822, 265007, 18108374, 264556
1510	95362643 (3019, 3020)	Novel Protein sim. GBank gij113161[sp]P28614[ACOR_ALCEU - ACETOIN CATABOLISM REGULATORY PROTEIN			UNCLASSIFIED	264259, 29331822, 265007, 18108374, 264556
1511	86318073 (3021, 3022)	Novel Protein sim. GBank gij1728831[sp]P38188[ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII			UNCLASSIFIED	264259, 29331822, 29331824, 29331827, 264509, 264907, 264510, 264511, 265007, 264512, 265008, 87168559, 264288, 265022, 33657023, 35695855, 264637, 264638, 264563
1512	95345390 (3023, 3024)	Novel Protein sim. GBank gij4559353[gb]AAD23014.1[AC00858] putative extragenic suppressor protein [Arabidopsis thaliana]		Contains protein domain (PF01163) - RIO1/ZK632.3/MJ0444 family		52845156, 18108398, 56994075, 60432289, 265008, 60433358, 60433436, 21908754, 87168474, 87168559, 265018, 264762, 264763, 264687, 21908765, 21908769, 27486282, 35695763, 18108374, 35696423, 264555, 18108385, 18108387, 18108388, 87168518, 264482
1513	87436228 (3025, 3026)	Novel Protein sim. GBank gij1330394 (U58761) - C01F1.6 gene product [Caenorhabditis elegans]				35698052, 264905, 264906, 264907, 264908, 264909, 264910, 264591, 264766, 264689, 264692, 264629, 264636

1514	95345392 (3027, 3028)	Novel Protein sim. GBank gi 4559353 gb AAD23014.1 AC00658 - (AC006585) putative extragenic suppressor protein [Arabidopsis thaliana]	Contains protein domain (PF01163) - RIO1/ZK632.3/MJ0444 family	UNCLASSIFIED	52644507, 52645156, 52646365, 52646842, 65274572, 22278994, 35698288, 56994075, 264259, 52645080, 29331822, 29331825, 35698052, 29331830, 52644045, 56182435, 265006, 60433358, 60433438, 55812038, 21906754, 52646317, 52644296, 87168474, 87168559, 264448, 52644228, 21906785, 21906788, 21906787, 21906788, 35695917, 265020, 52644150, 33657023, 52645129, 33657109, 33657182, 27488261, 27488262, 27488264, 27488265, 35695763, 18108378, 35698423, 35695855, 52644332, 18108385, 18108387, 87168518, 60432113 265020, 264639
1515	79163538 (3028, 3030)	Novel Protein sim. GBank gi 3879501 emb CAA87795 - (Z47812) similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33368 comes from this gene; cDNA EST EMBL:D33965 comes from this gene; cDNA EST EMBL:D33822 comes from this gene; cDNA EST EMBL:D34547 comes from this ge...	ubiquitin		
1516	88073539 (3031, 3032)	Novel Protein sim. GBank gi 498015 (L27479) - X123 [Homo sapiens]		UNCLASSIFIED	265008, 56182323, 22279002
1517	87793325 (3033, 3034)	Novel Protein sim. GBank gi 3415134 (AF082024) - Phyb1 [Pimpinella bractycarpa]			264091, 18108370, 264404
1518	87350697 (3035, 3036)	Novel Protein sim. GBank gi 728838 sp P39195 ALU8_HUMAN - IIII ALU SUBFAMILY SX WARNING ENTRY IIII	tm7		66714117, 264508, 264509, 264905, 264510, 264910, 264591, 264595, 264288, 264768, 264769, 18108374, 264638, 264638, 264486 264589, 264489, 60432049, 265008, 33657402, 264588, 21908754, 265019, 264368, 21908785, 21908788, 21908789, 264691, 65274620, 33657182, 27488261, 18108374, 264557, 264639, 87168518, 22279002
1519	94328689 (3037, 3038)	Novel Protein sim. GBank gi 5262681 emb CAB45771.1 - (AL080198) hypothetical protein [Homo sapiens]			
1520	87592855 (3039, 3040)	Novel Protein sim. GBank gi 2662161 dbj BAA23712 - (AB007800) H0452 cDNA clone for KIAA0440 has a 438- bp insertion at position 1711 of the sequence of KIAA0440. [Homo sapiens]	UNCLASSIFIED		18108392, 60432049, 264259, 29331824, 265007, 60433358, 265010, 21908788, 264636
1521	86970696 (3041, 3042)	Novel Protein sim. GBank gi 5052351 gb AAD38518.1 AF13542 - (AF135421) GDP- mannose pyrophosphorylase B [Homo sapiens]	Contains protein domain (PF00483) - Nucleotidyl transferase	synthase	18108384, 264259, 66714117, 265011, 264603, 265019, 18108384, 35698423, 264557, 264558, 18108388
1522	78960687 (3043, 3044)			UNCLASSIFIED	29331824, 265018, 265020, 265021
1523	91005151 (3045, 3046)	Novel Protein sim. GBank gi 3776567 (AC005388) - Strong similarity to F2187.33 gi 2809264 from A. thaliana BAC gb AC002560. EST gb N65119 comes from this gene. [Arabidopsis thaliana]		UNCLASSIFIED	65274572, 21908788, 264693
1524	80203723 (3047, 3048)				
1525	87799867 (3049, 3050)	Novel Protein sim. GBank gi 4759040 ref NP_004283.1 pRIN1 - ras inhibitor		UNCLASSIFIED	264112, 21908754, 263974
				UNCLASSIFIED	264683, 264687, 264689, 264690, 264692, 264693

1526	95105344 (3051, 3052)	Novel Protein sim. GBank gi 728850 sp P08640 AMYH_YEAST - GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)			glycoprotein	35896286, 56182181, 60431735, 264595, 55812038, 264605, 264683, 21906785, 55811957, 265020, 65274791, 264555, 264556, 264557, 264558, 264559, 83373044
1527	88262512 (3053, 3054)	Novel Protein sim. GBank gi 2792486 (AF041107) - tulip 2 [Rattus norvegicus]				56182575, 264258, 60432049, 29331822, 60432289, 264908, 68712502, 60433438, 87168559, 265017, 264288, 21906768, 21906769, 263977, 55811576, 56182323, 18108381
1528	94130918 (3055, 3056)				UNCLASSIFIED	22278995, 22278997, 264259, 66712502, 264598, 265017, 265019, 264682, 264448, 264683, 264764, 264685, 264686, 21906765, 21906766, 21906767, 21906768, 21906769, 265022, 264693, 83373044, 18108385
1529	94120793 (3057, 3058)	Novel Protein sim. GBank gi 408683 gb AAD20053 - (AF131826) Unknown [Homo sapiens]			UNCLASSIFIED	264488, 263994, 56182575, 22278995, 35896286, 22278997, 264259, 29331822, 60432289, 29331827, 35896052, 264509, 264906, 264907, 264908, 264909, 52644045, 56182435, 264511, 265009, 264810, 60433356, 60433438, 285017, 265018, 264760, 264448, 264764, 264369, 264288, 264766, 18108357, 264768, 52644229, 21906765, 21906766, 21906767, 21906768, 265021, 265022, 52644150, 33657109, 264629, 35895855, 60432113, 22279002, 264563, 264564, 264488, 264567
1530	85012765 (3059, 3060)	Novel Protein sim. GBank gi 2828710 (AF043842) - matrin cyclophilin [Rattus norvegicus]				264488, 264489, 35896286, 29331825, 35896052, 264508, 264905, 264906, 264907, 264909, 264510, 264511, 264512, 264910, 264592, 264595, 18108351, 264764, 264683, 264684, 264766, 264768, 18108357, 264769, 35895917, 264628, 264629, 18108374, 35895855, 264630, 264631, 264634, 264555, 264636, 264637, 264404, 264563, 264566, 264486
1531	85419351 (3061, 3062)	Novel Protein sim. GBank gi 1905874 (U90878) - carboxyl terminal LIM domain protein [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).		kinase	56182575, 35896286, 264087, 264259, 29331822, 29331825, 29331826, 29331827, 35896052, 264509, 56182435, 264510, 264511, 265007, 60433356, 55811386, 264681, 264369, 264288, 264766, 264687, 55811957, 35895917, 33657023, 35895763, 55810764, 35896423, 55811576, 263981, 60170394, 56182323, 83373044, 60432113, 264566

1532	85718224 (3063, 3084)	Novel Protein sim. GBank gi 3874716 emb CAA81265 - (Z88494) cDNA EST EMBL:D65271 comes from this gene; cDNA EST EMBL:D64845 comes from this gene; cDNA EST EMBL:D64449 comes from this gene; cDNA EST EMBL:D67438 comes from this gene; cDNA EST EMBL:D68087 comes from this gene; cDN...			UNCLASSIFIED	264689
1533	94239830 (3065, 3066)	Novel Protein sim. GBank gi 1490324 emb CAB01543 - (Z78141) unknown [Mus musculus]			struct	29331824, 29148499, 264907, 264112, 265008, 265011, 265017, 265018, 264762, 18108351, 263987, 20281149, 18108374, 263981, 264588
1534	85343941 (3067, 3068)	Novel Protein sim. GBank gi 81286 pir S22697 - extensin - Volvox carter (fragment)			UNCLASSIFIED	264905, 264907, 264766, 264637
1535	80936732 (3069, 3070)					65274572, 22278997, 264259, 60432049, 29331822, 60432288, 29331827, 29148499, 265008, 265008, 60170831, 60433438, 33109954, 87168559, 265018, 18108357, 21908768, 29148629, 265021, 265022, 18108377, 58182323, 60432113, 22278000, 22278002
1536	87602856 (3071, 3072)	Novel Protein sim. GBank gi 106024 pir B32891 - finger protein 2, placental - human	Contains protein domain (PF00096) - Zinc finger, C2H2 type		transcriptfactor	264686, 18108357, 18108394, 21906767, 21906768, 29148629, 35696286, 265020, 265021, 52844150, 264693, 66714117, 29331825, 29331826, 264508, 264905, 20281148, 264908, 18108374, 35696423, 35695855, 265008, 264634, 264636, 264638, 18108385, 58526488, 265017, 265018, 264563, 264762, 18108351, 264448, 264369, 264766
1537	85354556 (3073, 3074)	Novel Protein sim. GBank gi 3876332 emb CAB02096 - (Z79754) cDNA EST EMBL:T01054 comes from this gene; cDNA EST EMBL:D73600 comes from this gene; cDNA EST yk426f12.5 comes from this gene; cDNA EST yk342f10.5 comes from this gene; cDNA EST yk475c5.5 comes from this gene; cDNA ES...				65274572, 56182575, 60432049, 264259, 29331828, 265008, 265007, 60433358, 60433438, 284601, 18108351, 264448, 264369, 264288, 33857023, 65274620, 33857109, 60432113
1538	85724628 (3075, 3076)	Novel Protein sim. GBank gi 403440 (M81787) - [Gallus domesticus skeletal muscle mRNA, partial cds.], gene product [Gallus gallus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase		18108394, 18108397, 264909, 265008, 265009, 265010, 18108351, 264638, 18108382, 18108385, 18108388

1539	95337628 (3077, 3078)	Novel Protein sim. GBank gi 321841 emb CAA19575.1 - (AL023859) SPBC19C7.07c, putative tRNA splicing endonuclease gamma subunit, len:284aa, similar eg. to YAR008W, YAH8_YEAST, P39707, YAR008W, tRNA splicing endonuclease gamma subunit, (275aa), fasta scores, opt:269, E(1):6.4e-2...		nuclease	22278994, 22278996, 35696286, 56994075, 22278997, 22278998, 22278999, 60432049, 284259, 29331822, 29331824, 60424269, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 33656970, 56162435, 265009, 33657402, 60433356, 60433438, 55812038, 21906754, 87188559, 265017, 265018, 265019, 18108351, 264288, 52844229, 18108359, 21806764, 21906767, 21908768, 35695917, 265020, 265021, 52844150, 33657023, 33657109, 27486261, 18108370, 18108376, 35698423, 55811578, 65274791, 284558, 58182323, 60170394, 83373044, 87188518, 60432113, 22279000, 22279002, 284568
1540	95352858 (3079, 3080)	Novel Protein sim. GBank gi 5052634 gb AAD38647.1 AF14567 - (AF145672) BcDNA.GH12174 [Drosophila melanogaster]		UNCLASSIFIED	264369, 264691, 263978
1541	95317948 (3081, 3082)	Novel Protein sim. GBank gi 5052348 gb AAD38515.1 AF13501 - (AF135016) protein phosphatase 2A 48 kDa regulatory subunit [Homo sapiens]		phosphatase	264486, 264489, 22278999, 264259, 29331822, 35696052, 264508, 264509, 264905, 264907, 264908, 264511, 264512, 264910, 264592, 264781, 264782, 264448, 264764, 264288, 264887, 21908769, 55811957, 35695917, 265020, 264691, 33657023, 264692, 33657109, 264626, 18108374, 264632, 264634, 264635, 264639, 18108385, 264563, 264564, 264565, 264566, 264486
1542	90937549 (3083, 3084)	Novel Protein sim. GBank gi 5305702 gb AAD41779.1 AF12686 - (AF126867) calpain-like protease [Mus musculus]		cathepsin	18108392, 18108394, 65274572, 29331822, 264508, 265007, 265008, 265009, 265011, 264682, 18108354, 18108355, 52844150, 18108368, 264636, 18108381, 18108382
1543	94348768 (3085, 3086)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - III ALU SUBFAMILY SB WARNING ENTRY IIII		nuclease	264108, 33109954, 265019, 264683, 35695917, 264690, 264692, 33657109
1544	87757295 (3087, 3088)	Novel Protein sim. GBank gi 3493162 (AF084259) - bromodomain-containing protein BP75 [Mus musculus]	Contains protein domain (PF00439) - Bromodomain	nuc_rept	35696288, 56994075, 22278999, 35696052, 60433358, 60433438, 265011, 264683, 33657109, 35698423, 264631, 87188518, 22279000
1545	85757973 (3089, 3090)	Novel Protein sim. GBank gi 1086591 (U41007) - similar to S. carvisiae nuclear protein SNF2 (SP:P22082) in a region of gly-arg repeats [Caenorhabditis elegans]		UNCLASSIFIED	284112, 284692, 284693, 55811576
1546	79476589 (3091, 3092)			UNCLASSIFIED	284905, 284686
1547	86999594 (3093, 3094)	Novel Protein sim. GBank gi 2661132 (AF035683) - p21 [Mus musculus]		UNCLASSIFIED	284259, 29331822, 66714117, 265007, 55811386, 265010, 264600, 265017, 265018, 264288, 264768, 265020, 265022, 55811576, 18108380, 264563

1548	84233065 (3095, 3096)	Novel Protein sim. GBank gij3043692[dbj BAA25510] - (AB011156) KIAA0584 protein [Homo sapiens]		UNCLASSIFIED	29331824, 60431528, 264639, 56182323
1549	85330048 (3097, 3098)	Novel Protein sim. GBank gij589519[dbj BAA83043.1] - (AB028014) KIAA1091 protein [Homo sapiens]		eph	60424179, 22278995, 35696286, 22278998, 22278999, 264092, 264094, 29331822, 56182181, 29331824, 35696052, 264905, 264906, 264908, 264909, 265008, 264511, 265008, 60431735, 60433356, 21906754, 55811388, 87168559, 265017, 265018, 265019, 55811150, 264682, 264288, 264389, 56181562, 264788, 21906785, 21906788, 21906789, 55811957, 265020, 264691, 33657109, 60431528, 35696423, 35695855, 56526486, 60432113, 22279002, 264563, 264566
1550	85201807 (3099, 3100)	Novel Protein sim. GBank gij544483[sp P35350 GUSB_BOVIN - POSSIBLE GUSTATORY RECEPTOR TYPE B (PPR1 PROTEIN)]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	tm7	65274572, 60432289, 265008, 264910, 265011, 265017, 265019, 264788, 56182323
1551	86077111 (3101, 3102)	Novel Protein sim. GBank gij4758566[ref NP_004798.1 pH56S - heparan-sulfate 6-sulfotransferase]		UNCLASSIFIED	22278999, 29331822, 264508, 264509, 264908, 264907, 264909, 285007, 264512, 264910, 21906754, 265018, 265019, 264681, 264784, 264786, 264688, 264789, 21906789, 264692, 35695763, 264635, 264555, 264556, 264557, 264638, 264558, 264563
1552	87617114 (3103, 3104)			UNCLASSIFIED	264259, 29331828, 66712502, 264784, 264288, 264688, 33657109, 264556
1553	94725512 (3105, 3106)	Novel Protein sim. GBank gij4589570[dbj BAA76807.1] - (AB023180) KIAA0963 protein [Homo sapiens]	Contains protein domain (PF00304) - Gamma-thionins family	- dehydrogenase	56182575, 35696286, 29146499, 264509, 264907, 264908, 264909, 56182435, 265006, 265008, 265009, 264910, 264757, 264758, 265017, 55811150, 18108351, 264784, 56181562, 35695917, 264693, 33657109, 18108374, 35696423, 65274781, 35695855, 264635, 264555, 56182323, 18108382, 83373044, 22279000
1554	94233069 (3107, 3108)	Novel Protein sim. GBank gij3043692[dbj BAA25510] - (AB011156) KIAA0584 protein [Homo sapiens]	Contains protein domain (PF00446) - Gonadotropin-releasing hormones	transferase	35696286, 22278997, 264259, 29331822, 29331824, 29331825, 29331828, 265007, 265009, 60432229, 33657402, 55812038, 265011, 265018, 264681, 264389, 264686, 264767, 264768, 21906785, 21906789, 35695917, 264693, 18108370, 60431528, 55811576, 264631, 60170394, 56182323, 83373044, 18108385, 22279000, 22279002

1555	87332970 (3109, 3110)	Novel Protein sim. GBank gjl2257495[dbj BAA21392] - (AB004534) pl015 [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264259, 28331826, 35696052, 264508, 264905, 284908, 284907, 284908, 52644045, 284909, 284910, 60432228, 60433358, 55812038, 284758, 284759, 33657084, 265011, 87188559, 284601, 285018, 265019, 284763, 284784, 284288, 264766, 284768, 21908765, 35695917, 265022, 264691, 33657023, 35696423, 35695855, 264635, 264555, 264636, 264638, 264639, 18108385, 56526488
1556	91228268 (3111, 3112)			UNCLASSIFIED	63373044, 264758, 265022, 264600, 35696052, 264630, 35696423, 265018, 264632, 264662, 29331822, 265020, 265011, 60432228, 284509, 284908, 284907, 284908, 264909, 264910, 284758, 55811386, 264761, 264762, 264766, 264769, 264690, 263978, 264634, 264635, 264639, 264594, 264486, 22278994, 22278998, 22278997, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331827, 264908, 264909, 60433356, 21908754, 265017, 265018, 264448, 21908767, 265021, 265022, 33657023, 33657109, 18108370, 55811576, 83373044, 87188518, 22279000, 22279002, 264259, 29331822, 60432289, 35696052, 264107, 264110, 21908754, 33109854, 87188559, 264760, 264763, 21908764, 21908765, 21908769, 265021, 264690, 35695855
1557	87640609 (3113, 3114)	Novel Protein sim. GBank gjl3329611 (AF078783) - contains similarity to C3HC4-type zinc fingers (Pfam; zfc3HC4.hmm, score: 34.08); most similar to drosophila goliath protein (SW: Q06003) [Caenorhabditis elegans]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	
1558	94840376 (3115, 3116)	Novel Protein sim. GBank gjl5360105[gbl AAD42871.1 AF155105] putative zinc finger protein NY-REN-34 antigen [Homo sapiens]			
1559	88224865 (3117, 3118)	Novel Protein sim. GBank gjl112808[sp P02750 A2GL_HUMAN - LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG)]	Contains protein domain (PF00560) - glycoprotein Leucine Rich Repeat		
1560	84580675 (3119, 3120)	Novel Protein sim. GBank gjl3880146[emb CAA82704] - (Z88319) Similarity to Human hnRNP F protein (PIR Acc. No. S43484); cDNA EST EMBL:D34218 comes from this gene; cDNA EST EMBL:D37248 comes from this gene; cDNA EST EMBL:D71817 comes from this gene; cDNA EST EMBL:D74531 comes from...		UNCLASSIFIED	264908, 264603, 264638
1561	86609159 (3121, 3122)			UNCLASSIFIED	264510, 264594
1562	83358682 (3123, 3124)			UNCLASSIFIED	263967
1563	85508894 (3125, 3126)			UNCLASSIFIED	264910, 284784, 264766
1564	87766371 (3127, 3128)	Novel Protein sim. GBank gjl1168287[sp P45953 ACDV_RAT - ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (VLCAD)]	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	UNCLASSIFIED	18108394, 35696286, 284259, 29331822, 60432289, 35696052, 29331828, 264508, 68712502, 264908, 56182435, 265007, 264910, 60170831, 21908754, 265011, 265017, 265018, 265019, 18108351, 264448, 264288, 264686, 21908765, 21908768, 265021, 60170615, 264692, 35696423, 35695855, 264557, 56182323, 60432113, 22278002, 264482

1565	87783361 (3128, 3130)	Novel Protein sim. GBank gi 129726 sp P05307 PDI_BOVIN - PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (PROLYL 4-HYDROXYLASE BETA SUBUNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55)			isomerase	264488, 264688, 18108388, 55811857, 264534, 264259, 264508, 264905, 264509, 264908, 18108372, 264510, 264511, 264512, 265008, 264630, 265009, 264910, 264635, 264638, 264591, 264555, 264592, 264637, 264593, 264594, 264595, 264598, 265011, 264603, 22279002, 18108351, 264762, 264565, 264567
1566	87424749 (3131, 3132)	Novel Protein sim. GBank gi 3880445 emb CAA20328 - (AL031266) VM106R.1 [Caenorhabditis elegans]			tnf	22278996, 22278998, 264259, 29331822, 29331824, 60432288, 29331827, 86712502, 264908, 265008, 18108351, 52644229, 21908765, 21908767, 21908768, 21908769, 33657109, 264555, 264638, 264482
1567	84999006 (3133, 3134)	Novel Protein sim. GBank gi 4929899 gb AAD34110.1 AF15187 - (AF151873) CGI-115 protein [Homo sapiens]			UNCLASSIFIED	56182575, 21906769, 264692
1568	87648761 (3135, 3136)	Novel Protein sim. GBank gi 4827063 ref NP_005072.1 pZNF1 - zinc finger protein 142 (clone pHZ-49)	Contains protein domain (PF00096) - Zinc finger, C2H2 type		transcriptfactor	29331827, 29331830, 264511, 265009, 264758, 21906767, 21906768, 264691, 264693, 22279000, 22279002
1569	90936668 (3137, 3138)	Novel Protein sim. GBank gi 5689451 dbj BAA83009.1 - (AB028980) KIAA1057 protein [Homo sapiens]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2		ubiquitin	65274572, 29331822, 29331824, 29331828, 264905, 56182435, 265007, 265019, 264764, 21908765, 21908769, 55811957, 60170615, 52644150, 264692, 33657023, 33657109, 18108377, 264563, 264567
1570	86943981 (3139, 3140)	Novel Protein sim. GBank gi 1255430 (U53155) - No definition line found [Caenorhabditis elegans]			UNCLASSIFIED	264595, 264682, 265021
1571	91210340 (3141, 3142)	Novel Protein sim. GBank gi 450773 ref NP_001061.1 pTUBG - tubulin, gamma polypeptide	Contains protein domain (PF00091) - Tubulin/FtsZ family		tubulin	22278996, 35696288, 22278997, 264091, 264259, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 56182435, 264510, 265007, 264758, 265011, 18108351, 264448, 264288, 264369, 21908765, 21906767, 21906768, 21908769, 35695917, 265020, 265021, 33657023, 264693, 18108370, 18108377, 35696423, 35695855, 264634, 264555, 264558, 18108384
1572	81201684 (3143, 3144)				UNCLASSIFIED	35696052, 264905, 264906, 264908, 284910, 264758, 264768, 35695917, 264637
1573	80207068 (3145, 3146)				UNCLASSIFIED	263972

1574	94216142 (3147, 3148)	Novel Protein sim. GBank gi 4758334 ref NP_004258.1 pFADS - delta-6 fatty acid desaturase	Contains protein domain (PF00173) - Heme-binding domain in cytochrome b5 and oxidoreductases	cytochrome	18108394, 264887, 18108397, 18108398, 22278996, 22278997, 22278998, 264259, 29331825, 29331827, 29148498, 29148499, 264107, 264907, 264909, 52644045, 264511, 265008, 264910, 265009, 264591, 21906754, 265011, 265019, 18108351, 264882, 264763, 264764, 18108354, 264369, 264288, 264685, 264766, 264688, 264768, 264688, 21906765, 21906766, 21906767, 21906768, 21906769, 29148629, 264690, 264691, 264693, 20281089, 18108370, 18108374, 18108378, 35695855, 264634, 18108384, 18108385, 22279002, 264563, 264566
1575	95340019 (3149, 3150)	Novel Protein sim. GBank gi 3881810 emb CAA94856 - (Z70783) similar to EF-hand calcium binding protein; cDNA EST EMBL:CO8700 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00036) - EF hand	phosphatase	56994075, 264259, 29331822, 29331824, 29331825, 60432289, 29331828, 264909, 265008, 265008, 265009, 265010, 87168559, 55811150, 264448, 18108354, 264369, 264288, 18108357, 55811957, 265020, 265021, 60170615, 264691, 33657023, 33657109, 60431528, 65274791, 35695855, 18108385, 60432113, 22279002, 264482
1576	95314018 (3151, 3152)	Novel Protein sim. GBank gi 2773195 (AF039711) - contains similarity to Physcomitrella patens glyceraldehyde 3-phosphate dehydrogenase (GB:X72381) [Caenorhabditis elegans]		UNCLASSIFIED	264568, 264082, 264084, 264095, 264259, 264508, 264905, 264509, 264907, 264909, 264510, 264511, 265006, 264910, 21906754, 265010, 265011, 87168559, 264761, 264762, 264288, 264766, 264769, 264691, 264693, 35695855, 264632, 264634, 264635, 264638, 83373044, 264486
1577	87613800 (3153, 3154)	Novel Protein sim. GBank gi 2489130 sp P70315 WASP_MOUSE - WISKOTT- ALDRICH SYNDROME PROTEIN HOMOLOG (WASP)		UNCLASSIFIED	264511, 265011, 264681, 264369, 264686, 264689, 264629, 264555, 264558, 264559
1578	87123138 (3155, 3156)				264259, 29331826, 265017, 264689, 264693, 60432113
1579	88085141 (3157, 3158)	Novel Protein sim. GBank gi 2978255 dbj BAA25190 - (AB007407) myeloid zinc finger protein-2 [Mus musculus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	35696286, 264908, 264909, 60433438, 55811386, 264369, 264685, 33657023, 264555, 264558, 264557, 87168518
1580	87255702 (3159, 3160)	Novel Protein sim. GBank gi 4324682 gb AAD16986 - (AF109674) late gestation lung protein 1 [Rattus norvegicus]	Contains protein domain (PF00188) - SCP-like extracellular protein	glycoprotein	22278999, 35696052, 29331830, 52644045, 55812038, 87168474, 265018, 264448, 265022, 264638, 56526486, 22279000
1581	95087431 (3161, 3162)	Novel Protein sim. GBank gi 2088838 (AF003386) - F59E12.4 gene product [Caenorhabditis elegans]			22278995, 29331822, 29331824, 29331826, 56182435, 264595, 55812038, 87168559, 265017, 264288, 21908764, 55811957, 35695917, 264692, 55811578, 264637, 56182323, 264559, 83373044, 60432113

1582	85358052 (3163, 3164)	Novel Protein sim. GBank gjl5420387[embjCAB46678.1] - (AJ243459) proteophosphoglycan [Leishmania major]		phosphatase	264259, 60432288, 29331827, 264509, 264905, 264906, 264907, 264909, 264910, 264782, 264288, 264788, 264789, 264832, 264555, 264639, 56526488, 22279000
1583	87622715 (3165, 3166)	Novel Protein sim. GBank gjl5578958[embjCAB51351.1] - (AL050306) dJ475B7.2 (novel protein) [Homo sapiens]		UNCLASSIFIED	60170031, 33657402, 264682, 21906768, 35695855, 264563
1584	85337722 (3167, 3168)	Novel Protein sim. GBank gjl5531815[gbjAAD4482.1] - (AF078850) steroid dehydrogenase homolog [Homo sapiens]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	60424179, 52646842, 65274572, 56182575, 22278995, 35688286, 22278996, 22278998, 22278999, 264259, 29331822, 56182181, 60424268, 60432289, 29331827, 29331828, 35696052, 28146498, 66712502, 29331830, 52644045, 56182435, 264510, 264512, 265008, 60433356, 33657402, 60433438, 55812038, 21906754, 55811386, 52644296, 87168474, 87168559, 265018, 265019, 264448, 264369, 264288, 18108358, 21906765, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 18108374, 55810764, 55811576, 35686423, 65274791, 35695855, 56182323, 83373044, 18108387, 87168518, 60432113, 22278002
1585	87626117 (3169, 3170)	Novel Protein sim. GBank gjl4240132[dbjBAA74846.1] - (AB020630) KIAA0823 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	phosphatase	35696286, 22278998, 264259, 29331822, 29331824, 29331825, 264805, 265008, 265007, 265008, 60433356, 33109954, 87168474, 265011, 265017, 264604, 264369, 264288, 264685, 264769, 18108359, 21906765, 18108384, 18108370, 264629, 263972, 18108383, 18108388, 264482, 264584
1586	88067081 (3171, 3172)	Novel Protein sim. GBank gjl3786494 (AF098993) - No definition line found [Caenorhabditis elegans]			285017, 265018, 264689, 33657023, 263978, 264638, 264563
1587	87617126 (3173, 3174)	Novel Protein sim. GBank gjl3253159 (AF005355) - translation initiation factor eIF2C [Oryctolagus cuniculus]		UNCLASSIFIED	264907, 264908, 264511, 264910, 264591, 264594, 264629, 264631, 264563, 264483, 264567
1588	87802536 (3175, 3176)	Novel Protein sim. GBank gjl1077573[pirjSS2680 - probable ribosomal protein L34, mitochondrial - yeast (Saccharomyces cerevisiae)]	Contains protein domain (PF00468) - Ribosomal protein L34	UNCLASSIFIED	264259, 29331828, 264905, 265008, 264758, 21906754, 264761, 264762, 21906765, 21906769, 60170615, 52644150, 33657109, 35695855, 56182323, 18108385
1589	90980653 (3177, 3178)	Novel Protein sim. GBank gjl2137756[pirjI48746 - semaphorin C - mouse (fragment)]		UNCLASSIFIED	65274572, 264480, 29331822, 66714117, 29331827, 29331828, 56182435, 265008, 60170831, 264595, 264758, 264588, 265011, 264688, 21908766, 21906768, 55811957, 27488265, 264639, 18108385, 56526486, 60432113

1590	95319825 (3179, 3180)				UNCLASSIFIED	284489, 22278998, 284259, 29331824, 29331825, 29331826, 29331827, 285006, 60433358, 21906754, 285017, 285018, 285019, 284448, 284765, 284288, 52844229, 21906765, 21906767, 21906788, 21906789, 285021, 284692, 27486285, 35695783, 58528488, 60432113, 22279000, 22279002, 284564
1591	86877160 (3181, 3182)					
1592	87882533 (3183, 3184)	Novel Protein sim. GBank gi 4557749 ref NP_000237.1 pMHC2 - MHC class II transactivator			MHC	284259, 284905, 29331830, 284595, 285017, 284448, 284288, 284690, 284629, 87188518
1593	94991661 (3185, 3186)				UNCLASSIFIED	65274572, 60432049, 264509, 60433356, 21906754, 21906767, 21906768, 18108370, 35698423, 22279000, 284585, 264587
1594	87773752 (3187, 3188)	Novel Protein sim. GBank gi 3877072 emb CAA87060 - (Z46937) similarity with ribosomal protein L21 [Caenorhabditis elegans]			UNCLASSIFIED	284488, 29331827, 284905, 284906, 264907, 284908, 284909, 284910, 284592, 284593, 284757, 284602, 284604, 284760, 284881, 284288, 284768, 284768, 29148629, 35695917, 284692, 284628, 284829, 284630, 284632, 284634, 284635, 284636, 284639, 284563, 284564, 284568
1595	79919425 (3189, 3190)	Novel Protein sim. GBank gi 3152703 (AF065389) - tetraspan NET-4 [Homo sapiens]	Contains protein domain (PF00335) - 4 transmembrane segments integral membrane proteins		UNCLASSIFIED	29331828, 284908, 55811957
1596	79933928 (3191, 3192)				UNCLASSIFIED	28146498, 284758, 263987
1597	88971857 (3193, 3194)	Novel Protein sim. GBank gi 5257114 gb AAD41244.1 AF094480 - (AF094480) cholesterol 24-hydroxylase [Homo sapiens]	Contains protein domain (PF00067) - Cytochrome P450		cyto450	284092, 29331824, 284508, 284682, 264369, 284886, 284630, 284563
1598	87862939 (3195, 3196)					284259, 284634
1599	87849829 (3197, 3198)	Novel Protein sim. GBank gi 4506797 ref NP_000324.1 pSCA7 - spinocerebellar ataxia 7 (olivopontocerebellar atrophy with retinal degeneration)	Contains protein domain (PF01581) - FMRFamide related peptide family		UNCLASSIFIED	52845080, 29331824, 29331828, 284511, 285009, 285011, 284605, 284448, 284764, 285020, 284692, 284893, 18108370, 284635, 18108385
1600	80058002 (3199, 3200)					29331826, 284603, 284691, 284563
1601	15023246 (3201, 3202)					284635
1602	86926987 (3203, 3204)	Novel Protein sim. GBank gi 5305704 gb AAD41780.1 AF12853 - (AF128535) cytoplasmic phosphoprotein PACSIN2 [Mus musculus]	Contains protein domain (PF00018) - SH3 domain		UNCLASSIFIED struct	29146499, 284112, 264762, 18108351, 29148627, 283974
1603	80502072 (3205, 3206)	Novel Protein sim. GBank gi 283920 pir S27939 - lensin - chicken			collagen	284490, 29331824, 264907, 264809, 284511, 265008, 284592, 265010, 285011, 284762, 284764, 284369, 284288, 284687, 284769, 284693, 284628, 284634, 284638, 284555, 284556, 284638, 284557, 284558, 284559, 18108385
1604	80221813 (3207, 3208)	Novel Protein sim. GBank gi 4768831 gb AAD28633.1 AF11682 - (AF116827) unknown [Homo sapiens]			ATPase-associated	263977

1605	91221129 (3209, 3210)				struct	284905, 284509, 284908, 284907, 284908, 284909, 284604, 284788, 284788, 284692, 284693, 33657109, 284629, 35695855, 284635, 284638, 284637
1606	94312703 (3211, 3212)	Novel Protein sim. GBank gi 4505313 ref NP_003794.1 pMYOM - UNKNOWN		Contains protein domain (PF00047) - Immunoglobulin domain	- struct	22278996, 22278998, 284259, 33657402, 265017, 18108351, 284448, 21906767, 21906769, 52644150, 284691, 87188518
1607	10871805 (3213, 3214)	Novel Protein sim. GBank gi 5174473 ref NP_005888.1 pPPI - Intracisternal A particle- promoted polypeptide			transcriptfactor	264689
1608	80428900 (3215, 3216)	Novel Protein sim. GBank gi 2224629 dbj BAA20802 - (AB002342) KIAA0344 [Homo sapiens]			UNCLASSIFIED	264094, 264906, 284907, 284909, 284910, 284591, 284603, 284768, 284693, 284634, 284635, 284637, 284639
1609	84311572 (3217, 3218)	Novel Protein sim. GBank gi 4884073 emb CAB43213.1 - (AL049934) hypothetical protein [Homo sapiens]				52644507, 52645156, 52646365, 52646842, 56182575, 22278994, 56994075, 35696288, 22278997, 22278998, 22278999, 284259, 52645080, 29147820, 29331828, 35696052, 33858970, 284508, 284509, 284907, 52644045, 56182435, 284510, 284511, 264512, 33657402, 21906754, 52646317, 33109954, 52644288, 87168474, 285017, 285018, 285019, 18108351, 284448, 284288, 284769, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 285021, 265022, 52644150, 33657023, 33657109, 52645129, 27486261, 27486262, 35695763, 264628, 18108370, 18108376, 35696423, 284638, 52644332, 18108387, 87168518, 22279000, 264583, 264486
1610	85488200 (3219, 3220)	Novel Protein sim. GBank gi 283920 pir S27939 - tensin - chicken			UNCLASSIFIED	284593, 284757, 55812038, 285018, 285020, 284691, 284692, 284693, 284631, 284634, 284635, 284555, 22279000, 284584
1611	84122843 (3221, 3222)	Novel Protein sim. GBank gi 107284 pir A35415 - peroxidase (EC 1.11.1.7), thyroid (Grave's disease) - human (fragment)		Contains protein domain (PF00008) - EGF-like domain	- peroxidase	35696288, 21906785, 284691, 35696423
1612	85746031 (3223, 3224)	Novel Protein sim. GBank gi 3874846 emb CAA94337 - (Z70307) Similarity to B.subtilis tetracycline resistance protein (SW:TCR2_BACSU); cDNA EST EMBL:C09951 comes from this gene; cDNA EST EMBL:C08265 comes from this gene [Caenorhabditis elegans]			UNCLASSIFIED	284488, 284509, 18108370, 18108387, 264486
1613	82247354 (3225, 3226)				UNCLASSIFIED	264759

1614	81228634 (3227, 3228)	Novel Protein sim. GBank gi 4680673 gb AAD27726.1 AF13295 - (AF132951) CGI-17 protein [Homo sapiens]	Contains protein domain (PF01605) - eRF1-like proteins	UNCLASSIFIED	22278995, 22278998, 22278997, 22278998, 22278999, 284259, 29331822, 284908, 264512, 265009, 265011, 265017, 265018, 265019, 18108351, 284683, 284288, 284766, 21906767, 21906768, 21906769, 35895917, 265021, 265022, 35896423, 35895855, 60170394, 56182323, 83373044, 284556 22278998, 35896288, 22278997, 29331822, 35896052, 29331828, 264508, 264808, 284909, 56182435, 264511, 265017, 285018, 284766, 284767, 284768, 265020, 264691, 284628, 284632, 284635, 284555, 284556, 56182323, 284558, 22279002
1615	86121809 (3228, 3230)	Novel Protein sim. GBank gi 5689485 dbj BAA83028.1 - (AB028997) KIAA1074 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	homeobox	22278998, 35896288, 22278997, 29331822, 35896052, 29331828, 264508, 264808, 284909, 56182435, 264511, 265017, 285018, 284766, 284767, 284768, 265020, 264691, 284628, 284632, 284635, 284555, 284556, 56182323, 284558, 22279002
1616	94311819 (3231, 3232)	Novel Protein sim. GBank gi 3876260 emb CAB01696 - (Z78418) cDNA EST EMBL:D71020 comes from this gene; cDNA EST EMBL:D73593 comes from this gene; cDNA EST EMBL:C07849 comes from this gene; cDNA EST EMBL:C09081 comes from this gene; cDNA EST yk399f2.3 comes from this gene; cDNA ...	UNCLASSIFIED	UNCLASSIFIED	284488, 52844507, 52845158, 52846365, 52846842, 22278994, 22278995, 35896286, 22278996, 22278997, 22278999, 52845080, 29331822, 29331824, 29331825, 29331827, 29331828, 35896052, 33856970, 284905, 284909, 284594, 52846317, 21906754, 33857084, 52844296, 87188474, 87188559, 265017, 265018, 285019, 284681, 284448, 264684, 52844229, 21906764, 284689, 21906765, 21906766, 21906769, 35895917, 265020, 265021, 52844150, 33857023, 52845129, 33857109, 33857182, 27486281, 27486282, 33857349, 27486285, 35895763, 18108378, 35898423, 35895855, 284557, 52844332, 284558, 18108385, 87188518 35896052, 284905, 284509, 284907, 284908, 284510, 284511, 264784, 284768, 284768, 284689, 284693, 18108374, 264635, 264636, 264638
1617	88090742 (3233, 3234)	Novel Protein sim. GBank gi 466053 sp P34879 YO41_CAEEL - HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III	Contains protein domain (PF01529) - DHHC zinc finger domain	peptidase	35896052, 284905, 284509, 284907, 284908, 284510, 284511, 264784, 284768, 284768, 284689, 284693, 18108374, 264635, 264636, 264638
1618	86272860 (3235, 3236)	Novel Protein sim. GBank gi 424023 dbj BAA74894.1 - (AB020678) KIAA0871 protein [Homo sapiens]		sinucl	35896286, 22278999, 264092, 29331824, 29331825, 35896052, 33857084, 21906765, 27486284
1619	95354580 (3237, 3238)	Novel Protein sim. GBank gi 5031763 ref NP_005515.1 pHRY - hairy (Drosophila)- homolog	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcriptfactor	52846842, 65274572, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35896052, 56182435, 265007, 265008, 284910, 80170831, 80432229, 80433358, 80433438, 285019, 284448, 284288, 284688, 21906768, 285021, 60170615, 33857023, 65274620, 33857109, 18108374, 18108378, 35898423, 35895855, 56182323, 56526488
1620	87344655 (3239, 3240)	Novel Protein sim. GBank gi 1351047 sp P45843 SCRT_DROME - SCARLET PROTEIN	UNCLASSIFIED	UNCLASSIFIED	264684

1621	87078708 (3241, 3242)	Novel Protein sim. GBank gj3822553 (AF098788) - nuclear calmodulin-binding protein [Gallus gallus]	Contains protein domain (PF00622) - SPRY domain	UNCLASSIFIED	264910
1622	94741739 (3243, 3244)			UNCLASSIFIED	18108392, 65274572, 18108398, 22278996, 22278997, 22278999, 29146498, 29148499, 264905, 264908, 264909, 264928, 52644045, 264592, 60433356, 21906754, 264602, 265017, 264389, 21906768, 55811957, 265021, 60170615, 264635, 264557, 60170394, 83373044, 18108385, 22279000, 22279002, 264568
1623	87779106 (3245, 3246)	Novel Protein sim. GBank gj731086/spjP40389JUV22_SCHPO - UV-INDUCED PROTEIN UV22		ribosomalprot	18108398, 264259, 264909, 56182435, 87168474, 264448, 21906768, 35685917, 264691, 87168518, 264563
1624	87338178 (3247, 3248)	Novel Protein sim. GBank gj3875669[embjCAB05478] - (Z83104) cDNA EST EMBL: T00015 comes from this gene; cDNA EST EMBL: D33865 comes from this gene; cDNA EST EMBL: D36540 comes from this gene; cDNA EST yk240f8.3 comes from this gene; cDNA EST yk387c8.3 comes from this gene; cDNA ES...		UNCLASSIFIED	66714117, 29331825, 264908, 265008, 264758
1625	85354748 (3249, 3250)	Novel Protein sim. GBank gj4589622[kbjBAA76833.1] - (AB023206) KIAA0989 protein [Homo sapiens]		kinase	264469, 22278994, 22278995, 22278998, 35686286, 22278997, 22278998, 22278999, 264092, 264259, 29331824, 29331825, 29331827, 29331828, 264102, 264106, 264508, 33657084, 265017, 265018, 18108351, 264683, 264369, 264288, 21906765, 21906766, 21906767, 21906769, 35695917, 265021, 264691, 65274620, 18108368, 263972, 18106376, 35696423, 264631, 264834, 22279000, 22279002
1626	94734369 (3251, 3252)	Novel Protein sim. GBank gj5678070[gjAAD4844.1]AF16090 - (AF160904) BcDNA.HL05936 [Drosophila melanogaster]			52644507, 52645156, 52646365, 52646842, 22278994, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 66714117, 29331826, 60432289, 29331827, 29331828, 35686052, 264906, 66712502, 264909, 265008, 265009, 60432229, 60433356, 60433438, 21906754, 52646317, 52644296, 265011, 87168559, 264604, 265018, 264448, 264369, 264288, 264768, 52644229, 264689, 21906765, 21906768, 35685917, 265021, 265022, 52644150, 33657023, 65274620, 27466261, 27466262, 27466265, 35695763, 263972, 52644332, 60170394, 87168516, 60432113, 264567
1627	83368773 (3253, 3254)			UNCLASSIFIED	264288
1628	85708459 (3255, 3256)	Novel Protein sim. GBank gj3568087 (AC004667) - hypothetical protein [Arabidopsis thaliana]		eph	264288, 264686, 264767, 22279002

1629	84993841 (3257, 3258)	Novel Protein sim. GBank gi 4240175 dbj BAA74866.1 - (AB020850) KIAA0843 protein [Homo sapiens]		struct	264555
1630	87779027 (3259, 3260)			UNCLASSIFIED	29331822, 29331827, 265010, 264693, 264634, 22279002
1631	87758454 (3261, 3262)	Novel Protein sim. GBank gi 1915892 emb CAA69995 - (Y08740) tom-1A protein [Gallus gallus]		UNCLASSIFIED	55811957, 264259, 33857023, 264693, 29331822, 29331824, 29331827, 29331828, 264908, 264908, 55811578, 264910, 264634, 264638, 264637, 58182323, 264559, 264758, 18108385, 264563, 264784, 264788
1632	87871692 (3263, 3264)	Novel Protein sim. GBank gi 2558501 dbj BAA22896 - (D63850) hepatoma-derived growth factor [Mus musculus]		UNCLASSIFIED	264687, 264768, 264691, 264692, 29148489, 264509, 264805, 264907, 264511, 264512, 264482, 264681, 264763, 264682, 264683
1633	87773683 (3265, 3266)				264488, 264259, 264907, 264908, 264909, 264628, 264628, 264631
1634	85892817 (3267, 3268)	Novel Protein sim. GBank gi 4887229 gb AAD32244.1 AF15075 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]	Contains protein domain (PF00435) - Spectrin repeat	struct	265007, 264637, 22279002
1635	94232800 (3269, 3270)			UNCLASSIFIED	65274572, 22278998, 35898052, 52644045, 264511, 265008, 265009, 265010, 265011, 265018, 265019, 264448, 264369, 21908765, 21908768, 265021, 264690, 264482
1636	80413227 (3271, 3272)			UNCLASSIFIED	22278995, 264594, 264763, 265020
1637	80070435 (3273, 3274)	Novel Protein sim. GBank gi 455751 ref NP_001339.1 pDAPK - death-associated protein kinase 3	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264558
1638	87101854 (3275, 3276)	Novel Protein sim. GBank gi 3420051 (AC004680) - unknown protein [Arabidopsis thaliana]			21906765, 21906767, 22278996, 35696288, 22278999, 264259, 264692, 264693, 29331824, 33657109, 264508, 264806, 18108370, 264629, 265007, 33657402, 21908754, 264602, 264604, 264764, 264683, 264586, 264288
1639	94322184 (3277, 3278)	Novel Protein sim. GBank gi 5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264488, 18108394, 65274572, 56182575, 35696286, 29331824, 29331826, 29331827, 35698052, 264908, 58182435, 264112, 265008, 265008, 264757, 264758, 55811386, 264603, 264760, 18108351, 264784, 264288, 264786, 264768, 21908767, 55811957, 264691, 33857023, 65274620, 18108370, 55810764, 55811578, 264558, 264639, 83373044, 18108385, 87168518

1840	94143185 (3279, 3280)	Novel Protein sim. GBank gij2842459[embjCAA16847.1] - (AL021747) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	56182575, 56994075, 35696286, 60432049, 60432289, 29331827, 35696052, 52644045, 56182435, 264510, 265006, 265007, 265008, 264910, 265009, 33657402, 55812038, 265010, 265011, 265017, 265018, 264288, 52644228, 21908765, 21908768, 21908768, 35695017, 265021, 60170615, 52644150, 33657023, 33657109, 33657348, 18108374, 35698423, 65274791, 35695655, 264632, 264555, 56182323, 22279000
1841	87625160 (3281, 3282)			UNCLASSIFIED	29146489, 265006, 265007, 265008, 265009, 55812038, 265010, 265011, 264555, 264556, 264558, 18108383
1842	94312557 (3283, 3284)	Novel Protein sim. GBank gij1575333 (U60416) - myr 6 myosin heavy chain [Rattus norvegicus]	Contains protein domain (PF01843) - struct DIL domain		22278999, 29147620, 29331828, 29331828, 33658970, 55812038, 265010, 265018, 265019, 18108351, 264689, 265020, 265022, 264690, 33657023, 65274620, 35695763, 52644332, 18108381, 60170394, 56182323, 18108388, 87168516, 22279002, 264564, 29331825, 29331827, 29331828, 21908754, 265019, 264286, 264693, 33657349, 18108370, 18108376, 264555, 63373044, 22279002, 264482
1843	94131766 (3285, 3286)				264905, 264907, 264908, 264910, 265009, 264757, 264758, 264761, 264762, 264763, 264766, 264768, 264769, 264828, 264829, 264630, 264631, 264632, 264563, 264564, 264565, 264566, 264567
1844	88095125 (3287, 3288)			UNCLASSIFIED	264685, 264693
1845	95013858 (3289, 3290)			UNCLASSIFIED	22278994, 56994075, 35696286, 264259, 29331824, 29331825, 29331826, 60432289, 264508, 60433356, 60433438, 87168559, 265016, 264687, 35695917, 264692, 33657023, 33657182, 27486281, 27486265, 33657349, 60432113, 264563, 264564
1846	95362691 (3291, 3292)	Novel Protein sim. GBank gij1076802[pirjS49915 - extensin like protein - maize		UNCLASSIFIED	29331822, 264908, 264908, 264369, 21908768, 60170615, 264639, 22279000
1847	94278428 (3293, 3294)	Novel Protein sim. GBank gij5002573[embjCAB44338.1] - (Y17468) alpha-N-acetylgalactosamine alpha-2,6-sialyltransferase [Fugu rubripes]		UNCLASSIFIED	265009, 264686, 55811957, 35695917, 55810764, 264556, 56182323, 264558, 18108385
1848	87842098 (3295, 3296)		Contains protein domain (PF00086) - Zinc finger, C2H2 type	UNCLASSIFIED	

1649	85347628 (3297, 3298)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		cadherin	264488, 22278995, 35696286, 22278996, 22278997, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264907, 66712502, 264908, 52644045, 264909, 56182435, 264511, 265007, 265008, 265009, 264591, 264593, 60433438, 264596, 55812038, 21908754, 265011, 264601, 264602, 265017, 265018, 265019, 264682, 264448, 264764, 264683, 264288, 264768, 264685, 264687, 264768, 264688, 264769, 52644229, 264689, 21906765, 21906766, 21908767, 21908768, 55811957, 35695917, 265021, 265022, 52644150, 264692, 33657023, 33657109, 20281149, 18108370, 264628, 18108374, 18108376, 35698423, 35695855, 264632, 264634, 264635, 264636, 18108380, 264639, 264558, 18108382, 18108384, 18108385, 18108387, 264080, 264404, 60432113, 22279000, 22279002, 264482, 264565, 264566, 264487, 265011, 264602, 21906767, 18108374, 18108377, 18108385
1650	87416539 (3299, 3300)	Novel Protein sim. GBank gi 3647335 emb CAA21059 - (AL031644) possible zinc-finger protein [Schizosaccharomyces pombe]			
1651	91639773 (3301, 3302)	Novel Protein sim. GBank gi 4894278 emb CAB43247.1 - (AL050037) hypothetical protein [Homo sapiens]		synthase	264488, 52645156, 18108397, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264508, 264908, 29331830, 264910, 60432229, 21906754, 265010, 265011, 265017, 265019, 264448, 18108354, 264288, 264688, 21906765, 21906766, 21906768, 21906769, 265022, 264692, 264693, 264629, 35695855, 264558, 264637, 264557, 264559, 83373044, 56526486, 22279000, 22279002, 264584, 22278997, 29146498, 56182435, 21906754, 264369, 21906765, 21906768, 21906769, 265020, 52644150, 33657108, 22279000, 22279002
1652	86598622 (3303, 3304)	Novel Protein sim. GBank gi 1657837 (U73200) - p116Rip [Mus musculus]	Contains protein domain (PF00169) - PH domain	struct	
1653	94255993 (3305, 3306)	Novel Protein sim. GBank gi 3776054 emb CAA06273 - (AJ004989) Tapasin [Gallus gallus]	Contains protein domain (PF00047) - Immunoglobulin domain	glycoprotein	18108398, 22278995, 22278998, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 29331830, 264909, 265006, 265009, 60432229, 60433356, 60433438, 21906754, 265017, 265019, 264448, 264683, 264288, 265021, 265022, 264692, 18108364, 65274781, 18108384, 60432113, 264587, 33657109, 264585
1654	79756471 (3307, 3308)			UNCLASSIFIED	

1655	86689346 (3309, 3310)	Novel Protein sim. GBank gi 3355717 emb CAA73496 - (Y13053) seryl-tRNA synthetase [Zea mays]		synthase	52844507, 35696286, 22278998, 22278999, 29331824, 29331825, 29331828, 33656970, 284908, 52844045, 284511, 284910, 52846317, 284288, 52844229, 33657023, 33657108, 52844332, 284557, 56182323, 56528488, 60432113
1656	79962297 (3311, 3312)	Novel Protein sim. GBank gi 1890141 db BAA18947 - (D83208) P24 protein [Mus musculus]		UNCLASSIFIED	29331822, 29331824, 29331825, 284563
1657	87771894 (3313, 3314)	Novel Protein sim. GBank gi 4557645 ref NP_001524.1 pHNRP - heterogeneous nuclear ribonucleoprotein L	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	29331827, 265009, 21906766, 21906767, 265020, 265022, 33657109, 284638, 56528488, 284482
1658	87773778 (3315, 3316)	Novel Protein sim. GBank gi 3877072 emb CAA87060 - (Z46937) similarity with ribosomal protein L21 [Caenorhabditis elegans]	Contains protein domain (PF00829) - Ribosomal prokaryotic L21 protein	UNCLASSIFIED	52846365, 35696286, 22278996, 22278997, 22278998, 22278999, 284259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 28148498, 284905, 284908, 52844045, 265008, 60433358, 284757, 60433438, 21906754, 285011, 18108351, 284448, 284369, 284288, 284766, 264768, 21906765, 21906767, 21906768, 21906769, 28148829, 265021, 265022, 18108362, 263969, 263971, 18108374, 35696423, 18108383, 22279000, 284482
1659	88230101 (3317, 3318)	Novel Protein sim. GBank gi 539218 pir S38038 - hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	52846317, 21906766, 21906767, 21906768, 87188518, 22278996, 265020, 22278999, 87188559, 284803, 265017, 284631, 285018, 285019, 22278002, 284482, 284635, 284565
1660	94315313 (3319, 3320)	Novel Protein sim. GBank gi 2497012 sp Q10010 YSV4_CAEEL - HYPOTHETICAL 28.6 KD PROTEIN T19C3.4 IN CHROMOSOME III		UNCLASSIFIED	284488, 35696286, 284259, 35696052, 284508, 284509, 284905, 284908, 284907, 284908, 284909, 284510, 284511, 285006, 285007, 284512, 265009, 284910, 284592, 284596, 265010, 284600, 284602, 265017, 285018, 284605, 284780, 284784, 284288, 284766, 284688, 284788, 284789, 284689, 21906766, 35695917, 284690, 33657023, 284693, 33657109, 284629, 35696423, 35695855, 284634, 284635, 284555, 284636, 284637, 284556, 284638, 284639, 264559, 18108385, 18108388, 284563, 284483, 284584, 284585, 284566, 284486, 284567

1661	94234071 (3321, 3322)	Novel Protein sim. GBank gi 4759100 ref NP_004759.1 pSFRS - splicing factor. arginine/serine-rich 11	Contains protein domain (PF000076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264488, 22278988, 264259, 29331824, 29331828, 29331827, 29331828, 264509, 66712502, 29331830, 264908, 52644045, 265007, 264512, 60433358, 60433438, 55812038, 21906754, 285019, 284448, 284786, 284768, 284768, 21906768, 21908769, 285020, 33657023, 33657109, 65274791, 87168518, 284482, 284563, 284564, 284565, 284567
1662	94135172 (3323, 3324)	Novel Protein sim. GBank gi 1730502 sp P52875 PF27_MOUSE - TRANSMEMBRANE PROTEIN PFT27			18108392, 29331822, 29331828, 20281100, 264106, 265006, 265007, 265008, 18108348, 21908766, 18108365, 18108366, 18108374, 83373044, 18108385
1663	94217146 (3325, 3326)	Novel Protein sim. GBank gi 4884136 emb CAB43275.1 - (AL050107) hypothetical protein [Homo sapiens]	Contains protein domain (PF00397) - WW domain	kinase	52645156, 56182575, 22278994, 22278995, 35696286, 22278998, 56994075, 22278997, 22278998, 22278999, 264259, 29331822, 29331826, 29331827, 29331828, 33658970, 29331830, 264908, 56182435, 264511, 60433358, 33657402, 33109954, 87168474, 87168559, 265017, 265018, 264805, 18108351, 264764, 264286, 264766, 264768, 21908765, 21908766, 21908767, 21908768, 21908769, 265021, 265022, 264891, 33657023, 264893, 263967, 33657109, 264630, 52644332, 83373044, 87168518, 60432113, 22278900
1664	94234076 (3327, 3328)	Novel Protein sim. GBank gi 3043692 db BAA25510 - (AB011156) KIAA0584 protein [Homo sapiens]		UNCLASSIFIED	264488, 263994, 35696286, 29331824, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265008, 264910, 60170831, 264591, 264592, 264595, 87168474, 265011, 264800, 264801, 264604, 264605, 264760, 264762, 18108351, 264681, 264682, 264763, 264683, 264764, 264288, 264684, 264766, 264687, 264768, 264769, 21908764, 21908765, 21908767, 35695917, 265021, 284534, 60170615, 264690, 264691, 264692, 33657109, 33657182, 264628, 18108370, 264629, 35698423, 35698555, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 264558, 83373044, 87168518, 284563, 284568, 284486

1665	91226852 (3329, 3330)	Novel Protein sim. GBank gi 1083506 pir S50065 - siadhesin - mouse	Contains protein domain (PF00047) - Immunoglobulin domain	immunoglob	264488, 29331826, 29331828, 264509, 264908, 284907, 284909, 284510, 284511, 284910, 284592, 264593, 264595, 264758, 264598, 264600, 284760, 264762, 284764, 284768, 284768, 284629, 284630, 284634, 284638, 83373044, 264584, 264586, 264587, 264688
1666	85358160 (3331, 3332)	Novel Protein sim. GBank gi 3913431 sp O42843 DDX8_SCHPO - PUTATIVE PRE- MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C	Contains protein domain (PF00575) - S1 RNA binding domain	helicase	56984075, 22278989, 264259, 29331824, 29331826, 29331827, 29146498, 265009, 33109954, 87168559, 265019, 264288, 264688, 21908767, 21908769, 264891, 33857182, 18108370, 18108374, 18108385, 22279002
1667	91228655 (3333, 3334)	Novel Protein sim. GBank gi 5689535 dbj BAA83051.1 - (AB029022) KIAA 1099 protein [Homo sapiens]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	transport	284259, 29331822, 29331828, 264905, 284908, 284908, 264510, 265009, 264595, 284758, 265011, 87168559, 265017, 265018, 265019, 284448, 284768, 264688, 21908765, 21906767, 21906769, 265020, 265021, 60170815, 264690, 264692, 264693, 18108368, 18108370, 263972, 55810764, 264555, 83373044, 60432113, 22279000, 22279002
1668	88085135 (3335, 3336)	Novel Protein sim. GBank gi 2078894 gb AAB53983.1 - (AF002197) short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG_PE- bind). Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]		kinase	66714117, 264508, 264509, 264906, 264907, 284908, 264511, 264810, 264784, 264687, 264689, 33857109, 35698423, 35698555, 264632
1669	91227846 (3337, 3338)	Novel Protein sim. GBank gi 3875371 emb CAA85414.1 - (Z36948) contains a valine and arginine rich domain, possesses weak similarity with the RNA binding domains from RNA splicing factor U2AF 65 KD subunit; cDNA EST EMBL:D84658 comes from this gene; cDNA EST EMBL:D66829 comes fr...		UNCLASSIFIED	29331825, 33109954, 284369, 284767, 284689, 33857109, 83373044
1670	87628009 (3339, 3340)			UNCLASSIFIED	264259, 29331824, 29331827, 60433438, 265022, 264638
1671	87346372 (3341, 3342)	Novel Protein sim. GBank gi 462451 sp P34244 KKK1_YEAST - PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	35896288, 22278997, 28331825, 264809, 21906754, 265017, 265018, 265019, 264682, 264683, 284768, 264688, 21908766, 21906767, 21908768, 21908769, 264691, 264555, 264558, 22279000, 264566
1672	88291834 (3343, 3344)	Novel Protein sim. GBank gi 1814270 (U74586) - double- stranded RNA specific adenosine deaminase [Rattus norvegicus]		deaminase	264908, 264809, 264632, 18108381

1673	88095137 (3345, 3346)	Novel Protein sim. GBank gj2076894[gbjAAB5383.1] - (AF002197) short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG_PE-bind). Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00130) - Phorbol esters/diacylglycerol binding domain (C1 domain)	kinase	264488, 264569, 18108394, 56994075, 22278996, 264259, 35698052, 264508, 264905, 264509, 264908, 264907, 264908, 264909, 264510, 264910, 60170831, 264592, 264594, 264595, 264758, 264601, 264760, 264762, 264683, 264764, 264288, 264766, 264686, 264768, 264687, 264769, 264689, 264680, 33857023, 264692, 264693, 33857109, 264628, 264629, 18108374, 35698423, 35695855, 264631, 264632, 264634, 264635, 264637, 264556, 264638, 264639, 264563, 264482, 264584, 264585, 264568, 264567, 264486
1674	88258028 (3347, 3348)	Novel Protein sim. GBank gj5262467[embjCAB45693.1] - (AL080082) hypothetical protein [Homo sapiens]		kinase	29331822, 29331824, 284908, 52644045, 60433356, 87188559, 284448, 284288, 284688, 264691
1675	87608466 (3349, 3350)	Novel Protein sim. GBank gj3128366 (AF010496) - 50S ribosomal protein l9 [Rhodobacter capsulatus]		UNCLASSIFIED	56181886, 35698286, 22278997, 22278998, 264259, 29331824, 29331827, 35698052, 66712502, 264764, 264288, 264686, 264687, 35695917, 265020, 284690, 264693, 35695763, 18108370, 35698423, 35695855, 264637, 264639, 18108385, 264564
1676	95358086 (3351, 3352)	Novel Protein sim. GBank gj4184065[gbjAAD05327] - (AF111081) latrophilin 3 splice variant bbaf [Bos taurus]		UNCLASSIFIED	264259, 29331827, 29331828, 264106, 264907, 265009, 264600, 265019, 264288, 21908765, 265020, 265022, 35695855, 83373044, 18108385
1677	87408587 (3353, 3354)	Novel Protein sim. GBank gj3327046[dbjBAA31591] - (AB014516) KIAA0616 protein [Homo sapiens]		UNCLASSIFIED	264908
1678	86868829 (3355, 3356)			UNCLASSIFIED	29331824, 284102
1679	91214106 (3357, 3358)	Novel Protein sim. GBank gj550452 (U08469) - 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)	carboxylase	264488, 18108392, 18108394, 52646842, 18108397, 18108398, 35698286, 29331824, 265006, 265007, 265008, 265009, 18108348, 265011, 18108351, 264683, 18108354, 18108358, 18108359, 21906785, 29148627, 29148628, 264690, 18108361, 18108362, 18108364, 18108365, 18108368, 264628, 18108378, 35698423, 35695855, 264635, 18108381, 18108382, 18108383, 18108384, 18108385, 18108388
1680	91005372 (3359, 3360)	Novel Protein sim. GBank gj2394478 (AF024500) - No definition line found [Caenorhabditis elegans]		transport	65274572, 22278994, 22278999, 66714117, 29331827, 56182435, 21906754, 265018, 264288, 21908769
1681	94324150 (3361, 3362)	Novel Protein sim. GBank gj5689537[dbjBAA83052.1] - (AB028023) KIAA1100 protein [Homo sapiens]		UNCLASSIFIED	22278996, 29331822, 264908, 264593, 264604, 265019, 264683, 55811957, 264690, 33657023, 35698423, 83373044, 264583
1682	86042710 (3363, 3364)			UNCLASSIFIED	264909, 265017, 264605

1683	94316213 (3365, 3368)	Novel Protein sim. GBank gi 5031717 ref NP_005704.1 pGPBP - goodpasture antigen- binding protein	Contains protein domain (PF01852) - START domain	UNCLASSIFIED	263994, 35696286, 35696052, 264508, 264508, 264905, 264906, 264907, 264908, 264908, 264511, 265006, 265007, 265009, 264910, 264593, 264758, 265010, 265011, 264760, 264761, 264762, 264763, 264764, 264368, 264766, 264768, 35695917, 264692, 33657109, 35698423, 35695855, 264634, 264635, 264636, 264638, 264639, 83373044, 264486
1684	80063409 (3367, 3368)			UNCLASSIFIED	264563, 264566
1685	94323182 (3369, 3370)	Novel Protein sim. GBank gi 1255371 (U53147) - coded for by C. elegans cDNA yk34a9.5; coded for by C. elegans cDNA yk34a9.3; Similar to guanylate kinase. [Caenorhabditis elegans]	Contains protein domain (PF00625) - Guanylate kinase	UNCLASSIFIED	60424179, 52846842, 22278984, 35686286, 22278998, 264259, 52845080, 29331824, 29331828, 265007, 33657084, 265018, 264681, 264448, 264683, 264369, 264689, 21908765, 21908767, 21908768, 21908769, 265021, 264692, 65274620, 33657109, 27488262, 264635, 52844332, 56162323, 22278000
1686	87820710 (3371, 3372)	Novel Protein sim. GBank gi 2244707 dbj BAA21115.1 - (AB005287) thrombospondin 1 [Bos taurus]		UNCLASSIFIED	56182575, 264259, 264508, 264905, 264509, 264907, 264908, 264510, 264511, 265006, 264512, 265009, 264910, 264758, 265010, 265011, 264605, 18108351, 264764, 264766, 18108357, 264766, 18108362, 264628, 264630, 264631, 264634, 264635, 264637, 264638, 264639, 264565, 264486, 264567
1687	94716400 (3373, 3374)	Novel Protein sim. GBank gi 4680679 gb AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	35695917, 264906, 264907, 264908, 264510, 265006, 265007, 264910, 264558, 18108361, 18108383, 265011
1688	82158442 (3375, 3376)			UNCLASSIFIED	264905, 264910, 264760, 264629, 264555
1689	94325049 (3377, 3378)	Novel Protein sim. GBank gi 4240193 dbj BAA74875.1 - (AB020659) KIAA0852 protein [Homo sapiens]		UNCLASSIFIED	264569, 35698286, 22278999, 264508, 264908, 264909, 56182435, 33657402, 60433438, 55812038, 265017, 265018, 264448, 264764, 264288, 264686, 29148629, 35695917, 265020, 265021, 263972, 18108374, 65274791, 83373044, 264089
1690	83255346 (3379, 3380)	Novel Protein sim. GBank gi 3800736 (AF031572) - seven- pass transmembrane receptor precursor [Mus musculus]	Contains protein domain (PF00028) - Cadherin domain	cadherin	264369, 21906766, 264692, 264639, 87168518
1691	88095223 (3381, 3382)	Novel Protein sim. GBank gi 2773208 (AF039713) - No definition line found [Caenorhabditis elegans]			264768, 33657109, 29331827, 26148628, 264510, 264106, 264910, 264109, 264508, 60170831, 264563, 264905, 264584, 264691, 264637, 264628, 264907, 264908, 33657023, 264567, 264766, 263974
1692	86106709 (3383, 3384)				264106
1693	87012775 (3385, 3386)	Novel Protein sim. GBank gi 121271 sp P02207 GLB_LAMFL - GLOBIN	Contains protein domain (PF00042) - Globin	UNCLASSIFIED	29331826, 264508, 264905, 264907, 264595, 265010, 265011, 21908768, 33657023, 264629, 263976, 264558

1694	94203168 (3387, 3388)	Novel Protein sim. GBank gi 5453932 ref NP_006225.1 pPOLR - polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)	Contains protein domain (PF01193) - RNA polymerases L / 13 to 18 kDa subunit	mapolymerase	35698286, 22278998, 22278998, 22278998, 264259, 29331822, 29331825, 29331826, 29331828, 35698052, 29146499, 264905, 264908, 52644045, 264511, 265006, 265007, 265009, 264592, 60433356, 21906754, 265010, 265011, 18108351, 264763, 264682, 264448, 264683, 264288, 264768, 264689, 21906768, 60170615, 264691, 264692, 264693, 18108370, 18108374, 263978, 35698423, 35695855, 264558, 18108381, 18108385, 87168518, 264482, 264486 264634
1695	94719325 (3389, 3390)	Novel Protein sim. GBank gi 4680879 gb AAD27729.1 AF13285 - (AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	
1696	87824038 (3391, 3392)	Novel Protein sim. GBank gi 4220517 emb CAA22890 - (AL035356) hypothetical protein [Arabidopsis thaliana]			22278997, 264259, 265010, 18108351, 264764, 21906768, 18108370 264682
1697	85740963 (3393, 3394)	Novel Protein sim. GBank gi 505652 (U10382) - GP38b glycoprotein [Homo sapiens]		glycoprotein	
1698	87445285 (3395, 3396)	Novel Protein sim. GBank gi 5052031 gb AAD3841.1 AF15573 - (AF155739) axotrophin [Mus musculus]			56994075, 22278998, 22278999, 264509, 33657402, 264758, 87168474, 87168559, 265017, 265018, 264448, 264687, 29146627, 21906769, 29146629, 265020, 265022, 33657023, 284558, 87168518, 22278002 35696286, 284635
1699	87424793 (3397, 3398)			UNCLASSIFIED	
1700	87859161 (3399, 3400)	Novel Protein sim. GBank gi 543344 pir S41647 - zinc finger 5 protein - mouse	Contains protein domain (PF00096) - Zinc finger, C2H2 type	nuc_recpt	29331824, 52844045, 265008, 265009, 263969, 263971
1701	86570488 (3401, 3402)			UNCLASSIFIED	
1702	87795092 (3403, 3404)	Novel Protein sim. GBank gi 3877439 emb CAA96652 - (Z72510) similarity to yeast UTR3 protein (Swiss Prot accession number P21374); cDNA EST EMBL:D72822 comes from this gene; cDNA EST EMBL:D75763 comes from this gene; cDNA EST yk274e3.3 comes from this gene; cDNA EST yk274e3.5 c...		MHC	264092, 264110, 263977 22278995, 22278997, 284092, 29146498, 29146499, 284107, 284508, 284907, 284110, 284112, 265008, 60170631, 21906754, 265011, 265017, 264762, 18108351, 264288, 21906765, 35695917, 265021, 60170615, 263967, 33657109, 18108370, 263972, 263974, 18108374, 263978, 35695855, 284555, 263981, 60170394, 18108385, 56528486, 87168518, 60432113 264909, 265017, 264628, 264629, 264638
1703	78568651 (3405, 3406)	Novel Protein sim. GBank gi 451544 (U04267) - proline-rich cell wall protein [Gossypium barbadense]		UNCLASSIFIED	
1704	86622979 (3407, 3408)	Novel Protein sim. GBank gi 263289 (U47856) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	264389
1705	87795175 (3409, 3410)	Novel Protein sim. GBank gi 4519621 dbj BAA75670.1 - (AB017614) OASIS protein [Mus musculus]			264589, 35696286, 284907, 265010, 264687, 264768, 264692, 264693, 264636, 264586 22278996, 22278998, 264259, 264509, 265018, 264764, 264685, 264686, 21906768, 21906769, 265022, 264691, 284558, 22279000
1706	87790987 (3411, 3412)	Novel Protein sim. GBank gi 3123034 sp Q15011 Y025_HUMAN - HYPOTHETICAL PROTEIN KIAA0025			

1707	88041230 (3413, 3414)	Novel Protein sim. GBank gij4321664[jb AAD15797] - (AF055470) ZNF258 [Homo sapiens]		UNCLASSIFIED	18108398, 22278997, 264259, 29147820, 29331826, 29146498, 284905, 284908, 285008, 284593, 284595, 284758, 284596, 285018, 284780, 18108351, 284764, 284766, 284889, 284693, 18108370, 35698423, 55811576, 284558, 87185518, 60432113, 284567
1708	91220519 (3415, 3416)	Novel Protein sim. GBank gij5174591[ref NP_005947.1 pMTHF - 5,10-methylenetetrahydrofolate dehydrogenase, 5,10-methylenetetrahydrofolate cyclohydrolase, 10-formyltetrahydrofolate synthetase	Contains protein domain (PF01268) - Formate-tetrahydrofolate ligase	synthase	56182575, 22278998, 56994075, 284259, 29331822, 29331824, 29331826, 29331827, 29331828, 29146498, 29146499, 29331830, 285009, 60170831, 33857402, 33108954, 87188559, 285019, 18108351, 284448, 21908765, 21908767, 21908768, 29148627, 29148629, 29148784, 60170615, 52644150, 33657023, 33657109, 18108374, 55811576, 284558, 18108385, 22279000, 284563
1709	80222583 (3417, 3418)			UNCLASSIFIED	284107, 55811957, 263974, 263976, 263977, 263981
1710	20754572 (3419, 3420)			UNCLASSIFIED	284558
1711	91013729 (3421, 3422)	Novel Protein sim. GBank gij5031735[ref NP_005760.1 pHEC- - N-acetylglucosamine 6-O-sulfotransferase		sulfotransferase	85274572, 29331824, 29331826, 284788, 80431528, 35698423, 60432113, 284563
1712	95330184 (3423, 3424)	Novel Protein sim. GBank gij5454168[ref NP_006453.1 pXAP4 - HBV associated factor	Contains protein domain (PF00641) - Zn-finger in Ran binding protein and others.	kinase	56994075, 264093, 284259, 29331822, 284099, 29331824, 29331827, 284107, 284110, 284511, 284592, 265011, 265018, 284683, 284686, 284689, 285020, 33657023, 263967, 33657109, 263974, 35698423, 35695855, 284630, 284636, 284558, 284568
1713	94143453 (3425, 3426)	Novel Protein sim. GBank gij180409 (M69183) - mature-parasite-infected erythrocyte surface antigen [Plasmodium falciparum]	Contains protein domain (PF00843) - B-box zinc finger.	UNCLASSIFIED	22278995, 284508, 284758, 18108351, 18108370, 263974, 18108374, 284634, 56182323, 83373044, 60432113
1714	87420048 (3427, 3428)				22278997, 284757, 21908765, 285020, 285021, 284692, 56528486
1715	94260257 (3429, 3430)	Novel Protein sim. GBank gij5689537[jb BAA83052.1 - (AB028023) KIAA1100 protein [Homo sapiens]		UNCLASSIFIED	284509, 284905, 284908, 284907, 284908, 284909, 284910, 284591, 285011, 284788, 284768, 284769, 284691, 284692, 284632, 284634, 284635, 284636, 284637, 284558, 284639, 284584
1716	87400448 (3431, 3432)	Novel Protein sim. GBank gij4589468[jb BAA76761.1 - (AB012808) mBOCT [Mus musculus]		transport	56182575, 29331824, 60432289, 284109, 284909, 285007, 284600, 285019, 284686, 285020, 284693, 55811576, 284558, 60432113, 22279002

1717	87563223 (3433, 3434)	Novel Protein sim. GBank gi 2765411 emb CAA74749 - (Y14381) GTP-binding protein [Homo sapiens]		UNCLASSIFIED	264568, 264259, 29331825, 29331828, 29331828, 35696052, 264509, 264905, 264907, 264908, 264909, 264512, 265009, 264910, 264592, 264595, 264758, 264759, 265017, 264681, 264764, 264766, 264686, 18108357, 35695917, 264690, 264692, 264693, 264628, 264629, 35696423, 264630, 264631, 264635, 264636, 18108380, 264638, 264639, 18108388, 18108391
1718	87032628 (3435, 3436)	Novel Protein sim. GBank gi 2833262 sp Q14999 Y076_HUMAN - HYPOTHETICAL PROTEIN KIAA0076 (HA0936)		UNCLASSIFIED	285011, 284681, 284682, 264684, 264688, 264689, 21906765, 265021, 264691, 33657023, 264693, 18108370, 35695855, 264632, 264634, 264636, 18108388, 22279002
1719	94315259 (3437, 3438)	Novel Protein sim. GBank gi 4505197 ref NP_003473.1 pMLL2 - myeloid/lymphoid or mixed-lineage leukemia 2		UNCLASSIFIED	18108396, 65274572, 35696286, 22278997, 60432049, 58182181, 68714117, 60432289, 29331826, 35696052, 29331828, 264906, 29331830, 56182435, 264592, 60431735, 60433438, 55812038, 264759, 265010, 264600, 264601, 265017, 264448, 264764, 264288, 264769, 21906766, 21906769, 55811957, 285020, 285021, 52644150, 33657023, 33657109, 33657182, 27486262, 33657349, 35695783, 18108370, 60431528, 18108374, 35696423, 55811576, 35695855, 264631, 56182323, 264559, 264584, 264486, 56182575, 22278999, 264259, 29331824, 60432289, 29331827, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 264758, 21906754, 265011, 264601, 264760, 264762, 264288, 264768, 264686, 18108357, 264689, 21906765, 55811957, 264693, 20281149, 264629, 18108374, 55811576, 65274791, 264630, 20281071, 264634, 264635, 264636, 264637, 264558, 264638, 264639, 56182323, 87168518
1720	94853063 (3439, 3440)	Novel Protein sim. GBank gi 2129478 pir S51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	22278994, 22278999, 28331822, 265006, 265007, 265008, 55812038, 21906754, 60174639, 285011, 87168559, 18108351, 18108354, 21906765, 21906766, 21906768, 21906769, 265020, 33657109, 18108370, 18108374, 264556, 60170394, 83373044, 18108385, 264486
1721	91722288 (3441, 3442)	Novel Protein sim. GBank gi 488646 emb CAB43381.1 - (AL050280) hypothetical protein [Homo sapiens]		UNCLASSIFIED	56894075, 29331824, 29331828, 265009, 18108351, 21906768, 265020, 33657023, 18108374, 83373044
1722	94134549 (3443, 3444)	Novel Protein sim. GBank gi 5689375 dbj BAA82868.1 - (AB030644) tudor repeat associator with PCTAIRE 2 [Rattus norvegicus]	Contains protein domain (PF00567) - kinase Tudor domain		

1723	95358181 (3445, 3448)	Novel Protein sim. GBank gij4426962[gblAAD20533] - (AF126062) Arf-like 2 binding protein BART1 [Homo sapiens]		UNCLASSIFIED	264488, 284887, 284769, 21906767, 21908768, 58182575, 55811957, 22278997, 22278998, 285020, 284258, 284692, 33857023, 29331822, 29331824, 29331825, 60432289, 33657182, 33656870, 33857349, 29146489, 284508, 284807, 18108370, 264629, 284808, 284809, 18108374, 55811576, 284510, 265008, 284511, 285007, 284910, 284632, 284591, 60432229, 284592, 60433356, 284594, 60433438, 264595, 83373044, 55812038, 33109954, 33657084, 87168518, 87168474, 265010, 265011, 87168558, 284600, 60432113, 264604, 265019, 284563, 284448, 284682, 264566, 284764, 284288, 284567, 284488, 284389, 284788
1724	87713806 (3447, 3448)	Novel Protein sim. GBank gij2340162 (AF005083) - dsRBP-ZFa [Xenopus laevis]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	UNCLASSIFIED	284905, 18108359, 284693, 284628, 264631, 264636, 284555, 284556, 284558, 284559
1725	85655191 (3449, 3450)	Novel Protein sim. GBank gij3152662 (AF064604) - KE03 protein [Homo sapiens]	Contains protein domain (PF00023) - homeobox Ank repeat		35698286, 284259, 29331822, 356986052, 284508, 284509, 284905, 284906, 284907, 284908, 284909, 284910, 285009, 284591, 284601, 284760, 18108351, 284681, 284764, 264286, 284768, 284788, 21908769, 35695917, 264628, 356986423, 264630, 284631, 264632, 264635, 284636, 284638, 87168518, 284568
1726	85754255 (3451, 3452)			UNCLASSIFIED	29148498, 284683, 284689
1727	85296362 (3453, 3454)	Novel Protein sim. GBank gij4689348[gblAAD27861.1]AF13256 - (AF132562) BcDNA.LD14270 [Drosophila melanogaster]		UNCLASSIFIED	284905, 285011, 284689, 21908768

1728	85348515 (3455, 3456)	Novel Protein sim. GBank gij4406549[gbjAAD20027] - (AF131738) Unknown [Homo sapiens]		UNCLASSIFIED	60424179, 18108397, 56182575, 22278995, 56994075, 35698286, 22278997, 22278998, 22278998, 264094, 60432049, 264259, 28331822, 29331824, 56182181, 28331825, 60432289, 29331826, 29331827, 35698052, 264905, 264908, 264907, 29331830, 66712502, 264908, 56182435, 264511, 285008, 265009, 60432229, 60433356, 33657402, 60433436, 264759, 21908754, 87188474, 265010, 265011, 87188559, 265017, 265018, 265019, 55811150, 264681, 284448, 284682, 284763, 284683, 284288, 284684, 284369, 284685, 284766, 284687, 284769, 21908764, 284689, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 265021, 265022, 284535, 264891, 264682, 33657023, 264693, 33657109, 18108370, 264628, 263972, 264628, 18108374, 18108376, 55810784, 65274791, 35695855, 264631, 264634, 264635, 60431850, 264636, 264638, 60170394, 284639, 83373044, 58528486, 87188518, 60432113, 22279000, 22279002, 284564, 284566
1729	81227948 (3457, 3458)	Novel Protein sim. GBank gij854065[embjCAA58337] - (X83413) U88 [Human herpesvirus 8]		UNCLASSIFIED	284906, 284907, 284908, 284511, 284555, 83373044, 284596, 284566
1730	85483474 (3459, 3460)			UNCLASSIFIED	29331822, 29331825, 29331828, 264907, 284908, 264909, 285011, 284784, 284629
1731	88266088 (3461, 3462)	Novel Protein sim. GBank gij831600[prjIS47094 - hypothetical protein - rabbit]		UNCLASSIFIED	52646842, 284907, 284909, 56182435, 55811386, 87188559, 285018, 285019, 284760, 52844229, 55811576
1732	81218878 (3463, 3464)	Novel Protein sim. GBank gij4240231[dbjBAA74894.1] - (AB020678) KIAA0871 protein [Homo sapiens]		struct	56182575, 29331822, 29331824, 29331827, 66712502, 264591, 33657402, 60433356, 265019, 21906768, 21906769, 35695917, 265020, 265021, 264638, 56182323
1733	87617178 (3465, 3468)	Novel Protein sim. GBank gij1575756 (U70674) - m-Numb [Mus musculus]	Contains protein domain (PF00640) - synthase Phosphotyrosine interaction domain (PTB/PID).		284907, 284910, 33657402, 265010, 264681, 284683, 284684, 284686, 284769, 284681, 284692, 284693, 284628, 284636, 284558
1734	87795261 (3467, 3468)				284693

1735	88318638 (3469, 3470)	Novel Protein sim. GBank gi 4836807 gb AAD30566.1 AF14679 - (AF146793) PFT27 [Mus musculus]	Contains protein domain (PF01169) - Uncharacterized protein family UPF0016		264488, 18108394, 18108398, 22278998, 60432049, 284259, 29331822, 264908, 265006, 265007, 265008, 265009, 264591, 33657402, 265010, 265011, 87168559, 265017, 18108351, 264682, 18108354, 264769, 264689, 21906785, 21906768, 21906769, 29148629, 29148784, 265021, 265022, 52644150, 18108364, 18108365, 33657109, 18108370, 18108374, 18108380, 18108385, 87168518, 264563, 18108390
1736	95362884 (3471, 3472)	Novel Protein sim. GBank gi 4885647 ref NP_005472.1 pTRAP - thyroid hormone receptor-associated protein complex component		UNCLASSIFIED	264490, 264259, 66714117, 66712502, 56182435, 265006, 265008, 264910, 60433356, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264556, 264639, 264564
1737	88165549 (3473, 3474)	Novel Protein sim. GBank gi 2143607 pir S68695 - B/K protein - rat	Contains protein domain (PF00168) - C2 domain	kinase	29331822, 29331830, 264591, 265011, 265018, 265019, 22278902
1738	85788811 (3475, 3476)	Novel Protein sim. GBank gi 222594 emb CAA69714 - (Y08460) Mdes protein [Mus musculus]		UNCLASSIFIED	264908, 264909, 265008, 264910, 264566
1739	87328576 (3477, 3478)		Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	UNCLASSIFIED	35696052, 264603, 264557
1740	83592939 (3479, 3480)	Novel Protein sim. GBank gi 4809 emb CAA44309 - (X62452) YCR801 [Saccharomyces cerevisiae]		traffic	264604, 21906764, 18108364, 264629, 35695855, 264636
1741	95010100 (3481, 3482)	Novel Protein sim. GBank gi 4883898 gb AAD31695.1 AF13042 - (AF130420) serine protease-like protein isoform [Homo sapiens]	Contains protein domain (PF01363) - FYVE zinc finger	UNCLASSIFIED	60432289, 29331827, 264509, 265009, 60432229, 264759, 265017, 264767, 264688, 264689, 21908769, 265020, 33657109
1742	85788814 (3483, 3484)	Novel Protein sim. GBank gi 4505193 ref NP_003667.1 pMLD - membrane fatty acid (lipid) desaturase		UNCLASSIFIED	264908, 264910, 264758, 265011, 264631, 264638, 264566
1743	86966475 (3485, 3486)				265017, 265020, 264692
1744	91224003 (3487, 3488)	Novel Protein sim. GBank gi 726832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII		UNCLASSIFIED	22278998, 264508, 264907
1745	20290075 (3489, 3490)			UNCLASSIFIED	264558
1746	94326110 (3491, 3492)	Novel Protein sim. GBank gi 731756 sp P38673 YHY6_YEAST - HYPOTHETICAL 175.8 KD PROTEIN IN GND1-JK11 INTERGENIC REGION	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	65274791, 264639, 264559
1747	94324333 (3493, 3494)	Novel Protein sim. GBank gi 1658503 U75467 - Alu [Drosophila melanogaster]		transcript factor	52646842, 28331824, 28331825, 52644045, 56182435, 265007, 52646317, 87168474, 265018, 18108351, 264389, 264769, 264689, 35695917, 60170615, 264691, 33657023, 65274791, 35695855, 60170394, 22279000, 284482

1748	88003580 (3495, 3498)	Novel Protein sim. GBank gil4504511[ref]NP_001530.1[pHSJ2 - heat shock protein, DNAJ-like 2	Contains protein domain (PF00684) - DnaJ central domain (4 repeats)	eph	284489, 56182575, 28331824, 56182435, 284112, 285007, 285019, 284784, 21908768, 285020, 284891, 55811578, 284835, 284555, 284556, 284557, 284559
1749	83363091 (3497, 3498)	Novel Protein sim. GBank gil5650780[g]bAAD45948.1[AF15196 - (AF151968) RGS protein RGS-17 (Gallus gallus)]	Contains protein domain (PF00615) - Regulator of G protein signaling domain	oncogene	284106
1750	94321664 (3499, 3500)	Novel Protein sim. GBank gil4996894[g]bAAC28444.2] - (AF065164) hyperpolarization-activated, cyclic nucleotide- gated channel 2 [Homo sapiens]			33657402, 284288, 52844150, 263874, 83373044
1751	83373058 (3501, 3502)	Novel Protein sim. GBank gil2760161[d]b]BAA24184] - (AB010054) outer arm dynein light chain 2 [Anthodaris crassispina]	Contains protein domain (PF00560) - Leucine Rich Repeat	ATPase_associated	265010, 284369
1752	88456530 (3503, 3504)	Novel Protein sim. GBank gil3915482[sp]P74346]YG29_SYN3 - HYPOTHETICAL 36.0 KD PROTEIN SLR1629	Contains protein domain (PF00849) - RNA pseudouridylylase synthase	deaminase	264510, 284593, 264682, 21906765, 18108370
1753	94235159 (3505, 3506)	Novel Protein sim. GBank gil2852636 (AF007155) - unknown [Homo sapiens]	Contains protein domain (PF01553) - Acytransferase	phosphatase	56994075, 22278996, 284908, 60170831, 284682, 284784, 284389, 284288, 284685, 284687, 21908768, 284692, 284693, 65274620, 65274781, 35685855, 284637, 284584
1754	88095323 (3507, 3508)	Novel Protein sim. GBank gil731421[sp]P39881]YEH4_YEAST - HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION		transport	284488, 35698288, 284509, 284906, 284907, 284908, 284909, 284511, 284910, 284591, 33657402, 284594, 284757, 284758, 284600, 284604, 284762, 284763, 284685, 284768, 284691, 284628, 35698423, 284632, 284634, 284637, 284638, 283981, 284558, 284639, 284563, 284584, 284565, 284566, 284567, 284686
1755	79470282 (3509, 3510)	Novel Protein sim. GBank gil1176422 (U43184) - rhophilin [Mus musculus]		UNCLASSIFIED	
1756	92862614 (3511, 3512)	Novel Protein sim. GBank gil4432860[g]bAAD20708] - (AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]			52646842, 22278984, 22278985, 56994075, 22278986, 22278987, 284259, 28331822, 60432289, 28331827, 33858970, 285006, 285009, 60432229, 60433356, 60433438, 33109954, 21906754, 285017, 285018, 285019, 284448, 284389, 284288, 21908765, 21908768, 21908767, 21908768, 21908769, 285020, 285021, 285022, 284692, 27486262, 27486264, 18108376, 20281152, 284558, 18108388, 87168518, 60432113, 22279000, 22279002, 284482
1757	95357380 (3513, 3514)	Novel Protein sim. GBank gil5441615[emb]CAB46856.1] - (AJ388557) zinc finger protein [Canis familiaris]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_ma_bind	22278987, 284259, 60432289, 28331827, 284908, 52644045, 285008, 284593, 285019, 284768, 21908768, 65274620, 18108385, 60432113, 284566, 284487

1758	87612971 (3515, 3518)	Novel Protein sim. GBank gjl388104Q[embjCAA16403] - (AL021497) predicted using Genefinder [Caenorhabditis elegans]		UNCLASSIFIED	22278994, 22278999, 29331822, 29331824, 29331825, 33656970, 264508, 265008, 265007, 265009, 264591, 33657402, 33109854, 87168474, 264600, 265017, 265018, 21906769, 265020, 265021, 33657023, 33657109, 264629, 18108374, 35695855, 264632, 52844332, 22279002, 264563
1759	36984372 (3517, 3518)			UNCLASSIFIED	264759
1760	87329716 (3519, 3520)	Novel Protein sim. GBank gjl5262748[embjCAB45688.1] - (AJ133120) Proline rich synapse associated protein 2 [Rattus norvegicus]		UNCLASSIFIED	56182575, 60432048, 35696052, 264805, 264906, 264907, 264908, 264909, 265006, 265008, 264910, 60432228, 264592, 264595, 55812038, 264758, 264762, 18108351, 264784, 264788, 264789, 21906765, 55811957, 35695917, 264690, 264692, 264628, 264629, 55811576, 35696423, 264632, 264634, 264636, 264557, 264639, 60432113, 264565, 264486
1761	87408586 (3521, 3522)	Novel Protein sim. GBank gjl127749[spP10569]MYSC_ACACA - MYOSIN IC HEAVY CHAIN	Contains protein domain (PF00818) - Guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif	UNCLASSIFIED	29331822, 264910, 264685, 264686
1762	95319887 (3523, 3524)	Novel Protein sim. GBank gjl3169158 (AC004770) - BC269730_2 [Homo sapiens]	Contains protein domain (PF00173) - Heme-binding domain in cytochrome b5 and oxidoreductases	desaturase	22278999, 264259, 264905, 264907, 60170831, 265010, 265011, 265017, 264448, 21908765, 21908768, 21908767, 21908768, 265021, 264690, 33657109, 18108374, 264558, 60170394
1763	91224013 (3525, 3526)	Novel Protein sim. GBank gjl4809026[gbjAAD30062.1] - (AF132858) suppressor of G2 allele of skp1 homolog [Homo sapiens]			56181686, 29331825, 35696052, 264905, 264908, 264909, 264763, 264682, 264769, 35695917, 265022, 33657023, 18108374, 35696423, 264634
1764	87757697 (3527, 3528)	Novel Protein sim. GBank gjl1360669[pirjICGHU1V - collagen alpha 1(V) chain precursor - human	Contains protein domain (PF01410) - Fibrillar collagen C-terminal domain	collagen	22278998, 264259, 35696052, 29331828, 56182435, 265008, 265017, 265018, 264448, 264288, 21906768, 21906767, 29148627, 35695917, 264691, 33657023, 60432113, 22279002
1765	91230091 (3529, 3530)	Novel Protein sim. GBank gjl486806[pirjIS35503 - finger protein neutralized - fruit fly (Drosophila melanogaster)]		UNCLASSIFIED	264488, 18108394, 22278995, 22278997, 22278999, 264259, 264104, 264508, 264905, 264907, 264511, 265007, 265008, 264910, 265009, 21906754, 265010, 265017, 264603, 265018, 265019, 18108351, 264682, 264448, 264369, 264288, 264768, 18108359, 21908768, 21906767, 29148627, 29148629, 35695917, 265020, 265021, 264692, 264628, 264629, 18108374, 263976, 264636, 83373044, 22279000, 22279002

1766	95081201 (3531, 3532)	Novel Protein sim. GBank gi 2499087 sp Q09332 UGGG_DROME - UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)			glycoprotein	52845156, 87168559, 80170615, 33857023, 284893, 33857109, 27486261, 284555, 83373044
1767	87755998 (3533, 3534)	Novel Protein sim. GBank gi 4176443 emb CAA18263.1 - (AL022238) dJ1042K10.4 (novel protein) (Homo sapiens)			UNCLASSIFIED	285017, 285019, 284688, 284768, 285020, 284892
1768	80253216 (3535, 3536)				UNCLASSIFIED	29331824, 29331825, 284591, 56182323
1769	87388988 (3537, 3538)				UNCLASSIFIED	264563
1770	95413144 (3539, 3540)	Novel Protein sim. GBank gi 115204 sp P00736 C1R_HUMAN - COMPLEMENT C1R COMPONENT PRECURSOR	Contains protein domain (PF00089) - Trypsin		complement	284488, 284768, 284769, 56182575, 55811957, 284690, 284691, 35696052, 284905, 284509, 284908, 284907, 284828, 284808, 284909, 284910, 284634, 284635, 284636, 284556, 284757, 284758, 55812038, 85274444, 284760, 284563, 284762, 284764, 284884, 284766
1771	94233542 (3541, 3542)	Novel Protein sim. GBank gi 3914191 sp P58558 OGT1_RAT - UDP-N- ACETYLGLUCOSAMINE-PEPTIDE N- ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (O-GLCNAC TRANSFERASE P110 SUBUNIT)	Contains protein domain (PF00515) - TPR Domain		transferase	284758, 284600, 284369, 55811957, 285020, 83373044, 22278000
1772	87643510 (3543, 3544)	Novel Protein sim. GBank gi 4959442 gb AAD34351.1 AF12136 - (AF121360) DNZDHC/NEW1 zinc finger protein 11 [Drosophila melanogaster]	Contains protein domain (PF01529) - DHHC zinc finger domain			22278998, 29331828, 33109954, 285018, 285019, 284784, 21908765, 285020, 285021, 284556
1773	94116824 (3545, 3546)	Novel Protein sim. GBank gi 3978464 (AF085693) - G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein [Rattus norvegicus]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf		potassium_channel	65274572, 56182575, 22278998, 35698286, 22278998, 284259, 29331824, 60424269, 29331825, 60432289, 35696052, 284108, 284509, 284908, 284907, 29331830, 284908, 52644045, 284511, 285008, 285007, 285008, 60170831, 60433438, 284758, 55811388, 87188559, 285017, 284604, 285019, 55811150, 284288, 56181562, 284689, 21908768, 21908767, 21908768, 21908769, 55811957, 285020, 285022, 52844150, 284691, 33857023, 284682, 284683, 60431528, 35698423, 35695855, 284636, 56182323, 18108387, 56526488, 22278000, 22278002, 284563, 284564, 284565, 284566, 284567
1774	94232573 (3547, 3548)	Novel Protein sim. GBank gi 24956899 sp Q15034 Y032_HUMAN - HYPOTHETICAL PROTEIN KIAA0032	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)		UNCLASSIFIED	65274572, 56182575, 35696052, 55812038, 33109954, 21908754, 285017, 21908767, 21908768, 21908769, 285020, 284691, 284636, 56182323, 22278002

1775	95359330 (3549, 3550)	Novel Protein sim. GBank gi 1469199 dbj BAA09487 - (D50928) The KIAA0138 gene product is novel. [Homo sapiens]		UNCLASSIFIED	65274572, 56182575, 56994075, 35696288, 22278997, 29331822, 29331826, 60432289, 29331828, 35696052, 29331830, 66712502, 264828, 56182435, 284511, 265007, 265009, 60170831, 60432229, 60433438, 55812038, 21908754, 85658542, 87168559, 264601, 265017, 265018, 265019, 264762, 264448, 264288, 264689, 21908765, 21908768, 21908767, 21908768, 265020, 265021, 265022, 264691, 33657023, 264692, 33657109, 27486261, 33657349, 18108370, 18108377, 35696423, 55811576, 35695855, 264632, 264634, 264636, 264639, 56182323, 83373044, 56526488, 87168518, 60432113, 22279000, 22279002, 264482, 264486, 264910
1776	94133756 (3551, 3552)	Novel Protein sim. GBank gi 4589678 dbj BAA76857.1 - (AB023230) KIAA1013 protein [Homo sapiens]			
1777	87447171 (3553, 3554)	Novel Protein sim. GBank gi 3219939 sp P87115 YDK9_SCHPO - HYPOTHETICAL 116.5 KD PROTEIN C20G8.08C IN CHROMOSOME I		nucl_recpi	56884075, 29331826, 265008, 87168474, 265017, 265018, 264761, 55811150, 264764, 56181562, 264689, 21908765, 21906768, 21906769, 35695917, 264690, 33657023, 35695763, 60431528, 35696423, 55811576, 35695855, 22279000, 22279002, 264564
1778	94851624 (3555, 3556)	Novel Protein sim. GBank gi 3875648 emb CAA91454.1 - (Z68561) Similarity to Human rab13 protein (PIR Acc. No. A49847). Contains the ATP/GTP-binding site motif (PROSITE PS00017): cDNA EST EMBL:M89412 comes from this gene; cDNA EST yk212g9.3 comes from this gene; cDNA EST yk212g9...		UNCLASSIFIED	29331826, 29331827, 35696052, 264512, 265007, 265009, 265017, 265019, 264762, 18108351, 264769, 21908765, 21908768, 21908767, 21908768, 21908769, 265020, 265021, 264691, 264693, 18108370, 264556, 83373044
1779	94133758 (3557, 3558)	Novel Protein sim. GBank gi 4589676 dbj BAA76857.1 - (AB023230) KIAA1013 protein [Homo sapiens]		UNCLASSIFIED	29148627, 35696286, 29147620, 265006, 265007, 265008, 18108365, 65274727, 264482, 264369, 264768
1780	87023497 (3559, 3560)		Contains protein domain (PF00807) - Apidaecin	UNCLASSIFIED	264107, 33657109, 56526486
1781	84047477 (3561, 3562)			UNCLASSIFIED	264508, 264906, 264639
1782	88094607 (3563, 3564)	Novel Protein sim. GBank gi 729225 sp P41237 CTXN_RAT - CORTEXIN			264259, 29331822, 264508, 264905, 264908, 264907, 264908, 265007, 265009, 264910, 264591, 264758, 264764, 264288, 264768, 264769, 264635, 264636, 264637, 264639, 264583
1783	85717905 (3565, 3566)	Novel Protein sim. GBank gi 2257543 dbj BAA21436 - (AB004538) protein arginine N-methyltransferase [Schizosaccharomyces pombe]		interferon	264768

1784	95197093 (3567, 3568)	Novel Protein sim. GBank gj1755049 (U55042) - myosin X [Bos taurus]	Contains protein domain (PF00169) - struct PH domain	35696286, 284259, 35696052, 264508, 284905, 264908, 264907, 66712502, 284908, 284909, 265007, 265008, 265009, 264910, 264591, 264594, 264757, 264758, 264759, 265010, 265011, 284601, 264602, 264604, 264605, 18108351, 284762, 264763, 284764, 264368, 264766, 264687, 264788, 264888, 21906768, 35695917, 264690, 264691, 264692, 264693, 264628, 18108374, 35698423, 284631, 284632, 284635, 284637, 284638, 264639, 18108385, 22279000, 22279002, 284565, 264566, 264488
1785	95357475 (3569, 3570)	Novel Protein sim. GBank gj4589552[jdbj]BAA76798.1] - (AB023171) KIAA0954 protein [Homo sapiens]	UNCLASSIFIED	65274572, 284259, 29331822, 29331824, 29331825, 29331827, 29331828, 264905, 264906, 284908, 66712502, 58182435, 264511, 265007, 60433356, 55811150, 264683, 284389, 264687, 52644229, 21906767, 52644150, 33657023, 65274620, 33657182, 65274791, 35695855, 264555, 65274727, 22279002
1786	85298465 (3571, 3572)	Novel Protein sim. GBank gj117788[sp]P26770[CYA4_RAT ADENYLATE CYCLASE, TYPE IV (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE)]	UNCLASSIFIED	264908, 35698423, 264636
1787	87434784 (3573, 3574)	Novel Protein sim. GBank gj3877175[embj]CAA90338.1] - (Z50028) cDNA EST yk321h8.5 comes from this gene; cDNA EST EMBL:D88898 comes from this gene; cDNA EST yk395f9.5 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	284488, 284905, 264908, 264909, 264595, 264764, 284786, 284692, 60431528, 284629, 284636, 284564, 264586
1788	91228779 (3575, 3576)		UNCLASSIFIED	284488, 83373044
1789	88094529 (3577, 3578)	Novel Protein sim. GBank gj2088669 (AF003130) - F55A12.9 gene product [Caenorhabditis elegans]	UNCLASSIFIED	284488, 29331828, 264909, 18108351, 264288, 265021, 264555, 264636
1790	82489734 (3579, 3580)			35696052, 284905, 264908, 284907, 284908, 264909, 265008, 264910, 264758, 265011, 265019, 284764, 264766, 284769, 264628, 264635

1791	95197259 (3581, 3582)	Novel Protein sim. GBank gij2114321[dbj]BAA200371 - (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00047) - Immunoglobulin domain	glycoprotein	284488, 284686, 284887, 284768, 18108394, 284789, 18108397, 284259, 284691, 284892, 33857023, 284693, 284509, 284905, 284908, 284628, 284907, 284629, 284908, 284909, 284510, 285008, 284511, 285008, 284630, 285009, 284631, 284910, 284632, 284634, 284635, 284555, 284636, 284592, 284637, 284593, 284638, 18108381, 284639, 284758, 285010, 285011, 284602, 22279000, 284604, 284760, 284564, 284681, 284762, 284565, 284763, 284683, 284566, 284764, 284288, 284684, 284567, 18108354, 18108391, 284685, 284766
1792	87792690 (3583, 3584)	Novel Protein sim. GBank gij4337106[gb]AAD180821 - (AF129758) BAT4 [Homo sapiens]	Contains protein domain (PF01585) - G-patch domain	UNCLASSIFIED	22278997, 284259, 284508, 285007, 33857402, 87188559, 284389, 33857023, 35895855, 20281071, 284559, 18108387, 87188518
1793	95337877 (3585, 3586)	Novel Protein sim. GBank gij5579331[gb]AAD45504.1[AF145732] - (AF145732) endoplasmic reticulum alpha-mannosidase I [Homo sapiens]	Contains protein domain (PF01532) - Glycosyl hydrolase family 47	ATPase-associated	65274572, 22278995, 22278996, 22278997, 22278998, 284093, 284259, 29331824, 66714117, 60432289, 29331827, 29331828, 284103, 284105, 29331830, 285007, 284910, 285009, 60170831, 60433356, 21906754, 285010, 285017, 285018, 284681, 284682, 284288, 52644228, 21908765, 21908768, 21906767, 21908768, 21908769, 285020, 285021, 285022, 60170815, 52844150, 33857023, 33857109, 18108370, 18108374, 65274791, 20281071, 60432113, 22279000, 284482, 284564
1794	87759806 (3587, 3588)	Novel Protein sim. GBank gij4914604[emb]CAB3677.11 - (AL050389) hypothetical protein [Homo sapiens]	Contains protein domain (PF01798) - Putative snoRNA binding domain	UNCLASSIFIED	18108394, 22278995, 22278999, 284259, 29331822, 29331824, 29331825, 29146498, 29146499, 284508, 284905, 52844045, 284112, 285006, 285008, 284910, 60433356, 284757, 55812038, 87168474, 285011, 285017, 18108351, 284763, 284448, 284683, 284369, 21908765, 21908766, 21908767, 21908769, 28148784, 35685917, 80170815, 33857023, 284628, 18108374, 18108376, 35896423, 35895855, 284556, 284557, 284638, 284558, 18108385, 284564
1795	79747856 (3589, 3590)			UNCLASSIFIED	284632, 284635, 284636, 284595, 284596, 284907, 284568, 284909
1796	86588486 (3591, 3592)	Novel Protein sim. GBank gij585084[sp]Q07803[EFGM_RAT - ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)]		glycoprotein	284488, 284907, 284909, 284594, 284595, 284768, 284887, 21908765, 21908767, 284628, 284630, 284559

1797	91223219 (3593, 3594)	Novel Protein sim. GBank gl 1842111 (U87586) - decoy [Arabidopsis thaliana]		ribosomalprol	22278998, 22278997, 22278998, 22278999, 29331822, 264910, 60170831, 21906754, 52644229, 21906765, 21906768, 21906769, 35695917, 265022, 52644150, 264691, 33657023, 263967, 33657109, 22279000
1798	91221276 (3595, 3596)	Novel Protein sim. GBank gl 2832806[dbj BAA24608.1] - (D89340) dipeptidyl peptidase III [Rattus norvegicus]		peptidase	22278994, 56994075, 22278997, 22278998, 22278988, 264259, 29331826, 60432289, 29331828, 33656970, 265008, 60432229, 264757, 60433438, 21906754, 33657084, 87168559, 265017, 18108351, 264682, 264448, 264288, 21906765, 21906768, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 33657023, 33657182, 27486261, 27486265, 33657349, 263973, 18108374, 55811576, 35695855, 18108385, 87168518, 22279000, 264486
1799	86321713 (3597, 3598)	Novel Protein sim. GBank gl 5689541[dbj BAA3054.1] - (AB029025) KIAA1102 protein [Homo sapiens]		eph	264908, 21906754, 21906767, 21906769, 265020, 33657023, 264692, 264693, 264404, 22279000
1800	87080116 (3599, 3600)			UNCLASSIFIED	264691, 264556, 264566
1801	95060723 (3801, 3602)	Novel Protein sim. GBank gl 4680679[gb AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]			52844045, 265007, 264632
1802	87771012 (3603, 3604)	Novel Protein sim. GBank gl 134920[sp P21897 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)			35696286, 66714117, 264508, 264509, 56182435, 264512, 18108351, 264688, 55811957, 264692, 55811576, 35695855, 264486
1803	95060725 (3605, 3606)	Novel Protein sim. GBank gl 4680679[gb AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]			264686, 264488, 264687, 264489, 264768, 264769, 264689, 21906769, 35696288, 35695917, 264259, 264691, 264692, 264693, 20281098, 18108384, 35696052, 264508, 264509, 264905, 264906, 18108370, 264628, 264907, 66712502, 264808, 264908, 18108374, 18108376, 35696423, 35695855, 264510, 264511, 265006, 265007, 264512, 265008, 264910, 264631, 264632, 264634, 264635, 264591, 264636, 264637, 264592, 264638, 264593, 264639, 264594, 63373044, 264758, 264588, 18108385, 18108387, 265011, 264760, 264563, 18108351, 264762, 264564, 264448, 264565, 264763, 264683, 264764, 264586, 264288, 264486, 264567, 264765, 264766

1804	87770203 (3607, 3608)	Novel Protein sim. GBank gi 3879914 emb CAA98538.1 - (Z74043) predicted using Genefinder; cDNA EST EMBL:C13850 comes from this gene; cDNA EST EMBL:C11575 comes from this gene; cDNA EST yk343f4.5 comes from this gene [Caenorhabditis elegans]			52646365, 22278997, 22278999, 264905, 264908, 264909, 264910, 21906754, 264766, 21906765, 21906768, 35695917, 265020, 265022, 264691, 264637, 264639, 22279000, 264564, 264566
1805	95330375 (3609, 3610)	Novel Protein sim. GBank gi 5453844 ref NP_008461.1 pEBBP - estrogen-responsive B box protein			29331824, 29331825, 29331826, 29331827, 29331828, 87168559, 264288, 264687, 52644229, 35698423, 264636, 60432113
1806	94133762 (3611, 3612)	Novel Protein sim. GBank gi 4589676 db BAA76857.1 - (AB023230) KIAA1013 protein [Homo sapiens]	struc		264094, 264105, 264908, 35688423, 265008, 265007, 265008, 264555, 264592, 265011, 265018, 264369
1807	86943032 (3613, 3614)				29331824, 264908, 264910, 33657023, 263978
1808	87642711 (3615, 3616)	Novel Protein sim. GBank gi 4884079 emb CA843235.1 - (AL050008) hypothetical protein [Homo sapiens]	UNCLASSIFIED		264488, 35696286, 66714117, 35696052, 66712502, 264592, 80433438, 52644298, 265010, 264683, 264369, 264689, 55811957, 35695917, 33857109, 35695763, 55810764, 18108379, 35698423, 35695855, 56182323, 264563, 264564, 264487
1809	95321468 (3617, 3618)	Novel Protein sim. GBank gi 1916927 (U87965) - putative G protein [Mus musculus]	UNCLASSIFIED		264594, 55811150, 264686, 29148629, 29148784, 264690, 264629, 18108374, 264556, 264557, 264558
1810	88086316 (3619, 3620)	Novel Protein sim. GBank gi 1352944 sp P47179 J9P_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR	UNCLASSIFIED		264488, 35698052, 264905, 264906, 264907, 264908, 264909, 264511, 265009, 264910, 264592, 264593, 264594, 33857402, 264757, 264595, 264758, 264596, 264759, 264600, 264601, 264762, 264683, 264764, 264288, 264684, 264768, 264767, 264686, 264766, 264687, 264769, 264689, 265021, 264690, 264691, 264693, 264628, 264629, 18108374, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264563, 264566, 264486, 264567
1811	88086272 (3621, 3622)	Novel Protein sim. GBank gi 2134984 pir I37275 - death-associated protein kinase (EC 2.7.1.-) - human	Contains protein domain (PF00023) - kinase Ank repeat		264488, 264259, 264508, 264509, 264905, 264908, 264907, 56182435, 264511, 264512, 264910, 264758, 265011, 264600, 264604, 18108354, 264766, 264686, 264769, 264534, 60170615, 33657023, 264629, 264631, 264639, 264563, 264482, 264483
1812	78245772 (3623, 3624)				29331822, 29331824, 265018, 18108351, 21908769

1813	88090972 (3625, 3626)	Novel Protein sim. GBank gi 5051636 gb AAD38326.1 AF07372 - (AF073727) EH domain-binding mitotic phosphoprotein [Homo sapiens]	Contains protein domain (PF01417) - ENTH domain	glucoamylase	56182575, 284259, 29331824, 66714117, 29331828, 35886052, 284509, 264905, 264908, 264907, 284908, 66712502, 264909, 265007, 264910, 284591, 284593, 55812038, 265011, 285018, 284760, 284682, 284784, 284883, 264369, 284768, 284768, 284769, 21908768, 21908768, 284691, 264693, 18108374, 35695855, 264634, 264635, 264637, 284639, 284559, 22278000, 22279002, 264568
1814	88178047 (3627, 3628)	Novel Protein sim. GBank gi 3643608 (AC005395) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 35696286, 22278998, 264092, 264094, 284259, 29331822, 29331824, 29331825, 60432289, 29331828, 29331827, 29331828, 264105, 264107, 52644045, 58182435, 265008, 60432229, 60433358, 87168474, 87168559, 264369, 264286, 21908765, 35695917, 265021, 265022, 33657023, 33657109, 18108374, 35696423, 264638, 58526488, 264482
1815	85296473 (3629, 3630)	Novel Protein sim. GBank gi 117788 sp P26770 CYA4_RAT ADENYLATE CYCLASE, TYPE IV (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE)		struct	22278999, 264508, 284509, 264907, 264908, 264910, 265011, 264760, 264768, 264634, 264636
1816	83738845 (3631, 3632)	Novel Protein sim. GBank gi 1176623 sp P41846 YO98_CAEEL - HYPOTHETICAL 93.9 KD PROTEIN T20812.6 IN CHROMOSOME III		UNCLASSIFIED	18108394, 18108397, 264509, 264907, 264908, 264909, 265009, 264591, 265011, 265017, 264687, 264689, 265022, 264691, 18108362, 18108368, 18108370, 18108374, 18108379, 264635, 264557, 264564, 264567
1817	88095268 (3633, 3634)	Novel Protein sim. GBank gi 3786377 emb CAA21428 - (AL031907) hypothetical protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	histone	264488, 22278997, 22278998, 60432048, 29331822, 29331824, 60432289, 52644045, 60170831, 265017, 265018, 265019, 18108351, 264682, 52644228, 21906765, 21908767, 21908768, 52644150, 33657023, 33657109, 27486262, 18108370, 18108374, 60170394, 58182323, 22279002
1818	85806775 (3635, 3636)	Novel Protein sim. GBank gi 3879121 emb CAA94370 - (Z70310) predicted using Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL: T01923 comes from this gene; cDNA EST EMBL: D32335 comes from this gene; cDNA EST EMBL: D32723 comes from this gene; cDNA EST E...	Contains protein domain (PF00023) - Ank repeat	transcriptfactor	35696288, 60433358, 284758, 284369, 264686, 21908768, 264693, 264632
1819	87759572 (3637, 3638)	Novel Protein sim. GBank gi 5031865 ref NP_005771.1 pLHFP - lipoma HMGIC fusion partner		UNCLASSIFIED	22278995, 22278997, 22278999, 264259, 29331826, 264908, 265007, 265008, 265009, 60432229, 265017, 265018, 265019, 264448, 264288, 21908768, 21908769, 265020, 18108381, 18108384, 22279000, 22279002, 264567

1820	87769455 (3639, 3640)				284905, 284907, 284584
1821	80431510 (3841, 3842)				284907, 284768, 263978
1822	91221523 (3843, 3844)	Novel Protein sim. GBank gi 4884130 emb CAB43272.1 - (AL050101) hypothetical protein [Homo sapiens]			22278995, 56994075, 22278996, 22278997, 22278998, 284259, 29331824, 29331825, 29331828, 35698052, 29331828, 284908, 29331830, 60170831, 284591, 284593, 60433358, 284598, 285017, 285018, 18108351, 284763, 284683, 21906765, 21908767, 21906768, 21908769, 35695917, 285020, 285021, 33657023, 18108364, 18108370, 35695855, 22279000, 22279002, 284488, 284259, 284511, 284288, 284768, 284693, 35698423, 284634, 18108385, 284486
1823	85522330 (3645, 3646)			UNCLASSIFIED	
1824	86612025 (3847, 3848)	Novel Protein sim. GBank gi 477072 pir A48018 - mucin 7 precursor, salivary - human	Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	284907, 284908, 284909, 284511, 284631, 284634, 284635, 284637, 284638, 284639, 264758, 284588
1825	87430125 (3849, 3850)	Novel Protein sim. GBank gi 30368803 emb CAA18493 - (AL022373) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	80432048, 264910, 284487
1826	91723612 (3651, 3652)	Novel Protein sim. GBank gi 4880885 gb AAD27732.1 AF13295 - (AF132857) CGI-23 protein [Homo sapiens]		ATPase_associated	52644507, 52645156, 52646842, 22278994, 22278998, 56994075, 284259, 60432049, 52645080, 35698052, 86712502, 52644045, 285008, 285009, 60432229, 60433356, 60433438, 52646317, 52644298, 285011, 87168559, 284448, 284288, 284369, 284688, 52644229, 284689, 21908765, 21908768, 285020, 60170815, 52644150, 33657023, 27486262, 27486264, 27486265, 35695763, 35698423, 35695855, 83373044, 87168518, 284404, 22279002
1827	81647212 (3653, 3654)				264758

1828	95074017 (3655, 3656)	Novel Protein sim. GBank gi 4503571 ref NP_001419.1 pENO1 - enolase 1, (alpha)	Contains protein domain (PF00113) - Enolase	oncogene	264488, 52646842, 56182575, 22278998, 35898288, 22278997, 22278999, 264091, 264093, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 264105, 264508, 264807, 68712502, 52644045, 56182435, 265006, 264511, 264512, 265007, 265008, 265009, 60170831, 60432229, 264593, 60433358, 60433436, 264758, 33109954, 21906754, 67188474, 265010, 265011, 67188559, 265017, 265019, 264761, 264762, 264448, 264764, 264683, 264288, 264369, 18108355, 264768, 18108357, 18108358, 264688, 264769, 264689, 21906768, 21906769, 35895917, 265021, 60170615, 33657023, 33657349, 263972, 55811576, 35895855, 264635, 264555, 264556, 264638, 264557, 67168518, 22279000, 22279002, 264563, 264482, 264565, 264484, 264587
1829	80197720 (3657, 3658)				264508, 264634, 264509, 264482, 29331827, 264908, 265009, 264910
1830	94312942 (3659, 3660)	Novel Protein sim. GBank gi 2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma- associated herpesvirus]		nuclease	52645156, 22278994, 22278995, 35696288, 22278998, 22278997, 22278998, 22278999, 29331822, 29331825, 35898052, 52646317, 52644298, 67168559, 265018, 21906765, 21906768, 21906767, 21906768, 21906769, 35895917, 265021, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 35895763, 263974, 35898423, 35895855, 52644332
1831	94138063 (3661, 3662)			UNCLASSIFIED	29331824, 35898052, 29331830, 264595, 264758, 265010, 265019, 265022, 264693, 65274791
1832	84521663 (3663, 3664)	Novel Protein sim. GBank gi 1330345 (U58755) - coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....			264602

1833	95314184 (3665, 3666)	Novel Protein sim. GBank gi 5174413 ref NP_006026.1 pCDC4 - CDC42-binding protein kinase beta (DMPK-like)	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	22278994, 22278997, 22278998, 22278999, 284259, 29331822, 29331824, 60432289, 29331827, 35696052, 29146499, 284508, 284508, 284908, 284907, 66712502, 284908, 5284045, 284909, 284512, 265008, 284591, 284593, 60433356, 21906754, 33657084, 285011, 285017, 284604, 265018, 285019, 284681, 18108351, 284683, 284288, 284685, 284766, 284687, 21906765, 21906768, 21906767, 21906768, 21906769, 29148629, 285020, 285021, 284690, 284692, 33657023, 65274620, 33657182, 27486264, 33657349, 65274791, 284634, 284635, 284556, 284557, 284558, 284559, 18108385, 56528486, 87168518, 60432113, 22279000, 22279002, 264553
1834	80562790 (3667, 3668)				284258, 284907, 264689, 22279000, 22279002
1835	94135718 (3669, 3670)			UNCLASSIFIED	22278998, 29331822, 29331826, 87168474, 284603, 21906768, 263976, 35895855, 83373044
1836	87348450 (3671, 3672)	Novel Protein sim. GBank gi 4759288 ref NP_004268.1 pUCP4 - uncoupling protein 4	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	29331825, 284908, 285019, 284764, 284686, 21906765, 284635
1837	94234287 (3673, 3674)	Novel Protein sim. GBank gi 3334400 sp Q24574 UBPE_DROME - UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E)	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	22278995, 29146499, 265006, 265008, 265009, 285010, 284683, 21906765, 29148627, 29148829, 285020, 265021, 285022, 65274620, 18108370, 18108374, 264556, 18108365
1838	94324369 (3675, 3676)	Novel Protein sim. GBank gi 1362599 pir A56154 - Abl substrate ena (enabled) - fruit fly (Drosophila melanogaster)	Contains protein domain (PF00568) - WH1 domain		29331822, 265017, 284760, 285020, 83373044
1839	87456508 (3677, 3678)	Novel Protein sim. GBank gi 2117310 emb CAB09116.1 - (Z95620) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	60433436, 284601, 21906765, 21906766, 265021, 33657109, 284556
1840	87391708 (3679, 3680)	Novel Protein sim. GBank gi 127560 sp P23249 MV10_MOUSE - PROTEIN MOV-10		UNCLASSIFIED	284693
1841	85818445 (3681, 3682)	Novel Protein sim. GBank gi 4572464 gb AAD23834.1 AF12365 - (AF123653) FEZ1 [Homo sapiens]			56182575, 29331824, 29331826, 60433356, 284764, 284288, 33657023, 263987, 18108370, 18108374, 284631, 284555, 284556, 264839

1842	90992645 (3683, 3684)	Novel Protein sim. GBank gi1326268 (U58728) - C54H2.1 gene product [Caenorhabditis elegans]		UNCLASSIFIED	85274572, 29331822, 29331824, 29331825, 86714117, 29331826, 29331827, 264907, 264908, 52644045, 56182435, 264510, 265006, 265007, 265009, 264910, 60433356, 264757, 60433438, 55812038, 265017, 18108354, 264688, 264768, 33657023, 264693, 18108384, 33657109, 18108368, 264628, 55810764, 56182323, 18108384, 264563, 264564
1843	95292692 (3685, 3686)			UNCLASSIFIED	264488, 56182435, 264769, 29331826, 29331828, 264511, 265006, 265007, 264910, 264631, 264508, 264690, 264636, 264564, 264891, 60432229, 60432049, 264259, 264629, 33657023, 264486, 264909, 264567, 264595, 264766
1844	87444764 (3687, 3688)	Novel Protein sim. GBank gi2496887[sp Q09232 YQ22 CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III]		UNCLASSIFIED	264908, 265022, 33657023, 87168518, 22279002
1845	95096673 (3689, 3690)	Novel Protein sim. GBank gi1175494[sp Q09819 YAC5_SCHPO - HYPOTHETICAL 45.0 KD PROTEIN C16C9.05 IN CHROMOSOME I]	Contains protein domain (PF00628) - PHD-finger	transcriptfactor	264259, 29331824, 264907, 264908, 86712502, 264510, 265007, 265008, 55812038, 265018, 21908765, 52644150, 33657109, 264555, 264556, 264557, 56182323, 18108382, 83373044, 18108385, 264564
1846	84287872 (3691, 3692)	Novel Protein sim. GBank gi1388108[emb CAA21739] - (AL032857) similar to EGF-like domain; cDNA EST yk299a12.3 comes from this gene; cDNA EST EMBL:D35398 comes from this gene; cDNA EST yk331h8.5 comes from this gene; cDNA EST yk299a12.5 comes from this gene; cDNA EST yk467g8.5 c...	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	264905, 264908
1847	87821497 (3693, 3694)	Novel Protein sim. GBank gi15059323[gb AAD38967.1 AF15152 - (AF151522) hairy and enhancer of split related-1 [Homo sapiens]	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcriptfactor	22278997, 264259, 29331824, 264909, 18108351, 263974, 22279002
1848	86789380 (3695, 3696)	Novel Protein sim. GBank gi15701854[emb CAB52191.1] - (AJ245417) G5b protein [Homo sapiens]		tm7	29331825, 29331826, 29331827, 265017, 264883, 264288, 264768, 264768, 21908767, 21908768, 264892, 22279002
1849	84287874 (3697, 3698)	Novel Protein sim. GBank gi14503685[ref NP_001988.1 pFBLN - fibulin 2 precursor]	Contains protein domain (PF00008) - EGF-like domain	ATPase_associated	56182575, 265018
1850	86689650 (3699, 3700)	Novel Protein sim. GBank gi14589582[dbj BAA76813.1] - (AB023188) KIAA0969 protein [Homo sapiens]	Contains protein domain (PF00169) - PH domain	struct	60432049, 264908
1851	95419789 (3701, 3702)	Novel Protein sim. GBank gi1220637[dbj BAA01477] - (D10627) zinc finger protein [Mus musculus]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	dna_ma_bind	29331824, 35686052, 264910, 60433438, 264688, 35685917, 265020, 52644150, 65274620, 52644332

1852	95413170 (3703, 3704)	Novel Protein sim. GBank gij5174828[ref]NP_006090.1 pPIAS - protein inhibitor of activated STAT3		UNCLASSIFIED	56182575, 35896286, 22278996, 22278997, 22278999, 284490, 80432049, 284259, 29331822, 29331824, 29331825, 29331826, 60432288, 29331827, 35896052, 52844045, 265007, 284910, 60432228, 60433358, 60433438, 55812038, 65274444, 265018, 265019, 18108351, 284448, 284688, 284687, 21806765, 21806767, 21806769, 265021, 265022, 52844150, 284693, 33657109, 18108370, 18108374, 55811576, 35895855, 56182323, 60432113, 22279002, 264583 264887, 264766, 52844507, 264769, 21806765, 21806767, 21806768, 22278995, 56994075, 22278999, 52844150, 264259, 264692, 29331822, 29331824, 52845128, 29331827, 33856970, 33657349, 35895763, 264508, 284908, 284628, 264907, 284629, 284909, 35898423, 35895855, 264510, 265006, 284511, 284512, 284630, 265008, 284631, 284910, 284634, 284635, 284637, 264593, 284638, 284639, 33857402, 18108385, 52846317, 52844286, 87168518, 87168559, 284602, 265017, 22279000, 265018, 264760, 284762, 284682, 284448, 264764, 284684, 284587, 284288, 284369, 264766 264592
1853	91222267 (3705, 3706)	Novel Protein sim. GBank gjj854065[emb]CAA58337] - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	
1854	86038152 (3707, 3708)	Novel Protein sim. GBank gjj2072984 (U93569) - putative p150 [Homo sapiens]		nuclease	
1855	91221459 (3709, 3710)	Novel Protein sim. GBank gjj4539520[emb]CAB39994.1] - (AL035424) dA22D12.1 (novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogenous set of other types of proteins) [Homo sapiens]	Contains protein domain (PF01344) - nucd_recp Ketch motif		18108392, 52846385, 65274572, 56182575, 22278994, 56994075, 22278996, 35896286, 22278998, 284259, 80432049, 284908, 264510, 265007, 265008, 265009, 284595, 21808754, 87168474, 265011, 87168559, 264681, 264288, 264768, 18108359, 21808764, 21806768, 29148627, 265020, 265021, 265022, 52844150, 33657023, 33657109, 18108372, 18108374, 18108376, 35896423, 284631, 284636, 18108381, 284482
1856	94231871 (3711, 3712)	Novel Protein sim. GBank gjj3954978[emb]CAA06945] - (AJ06278) acetylglucosaminyltransferase-like protein [Mus musculus]		UNCLASSIFIED	56994075, 284259, 29331828, 284511, 284910, 284758, 284693, 284637, 18108381, 83373044
1857	94324455 (3713, 3714)	Novel Protein sim. GBank gjj4322670[g]AAD16120] - (AF094508) dentin phosphoryn [Homo sapiens]		ATPase_associated	22278999, 284258, 284908, 60170831, 284448, 264686, 265020, 265022, 33657109, 60170394, 83373044

1858	87628311 (3715, 3718)	Novel Protein sim. GBank gi 4981903 gb AAD36415.1 AE00178 - (AE001788) ribosomal protein S15 [Thermotoga maritima]	Contains protein domain (PF00312) - Ribosomal protein S15	284757
1859	84407484 (3717, 3718)	Novel Protein sim. GBank gi 4240317 dbj BAA74937.1 - (AB020721) KIAA0914 protein [Homo sapiens]		22278986, 29331824, 285007, 33109954, 265019, 264389, 21908768, 29148784, 27486261, 52644332, 22279002 285019
1860	17929308 (3719, 3720)	Novel Protein sim. GBank gi 4009522 (AF099731) - connexin 31.1 [Homo sapiens]		
1861	88086370 (3721, 3722)	Novel Protein sim. GBank gi 2143637 pir I184505 - calcium- dependent actin-binding protein - rat	Contains protein domain (PF00285) - Citrate synthase	264887, 284259, 29331822, 29331824, 29331825, 265007, 265009, 264591, 33109954, 265010, 265019, 264389, 264288, 284886, 284691, 284693, 27486284, 18108370, 18108374, 283977, 55811576, 58182323, 284639, 22279000, 22279002, 264482
1862	87372923 (3723, 3724)	Novel Protein sim. GBank gi 125493 sp P07313 KMLC_RABIT - MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	35898286, 264259, 87168474, 284369, 21908768, 284558, 264563
1863	85775037 (3725, 3726)	Novel Protein sim. GBank gi 3820909 emb CAA09289 - (AJ010842) Dof protein [Drosophila melanogaster]	UNCLASSIFIED	284601, 284766, 29148627, 29148629, 284692, 284629, 284635
1864	85547832 (3727, 3728)	Novel Protein sim. GBank gi 432263 gb AAD15985 - (AF077738) metalloproteinase CPX-1 [Mus musculus]	Contains protein domain (PF00754) - F5/8 type C domain	22278989, 264259, 284907, 265018, 18108370, 284634, 264635, 264555, 264556, 284638, 18108387
1865	87740827 (3729, 3730)	Novel Protein sim. GBank gi 2495727 sp Q93073 Y258_HUMAN - HYPOTHETICAL PROTEIN KIAA0256		22278989, 264490, 29331822, 66714117, 66712502, 265006, 265007, 265008, 265009, 284591, 80433438, 265010, 265019, 284760, 284448, 284768, 29148627, 29148629, 285020, 265022, 18108385, 80432113
1866	87268816 (3731, 3732)	Novel Protein sim. GBank gi 5262817 emb CAB45748.1 - (AL080157) hypothetical protein [Homo sapiens]	kinase	18108374, 284769, 18108377, 21908765, 21908768, 35698423, 56182575, 21908769, 29148629, 35698288, 35698917, 265021, 264510, 284511, 284512, 284534, 284535, 60170831, 52644150, 284555, 284691, 284259, 264556, 264692, 264557, 33657023, 60433358, 29331822, 264559, 284595, 29331824, 18108385, 21908754, 33657182, 29331827, 35698052, 33658970, 87168518, 265017, 60431802, 22279000, 284508, 284509, 18108351, 284907, 264682, 264567, 18108372, 264765, 264486
1867	84579159 (3733, 3734)	Novel Protein sim. GBank gi 3859930 (AF078096) - forkhead/winged helix-like transcription factor 7 [Homo sapiens]	UNCLASSIFIED	284094

1868	87357459 (3735, 3736)	Novel Protein sim. GBank gi 3881525 emb CAA93884 - (Z70038) cDNA EST EMBL:D32579 comes from this gene; cDNA EST EMBL:D3254 comes from this gene; cDNA EST yk224b3.5 comes from this gene; cDNA EST yk357110.5 comes from this gene [Caenorhabditis elegans]		nuclease	264489, 22278997, 22278999, 29331825, 29331826, 265008, 265009, 33657402, 87168474, 18108351, 21906765, 21906768, 21906769, 265020, 265021, 60170615, 27486284, 264828, 18108374, 264631, 18108385, 67188518, 22279000, 22279002, 264568, 264567
1869	86977292 (3737, 3738)	Novel Protein sim. GBank gi 4826772 ref NP_004961.1 pIGFA - insulin-like growth factor binding protein, acid labile subunit	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264508, 264508, 264908, 264908, 264909, 264910, 264591, 264600, 18108351, 264883, 264768, 264768, 35695855, 264634, 264558, 264639, 18108385, 264563, 264488
1870	95349488 (3739, 3740)	Novel Protein sim. GBank gi 1869859 emb CAB06722 - (Z86099) very large tegument protein [human herpesvirus 2]		UNCLASSIFIED	29331824, 60424269, 265007, 265008, 21906754, 265017, 265018, 265019, 264288, 264768, 264888, 264888, 21906768, 21906769, 35695917, 60170615, 264692, 18108368, 35695763, 35698423, 65274791, 264638, 264639, 56528488
1871	80234464 (3741, 3742)			UNCLASSIFIED	284509, 284905, 284595, 284768, 264635, 264638, 264563, 264486
1872	80235355 (3743, 3744)	Novel Protein sim. GBank gi 2460316 (AF022147) - uterus-ovary specific putative transmembrane protein [Rattus norvegicus]		protease	284510, 284594, 264565
1873	80213890 (3745, 3746)				264508, 264512, 265009, 265011, 18108351, 264687, 264691, 18108370, 18108374, 264635
1874	95351138 (3747, 3748)		Contains protein domain (PF00293) - Bacterial mutT protein	UNCLASSIFIED	264488, 35695917, 264259, 264905, 264907, 264908, 264909, 263978, 264511, 264635, 264638, 264637, 264638, 33657402, 264558, 18108385, 264600, 264604, 264764, 264587, 264766
1875	87330516 (3749, 3750)	Novel Protein sim. GBank gi 4589520 dbj BAA76782.1 - (AB023155) KIAA0938 protein [Homo sapiens]		UNCLASSIFIED	35698286, 264828, 264592, 264557, 264558
1876	87112950 (3751, 3752)	Novel Protein sim. GBank gi 263810 bbs 122920 - collagen alpha chain [Riftia pachyptilla=tube worms, Peptide, 1027 aa]		UNCLASSIFIED	264259, 29331822, 60432289, 264908, 264909, 264604, 264764, 264288, 264769, 18108376, 264558, 264558, 264559, 18108385
1877	87315208 (3753, 3754)	Novel Protein sim. GBank gi 3983358 gb AAC83924.1 - (AF102545) riboflavin binding protein precursor [Scaphiopus couchii]		UNCLASSIFIED	264767, 264688, 264768, 263978, 264693, 264639, 265010, 264563, 264905, 264908, 264907

1878	95351058 (3755, 3758)	Novel Protein sim. GBank gi 4510345 gb AAD21434.1 - (AC006921) unknown protein [Arabidopsis thaliana]	Contains protein domain (PF01428) - AN1-like Zinc finger	ubiquitin	264568, 264488, 35898286, 56994075, 264259, 29331822, 29331824, 29331825, 35898052, 29331828, 29146498, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264510, 264511, 264512, 265009, 264910, 33857402, 264594, 264758, 55812038, 265011, 264602, 264760, 18108351, 264762, 264681, 264682, 264784, 264389, 264288, 264766, 264687, 264768, 264769, 21908766, 35895917, 265021, 60170815, 33857023, 264692, 264693, 33657109, 27486265, 264628, 18108370, 264629, 18108374, 35898423, 264634, 264635, 264555, 264638, 264639, 83373044, 18108385, 56526488, 87188518, 264563, 264584, 264588, 264488, 264587
1879	95310883 (3757, 3758)	Novel Protein sim. GBank gi 4929843 gb AAD34082.1 AF15184 - (AF151845) CGI-87 protein [Homo sapiens]		UNCLASSIFIED	264905, 264907, 264908, 265007, 264565, 264568
1880	91012978 (3758, 3760)	Novel Protein sim. GBank gi 1550785 emb CAA69283 - (Y08026) Immune associated protein 38 [Mus musculus]		UNCLASSIFIED	264766, 264691, 264692, 83373044
1881	80214949 (3761, 3762)	Novel Protein sim. GBank gi 93144 pir B40505 - hypothetical protein - suid herpesvirus 1 (strain Indiana-Funkhuser or Becker)		UNCLASSIFIED	264509, 264905, 264908, 264909, 264910, 264762, 264887, 33657023, 264632
1882	86582450 (3763, 3764)	Novel Protein sim. GBank gi 2384958 (AF022985) - No definition line found [Caenorhabditis elegans]			264908, 21908766, 18108370, 263974, 87188518
1883	94216817 (3765, 3766)	Novel Protein sim. GBank gi 1351218 sp P47226 TES2_MOUSE - TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]	Contains protein domain (PF00412) - LIM domain containing proteins	homeobox	264908, 264910, 87188559, 21908766, 264638

1884	95310885 (3767, 3768)	Novel Protein sim. GBank gij4929843 gb AAD34082.1 AF15184 - (AF151845) CGI-87 protein [Homo sapiens]		UNCLASSIFIED	264488, 18108384, 58181686, 22278998, 60432048, 264259, 29331822, 29331824, 29331825, 66714117, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 58182435, 264510, 264511, 265007, 264512, 265009, 264910, 264592, 264593, 33857402, 55812038, 264758, 55811388, 265010, 265011, 87168559, 264600, 265017, 264804, 265019, 264605, 264780, 55811150, 264781, 264682, 264763, 264683, 264784, 264288, 264389, 264786, 264686, 264768, 264789, 29148784, 35695917, 264890, 264891, 33857023, 264692, 264693, 33857109, 18108370, 264628, 60431528, 264628, 263973, 18108374, 55810764, 55811576, 35696423, 35695855, 264631, 264634, 60431850, 264637, 264638, 58182323, 264639, 18108382, 83373044, 18108385, 60432113, 22279002, 264563, 264564, 264565, 264566, 264486, 264567
1885	87644280 (3769, 3770)	Novel Protein sim. GBank gij2507155 sp P37370 VRP1_YEAST - VERPROLIN		UNCLASSIFIED	58182575, 264259, 264905, 264909, 265008, 264598, 264768, 265020, 264628, 60431528, 264634, 58528488, 264080, 264563
1886	86674082 (3771, 3772)	Novel Protein sim. GBank gj 2854158 gb AAC02577.1 - (AF045841) No definition line found [Caenorhabditis elegans]			22278998, 22278999, 60432049, 264910, 265018, 264786, 21908788, 29148629, 264690, 264693, 264628, 264555, 264486
1887	94139139 (3773, 3774)	Novel Protein sim. GBank gij5174421 ref NP_006023.1 pCPNE - copine VI (neuronal)	Contains protein domain (PF00168) - C2 domain	ATPase-associated	29331822, 29331824, 29331825, 29331826, 29331827, 264906, 265007, 264681, 264788, 29148627, 264693, 18108364, 35698423, 65274791, 35695855, 264632, 58182323, 264639, 264563
1888	87822804 (3775, 3776)	Novel Protein sim. GBank gj 3319831 emb CAB10841 - (Z88048) dJ1408.2 (Melanoma-Associated Antigen MAGE LIKE) [Homo sapiens]	Contains protein domain (PF01454) - MAGE family		263978
1889	91255783 (3777, 3778)	Novel Protein sim. GBank gj 1083308 pir A56559 - enhancer-trap-focus-1 protein - mouse (fragment)	Contains protein domain (PF00176) - SNF2 and others N-terminal domain	helicase	264906, 55812038, 264758, 265010, 265018, 265019, 18108351, 264288, 21908785, 21908788, 21908789, 265021, 33857023, 33857109, 58182323, 83373044, 18108385, 22279000, 22279002
1890	87626705 (3779, 3780)	Novel Protein sim. GBank gj 4240185 db BAA74876.1 - (AB020680) KIAA0853 protein [Homo sapiens]		UNCLASSIFIED	18108398, 29147620, 264807, 265009, 264600, 265018, 18108351, 264288, 264689, 21908785, 21908788, 21908789, 264691, 264692, 264693, 264628, 18108370, 264636, 264558, 264404

1891	87013895 (3781, 3782)				UNCLASSIFIED	264686, 264768, 264887, 264892, 264693, 29331822, 29331824, 264508, 264905, 264906, 18108370, 264828, 264907, 264908, 264909, 18108379, 265007, 265008, 264910, 264632, 264591, 264639, 264586, 18108384, 265010, 265011, 264601, 264605, 264563, 264369
1892	87642825 (3783, 3784)	Novel Protein sim. GBank gi 5689535 dbj BAA83051.1 - (AB028022) KIAA1099 protein [Homo sapiens]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	struct		22278995, 264509, 87168559, 18108351, 264448, 264882, 265020, 264693, 18108374, 22279000
1893	88533826 (3785, 3786)			laminin		264569, 65274572, 22278997, 22278999, 264259, 29331822, 29331824, 66714117, 29331828, 264906, 265006, 265008, 265009, 264592, 265018, 264681, 264448, 264883, 18108354, 264369, 264684, 264685, 264768, 264887, 264689, 21908768, 265020, 265022, 60170615, 52644150, 264690, 264691, 264692, 33657023, 264693, 33657109, 264628, 18108374, 35695855, 264630, 264632, 264634, 264557, 264558, 60170394, 18108381, 18108385, 22279000
1894	88989120 (3787, 3788)					264508, 264905, 264906, 264907, 264594, 264684, 264690, 264692, 264630, 264635, 264636, 264639, 264563
1895	87631891 (3789, 3790)	Novel Protein sim. GBank gi 5262574 emb CAB45729.1 - (AL080133) hypothetical protein [Homo sapiens]	Contains protein domain (PF00435) - Spectrin repeat			56182575, 264259, 60432289, 29331826, 264107, 264905, 264908, 264910, 60170831, 264758, 265010, 265018, 264448, 264288, 264768, 33657109, 264628, 55810764, 18108379, 264634, 56182323, 56526486
1896	85673555 (3791, 3792)		Contains protein domain (PF00627) - UBA domain	UNCLASSIFIED		264907, 265008, 264682, 264686, 21908768, 264629, 264631, 264634, 264555
1897	80565569 (3793, 3794)	Novel Protein sim. GBank gi 728836 sp P39193 ALU6_HUMAN - III ALU SUBFAMILY SP WARNING ENTRY III		cadherin		264259
1898	87617637 (3795, 3796)	Novel Protein sim. GBank gi 127580 sp P23248 MV10_MOUSE - PROTEIN MOV-10		helicase		22278996, 22278998, 22278999, 29331824, 29331825, 60432289, 29331827, 35698052, 29331828, 265008, 265019, 264681, 264682, 264448, 264369, 52644229, 21908765, 21908768, 21908768, 21908769, 60170615, 55810764, 22279000
1899	86673097 (3797, 3798)	Novel Protein sim. GBank gi 2909819 (AF031548) - erythrocyte membrane glycoprotein Rh50 [Homo sapiens]	Contains protein domain (PF00909) - Ammonium Transporter Family	glycoprotein		264259, 264508, 264909, 60432229, 264769, 21908765, 21908769
1900	87641858 (3799, 3800)	Novel Protein sim. GBank gi 4102881 (AF017250) - vitellogenin precursor [Oreochromis aureus]		UNCLASSIFIED		264683

1901	95196847 (3801, 3802)	Novel Protein sim. GBank gij585959[sp]P38378[S61A_RAT PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT	Contains protein domain (PF00242) - DNA polymerase (viral) N-terminal domain	transport	284488, 52844507, 52845156, 18108396, 52846385, 52846842, 18108397, 56182575, 22278984, 22278985, 56994075, 35698286, 22278997, 22278998, 284490, 60432049, 284259, 29331822, 52845080, 29331824, 29331825, 66714117, 29331826, 60432289, 29331827, 28331828, 35698052, 33656970, 29146498, 284908, 284907, 29331830, 284908, 52844045, 284909, 284112, 285006, 284512, 285008, 284910, 285009, 60170831, 60432229, 60433356, 33657402, 60433438, 55812038, 284758, 33109954, 21908754, 33657084, 52844298, 87188474, 265010, 265011, 87188558, 265017, 265018, 265019, 18108351, 264448, 264288, 264686, 52844229, 21908785, 21908768, 21906767, 21908769, 55811957, 35695917, 265020, 265021, 52844150, 18108362, 33657023, 284693, 283887, 33657109, 33657182, 27486284, 33657349, 35695763, 18108370, 18108376, 55811576, 35698423, 35695855, 60431850, 284636, 263981, 52844332, 60170394, 63373044, 18108385, 87188518, 60432113, 264584, 264107, 263976
1902	80202013 (3803, 3804)	Novel Protein sim. GBank gij426613[gb]AAD20451] - (AF098796) SLM-1 [Mus musculus]		dna_ma_bind	
1903	87778554 (3805, 3806)	Novel Protein sim. GBank gij3747107 (AF095741) - unknown [Rattus norvegicus]		UNCLASSIFIED	264259, 29331825, 29331827, 264508, 284907, 285008, 60170831, 60433356, 60433438, 284759, 21908754, 264448, 284288, 265021, 265022, 33657023, 284693, 55811576, 284555, 284556, 22278000
1904	80434213 (3807, 3808)	Novel Protein sim. GBank gij1352911[sp]P47147[YJ80_YEAST - HYPOTHETICAL 80.2 KD PROTEIN IN CPA2-NNF1 INTERGENIC REGION		struct	284508, 284905, 284908, 284907, 284908, 285007, 284910, 284886, 284768, 284837, 284769, 284693, 284628, 18108374, 284634, 284638, 284637, 284585
1905	95351140 (3809, 3810)	Novel Protein sim. GBank gij3043714[dbj]BAA25521] - (AB011187) KIAA0595 protein [Homo sapiens]	Contains protein domain (PF00293) - Bacterial muT protein		284488, 284768, 284769, 284689, 29148629, 35695917, 35698286, 284259, 284692, 18108362, 33657023, 29331824, 33657109, 29146499, 284508, 284509, 284905, 284906, 284907, 66712502, 284908, 284909, 35698423, 35695855, 264510, 264511, 284512, 284910, 284634, 284635, 284637, 284638, 33657402, 284758, 85658542, 284602, 284760, 284761, 284482, 284563, 284762, 284483, 284764, 284586, 284288, 284766
1906	12763822 (3811, 3812)			UNCLASSIFIED	284637

1907	95351144 (3813, 3814)	Novel Protein sim. GBank gi 4929585 gb AAD34053.1 AF15181 - (AF151816) CGI-58 protein [Homo sapiens]	Contains protein domain (PF00561) - alpha/beta hydrolase fold	- hydrolase	65274572, 22278998, 35898288, 22278998, 22278998, 264259, 60432049, 29331822, 29331825, 60424269, 29331828, 35898052, 284593, 60433356, 21908754, 55811386, 85858542, 87188559, 285018, 284881, 284882, 284884, 284288, 21906765, 21906768, 21906768, 285020, 265022, 284890, 52844150, 264682, 33657023, 284693, 33657109, 35895855, 284636, 284638, 60432113
1908	95313641 (3815, 3816)	Novel Protein sim. GBank gi 3986770 (AF109906) - NG22 [Mus musculus]		UNCLASSIFIED	264488, 65274572, 56182575, 56181688, 22278995, 22278998, 22278997, 22278998, 22278999, 60432049, 284259, 29331822, 60432289, 29331828, 29331827, 29331828, 29148489, 284905, 284908, 284907, 284908, 66712502, 284909, 58182435, 284510, 264511, 285008, 284910, 60170831, 284592, 60433356, 33657402, 264594, 60433438, 284598, 55812038, 33109954, 52846317, 285011, 285017, 284604, 285018, 265019, 284605, 55811150, 284681, 284448, 284288, 284888, 284688, 284769, 21908765, 21908768, 21908767, 21908768, 21908769, 55811957, 29148629, 35895917, 285020, 265022, 284691, 284692, 18108384, 85274620, 33657109, 33657349, 35895763, 18108374, 283978, 55810784, 55811578, 35898423, 65274791, 284631, 284632, 284556, 284557, 60170394, 56182323, 83373044, 18108385, 60432113, 22279000, 22279002, 284588, 284488
1909	85514505 (3817, 3818)	Novel Protein sim. GBank gi 2224653 dbj BAA20813 - (AB002354) KIAA0356 [Homo sapiens]		UNCLASSIFIED	284259, 284508, 264805, 264906, 284907, 284908, 284511, 284910, 284593, 284758, 284764, 284766, 18108370, 284634, 284637, 264486
1910	94216821 (3819, 3820)	Novel Protein sim. GBank gi 1351218 sp P47226 TES2_MOUSE - TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]	Contains protein domain (PF00412) - LIM domain containing proteins	- homeobox	35898288, 22278998, 22278999, 35898052, 284509, 284905, 284908, 284907, 284908, 284909, 284511, 285007, 284512, 284910, 284758, 265011, 284801, 284802, 284804, 284603, 284781, 284784, 284288, 284788, 284788, 284687, 284769, 35895917, 265021, 52844150, 284892, 284628, 18108370, 284629, 18108372, 18108374, 35895855, 284631, 284634, 284635, 284636, 284637, 284638, 18108385, 284565, 284568, 284486

1911	91725345 (3821, 3822)	Novel Protein sim. GBank gi 4809339 gb AAD30184.1 AC00653 - (AC006530) hypothetical protein [Homo sapiens]	Contains protein domain (PF01119) - DNA mismatch repair protein	nuclease	18108394, 56182575, 56182181, 29331826, 29331827, 33656970, 284906, 265007, 284591, 55812038, 87168559, 284448, 284389, 21908765, 21908768, 265022, 284691, 284693, 18108385, 55811576, 284556, 18108385, 18108388
1912	95413518 (3823, 3824)	Novel Protein sim. GBank gi 5689439 dbj BAA83003.1 - (AB028974) KIAA1051 protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, CCHC class	UNCLASSIFIED	18108397, 56182575, 56181686, 22278994, 22278995, 56994075, 22278996, 22278998, 284259, 29331822, 29331824, 56182181, 29331825, 88714117, 35896052, 284805, 284908, 284907, 284908, 52844045, 56182435, 265007, 265008, 284910, 265008, 284591, 284596, 65274444, 55811386, 87188474, 285011, 87168559, 265018, 265019, 264760, 18108351, 264681, 284389, 264684, 264288, 264686, 284768, 21908765, 21908766, 21908767, 21908768, 21908769, 55811957, 265020, 265021, 265022, 60170615, 284692, 33657023, 284693, 18108376, 55811576, 35896423, 65274791, 284637, 56182323, 83373044, 56526486, 22279002, 264563, 264566
1913	95305548 (3825, 3826)	Novel Protein sim. GBank gi 5032245 ref NP_005665.1 pZNF2 - zinc finger protein (C2H2) homologous to mouse MOK-2			56182575, 22278994, 22278995, 56994075, 22278996, 22278998, 22278999, 29331826, 29331827, 265006, 55812038, 265010, 265017, 265018, 265019, 264681, 18108351, 284683, 284764, 284369, 284288, 284685, 284686, 284769, 21908765, 21908766, 21908768, 21908769, 55811957, 265020, 265022, 284691, 55811576, 284634, 284635, 284638, 56182323, 83373044, 18108385
1914	83423982 (3827, 3828)	Novel Protein sim. GBank gi 4588604 dbj BAA76824.1 - (AB023197) KIAA0980 protein [Homo sapiens]	Contains protein domain (PF00036) - EF hand	struct	56182575, 29331824, 35896052, 264806, 284908, 264828, 284909, 284592, 284758, 87168559, 18108351, 18108354, 264684, 284686, 33657023, 284693, 284628, 284631, 284632, 284634, 284635, 284639
1915	95340459 (3829, 3830)	Novel Protein sim. GBank gi 5689415 dbj BAA82991.1 - (AB028962) KIAA1039 protein [Homo sapiens]		UNCLASSIFIED	284259, 29331824, 29331826, 29331827, 284508, 284909, 265009, 285017, 285019, 284768, 284769, 284689, 284628, 284635, 284637, 284639, 83373044, 284565
1916	79640761 (3831, 3832)				284693, 284639

1917	87821680 (3833, 3834)	Novel Protein sim. GBank gij5685391[dbj BAA82979.1] - (AB028850) KIAA1027 protein [Homo sapiens]		struct	284769, 284689, 21906765, 21906768, 22278986, 284259, 284691, 284693, 29331824, 29331825, 29331828, 29331828, 284905, 284906, 284628, 284907, 284908, 284909, 284510, 284630, 284910, 284634, 284635, 284638, 284637, 284638, 283981, 284639, 284758, 18108385, 21908754, 265011, 284604, 284563, 18108351, 284762, 284763, 284568, 284764, 284766
1918	95302795 (3835, 3838)	Novel Protein sim. GBank gij5281517[gb AAD41524.1 AF15483 - (AF154831) PV-1 [Rattus norvegicus]		struct	284488, 18108392, 18108357, 21908765, 21908767, 21908768, 58182575, 21908769, 22278994, 35696286, 35695917, 22278996, 22278997, 285021, 265022, 284534, 284690, 284691, 284692, 33857023, 284693, 29331824, 29331825, 33857109, 29331826, 52845129, 35698052, 29331828, 27486262, 27486264, 35695763, 284508, 284905, 284509, 284808, 284628, 284907, 18108370, 284908, 284629, 284909, 18108372, 18108374, 263978, 35698423, 35695855, 284510, 284511, 285006, 285007, 284512, 285008, 284631, 285009, 284910, 284634, 284635, 284555, 284636, 284556, 284637, 284557, 284593, 284638, 284594, 60170394, 284595, 284559, 284596, 83373044, 284758, 52846317, 18108385, 52844296, 56528486, 87168518, 265010, 265011, 87168559, 284600, 284601, 284602, 285017, 284603, 284604, 285018, 284605, 284760, 284761, 284482, 284584, 18108351, 284762, 284692, 284585, 284448, 284784, 284586, 284488, 284567, 284369, 284288, 284768, 284487, 284885
1918	94143847 (3837, 3838)	Novel Protein sim. GBank gij3878584[emb CAB01237] - (Z77687) cDNA EST EMBL:C08125 comes from this gene; cDNA EST EMBL:C09753 comes from this gene [Caenorhabditis elegans]		oxidase	22278997, 29331822, 285007, 60170831, 60432229, 80433438, 284448, 284682, 284288, 55811957, 33857023, 33857109, 85274791, 56182323, 22279002
1920	91229953 (3839, 3840)	Novel Protein sim. GBank gij1809231 (AC000115) - coded for by human cDNAs R76043 (NID:g850725), R65857 (NID:g838495) and H12866 (NID:g877688) [Homo sapiens]		UNCLASSIFIED	284510, 284511, 284512, 284568
1921	79555226 (3841, 3842)	Novel Protein sim. GBank gij4580887[gb AAD24571.1 AF12108 - (AF121081) CAMP inducible 2 protein [Mus musculus]		UNCLASSIFIED	284693

1922	87641863 (3843, 3844)	Novel Protein sim. GBank gi 138595 sp P02845 MIT2_CHICK - VITELLOGENIN II PRECURSOR (MAJOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LV): PHOSVITIN (PV): LIPOVITELLIN II (LVII): YGP40]		UNCLASSIFIED	264686, 264688, 264490, 18108370, 264909, 18108374, 265008, 264557, 264564, 18108351
1923	84323589 (3845, 3846)	Novel Protein sim. GBank gi 119110 sp P03211 EBN1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	264488, 264489, 22278995, 264094, 264259, 3569052, 264509, 264905, 264906, 264807, 264908, 66712502, 264908, 264511, 264512, 265007, 264910, 265008, 264591, 264592, 264593, 264594, 264595, 264758, 264598, 264759, 265011, 265017, 265018, 265019, 55811150, 264681, 264762, 264448, 264784, 264288, 264389, 264786, 264787, 264886, 264687, 264788, 264789, 58181562, 264689, 21908766, 264691, 33657023, 264693, 65274620, 33657109, 18108370, 264628, 264629, 35698423, 264630, 264631, 264632, 264634, 264555, 264638, 264637, 264638, 264639, 264558, 83373044, 87168518, 264563, 264564, 264565, 264566, 264567 28331826, 264906, 264908, 264585, 265017, 265018, 265019, 265021, 264691, 264693, 264637, 18108385, 264585
1924	87338925 (3847, 3848)	Novel Protein sim. GBank gi 3877655 emb CAA86657 - (Z72511) possible zinc finger protein; cDNA EST EMBL:M89115 comes from this gene; cDNA EST EMBL:D71533 comes from this gene; cDNA EST EMBL:D72314 comes from this gene; cDNA EST EMBL:D75184 comes from this gene; cDNA EST EMBL:C1...	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)		
1925	87628338 (3849, 3850)	Novel Protein sim. GBank gi 4981903 gb AAD38415.1 AE00178 - (AE001788) ribosomal protein S15 (Thermotoga maritima)	Contains protein domain (PF00312) - Ribosomal protein S15	ribosomalprot	22278995, 22278998, 22278997, 264259, 29331824, 66714117, 29146489, 264909, 52644045, 265008, 265009, 264758, 265011, 265017, 264605, 264448, 264288, 264692, 33657109, 18108374, 60170394 264905, 264908, 264907, 264910, 264593, 265018, 264760, 264764, 264288, 264692, 264693, 263978, 264631, 264634, 264637, 264583 264689, 264631
1926	88094739 (3851, 3852)	Novel Protein sim. GBank gi 2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma- associated herpesvirus]		struct	
1927	85654857 (3853, 3854)	Novel Protein sim. GBank gi 3043632 dbj BAA25480 - (AB011126) KIAA0354 protein [Homo sapiens]			
1928	87799054 (3855, 3856)	Novel Protein sim. GBank gi 1665761 dbj BAA13371 - (D87433) KIAA0248 [Homo sapiens]	Contains protein domain (PF00193) - Extracellular link domain	tnf	264489, 264259, 265017, 265021, 264692
1929	86987236 (3857, 3858)	Novel Protein sim. GBank gi 5001993 gb AAD37247.1 AF13432 - (AF134321) chimeric AFGP/hypsinogen-like serine protease precursor [Dissostichus mawsoni]		UNCLASSIFIED	264508, 264591, 33657402, 265017, 264768, 264632, 264556, 264639

1930	87889128 (3859, 3860)	Novel Protein sim. GBank gi 1708230 sp P52983 NBL4_MOUSE - NBL4 PROTEIN		phosphatase	35698286, 29331828, 284805, 284907, 284808, 284909, 284511, 284910, 284758, 284601, 285017, 285019, 284805, 284760, 284764, 284766, 284688, 284769, 285022, 35698423, 284638, 60432113
1931	87797279 (3861, 3862)	Novel Protein sim. GBank gi 404634 (U01840) - serine/threonine kinase [Mus musculus]	Contains protein domain (PF00089) - Eukaryotic protein kinase domain	kinase	284906, 284908, 60432229, 284758, 284764, 284288, 285020, 284692, 284634, 284637 284884, 284691, 284635
1932	15030972 (3863, 3864)			UNCLASSIFIED	284595
1933	11613888 (3865, 3866)			struct	56182575, 58182435, 284510, 284757, 284758, 55812038, 55811388, 285018, 55811150, 21908765, 284691, 284631, 284635, 284637
1934	84426360 (3867, 3868)	Novel Protein sim. GBank gi 4115748 dbj BAA36484 - (AB022023) nonmuscle myosin heavy chain B [Bos taurus]		UNCLASSIFIED	284686, 285011, 284511, 284805, 18108351, 284584, 284681, 284259, 18108370, 284586, 284764, 284369, 284595
1935	87752511 (3869, 3870)				60432288, 285007, 285010, 285011, 285019, 33657109, 18108374
1936	95414338 (3871, 3872)	Novel Protein sim. GBank gi 4827040 ref NP_005110.1 pTRAP - thyroid hormone receptor-associated protein, 150 kDa subunit			
1937	94847141 (3873, 3874)	Novel Protein sim. GBank gi 543187 pir S37771 - ankyrin, erythrocyte - mouse	Contains protein domain (PF00023) - Ank repeat	kinase	85658542, 21908767, 35695917, 60170615, 264683, 33657109
1938	87403277 (3875, 3876)	Novel Protein sim. GBank gi 4544431 gb AAD22340.1 AC00685 - (AC006955) hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00888) - Cullin family	collagen	264488, 28146498, 284905, 284559
1939	91004978 (3877, 3878)	Novel Protein sim. GBank gi 500858 dbj BAA03210 - (D14186) 50kDa lectin [Bombyx mori]		UNCLASSIFIED	65274572, 22278999, 60432289, 56182435, 60433356, 285017, 21908765, 21908766, 21908768, 55811957, 27486284, 35698423, 60432113, 284564
1940	87348810 (3879, 3880)	Novel Protein sim. GBank gi 1946300 emb CAA73132 - (Y12529) hypothetical protein [Silene latifolia]	Contains protein domain (PF00560) - Leucine Rich Repeat	struct	284488, 29331822, 284448, 284683, 284288, 285020, 33657023, 284631
1941	84147177 (3881, 3882)	Novel Protein sim. GBank gi 4206386 (AF060570) - rlg-1 protein [Mus musculus]		UNCLASSIFIED	58994075, 22278998, 284259, 29331824, 29331827, 284905, 265008, 33657084, 285017, 285018, 284288, 284687, 21908765, 21908766, 21908767, 285020, 52644150, 27486264, 83373044, 18108387, 60432113, 22279002, 284565
1942	87841870 (3883, 3884)	Novel Protein sim. GBank gi 4927204 gb AAD33048.1 AF13391 - (AF133911) ARL-6 interacting protein-4 [Mus musculus]		UNCLASSIFIED	264488, 18108398, 29331825, 27486261, 284509, 18108370, 18108374, 264482
1943	84325288 (3885, 3886)	Novel Protein sim. GBank gi 3128952 sp O15736 TIPD_DICD1 - TIPD PROTEIN	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	22278998, 29331822, 29331827, 35696052, 284511, 285008, 284592, 60432229, 285017, 285018, 285019, 284884, 284892, 33657109, 65274791, 284636

1944	94232958 (3887, 3888)	Novel Protein sim. GBank gij1798570[dbj BAA13432] - (D87671) TIP120 [Rattus norvegicus]		UNCLASSIFIED	65274572, 22278994, 22278995, 22278996, 22278998, 22278999, 264259, 52645080, 29331824, 29331826, 29331827, 66712502, 58182435, 284512, 284910, 60170831, 60432228, 60433358, 33657402, 60433438, 264598, 33109954, 21906754, 67168474, 67168558, 285017, 265018, 265019, 18108351, 284368, 284686, 284768, 21906765, 21908768, 21906767, 21906769, 35695917, 265020, 265021, 60170615, 284892, 33857023, 18108370, 18108374, 35698423, 35695855, 284634, 60170394, 284639, 83373044, 18108385, 56528486, 87168518, 60432113, 22279000, 284563
1945	87641872 (3889, 3890)	Novel Protein sim. GBank gij4927204[gb AAD33049.1 AF13391 - (AF13391) ARL-6 interacting protein-4 [Mus musculus]		UNCLASSIFIED	264488, 22278996, 264510, 284511, 18108351, 264683, 284488, 264567
1946	87443990 (3891, 3892)	Novel Protein sim. GBank gij2498104[sp Q27969 AD50_BOVIN - ADRENAL MEDULLA 50 KD PROTEIN]		UNCLASSIFIED	60432289, 29331827, 35686052, 265007, 285008, 60433356, 60433438, 284369, 58181562, 21906767, 52844150, 264693, 27488264, 284637, 87168518, 284563
1947	86438862 (3893, 3894)	Novel Protein sim. GBank gij3914801[sp O54888 RPA2_RAT - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT)]	rnapiymerase		22278998, 264905, 264906, 264908, 284909, 284512, 284758, 284762, 284682, 284683, 284764, 284288, 284768, 284688, 21908768, 284693, 18108374, 35695855, 284635, 284637, 284638, 18108385, 22279002
1948	95199174 (3895, 3896)	Novel Protein sim. GBank gij5420387[emb CAB46678.1] - (AJ243459) proteophosphoglycan [Leishmania major]	struct		284909, 60170831, 284591, 284594, 235010, 265011, 284764, 284369, 284689, 284631, 284638
1949	7640129 (3897, 3898)				264389
1950	87788531 (3899, 3900)	Novel Protein sim. GBank gij3876766[emb CAA93466.1] - (Z69637) predicted using Genefinder; Similarity to E.coli hypothetical protein YCAC (SW:YCAC_ECOLI) [Caenorhabditis elegans]	Contains protein domain (PF00857) - Isochorismatase family	UNCLASSIFIED	284488, 284768, 284688, 284689, 264259, 29331822, 33657109, 29331828, 264103, 264508, 18108370, 35695855, 264510, 285008, 265009, 33657402, 18108385, 285018, 284583, 55811150, 18108351, 284389, 284288, 18106354
1951	86988253 (3901, 3902)	Novel Protein sim. GBank gij2626753[dbj BAA23424] - (AB008782) sulfate transporter [Arabidopsis thaliana]	Contains protein domain (PF00916) - Sulfate transporter family	transport	58182575, 22278997, 52645080, 29331824, 29331825, 29331827, 55812038, 52848317, 265018, 265019, 284389, 21908765, 21908767, 55811957, 265020, 265021, 33657023, 284693, 35695763, 58182323, 22279002
1952	87089775 (3903, 3904)	Novel Protein sim. GBank gij4929833[gb AAD34077.1 AF15184 - (AF151840) CGI-82 protein [Homo sapiens]	Contains protein domain (PF00108) - short chain dehydrogenase	reductase	264591, 284593, 284594, 264595, 264555, 264556, 284557, 264558, 264565

1953	20470371 (3905, 3906)	Novel Protein sim. GBank gij1168715 sp P31721 C1QB_RAT - COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR	Contains protein domain (PF00388) - C1q domain		284259, 284558
1954	91226025 (3907, 3908)	Novel Protein sim. GBank gi 424027 dbj BAA74914.1 - (AB020698) KIAA0891 protein [Homo sapiens]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	264488, 263994, 18108394, 35698286, 22278998, 29331822, 66714117, 29331826, 29331827, 284508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265008, 265007, 265008, 264910, 265008, 60170831, 60432228, 265011, 265017, 264603, 264604, 265019, 18108351, 264685, 264768, 264769, 35895917, 265020, 265021, 264691, 33657023, 264692, 33657109, 264628, 18108374, 35698423, 55811576, 35695855, 264630, 264635, 264636, 264555, 264556, 264638, 264557, 264639, 264558, 264559, 83373044, 18108385, 264563, 264564, 264566, 264488, 264567
1955	95308310 (3909, 3910)			UNCLASSIFIED	56182575, 56181686, 22278994, 22278999, 284259, 29331822, 56182181, 29331824, 29331825, 29331826, 29331827, 35696052, 284508, 29331830, 265008, 265009, 264591, 55812038, 87168474, 265017, 265018, 265019, 264448, 264768, 21908765, 21906768, 21906767, 55811957, 265020, 265021, 52845128, 33657109, 27488264, 33657349, 35695763, 60431528, 18108374, 55811576, 35695855, 264635, 60431850, 264639, 83373044
1956	95092121 (3911, 3912)	Novel Protein sim. GBank gi 1655821 dbj BAA13407 - (D87469) Similar to D.melanogaster cadherin-related tumor suppressor [Homo sapiens]	Contains protein domain (PF00028) - Cadherin domain	cadherin	264488, 56182575, 22278998, 22278999, 284259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264508, 264908, 264909, 264909, 264511, 265007, 264910, 264591, 55812038, 265010, 265018, 18108351, 264768, 56181562, 264689, 21906768, 21906769, 265022, 264691, 264628, 18108374, 55810784, 55811576, 35695855, 264631, 264632, 264635, 264637, 264639, 60170394, 56182323, 83373044, 18108385, 22279000, 22279002, 264563, 264564

1957	94326510 (3913, 3914)	Novel Protein sim. GBank gi 4589674 dbj BAA78856.1 - (AB023228) KIAA1012 protein [Homo sapiens]		UNCLASSIFIED	52646842, 56182575, 22278997, 22278998, 22278999, 29331824, 66714117, 29331827, 28146498, 264593, 33657402, 33109954, 87168474, 265018, 264448, 264368, 264288, 264766, 21908768, 21908767, 21906768, 21908769, 265020, 265021, 264692, 65274620, 27488264, 33657349, 27486265, 35895855, 22278002, 284482
1958	95313902 (3915, 3916)	Novel Protein sim. GBank gi 4240227 dbj BAA74892.1 - (AB020676) KIAA0869 protein [Homo sapiens]		UNCLASSIFIED	22278999, 264092, 264094, 284259, 60432049, 29331824, 56182181, 66714117, 264107, 264109, 264909, 264511, 60170831, 60432229, 21908754, 265010, 21908769, 35895917, 265022, 65274620, 263987, 263976, 35898423, 264631, 264632, 264634, 264635, 18108385, 22279000, 22278002, 264593, 265019
1959	85701470 (3917, 3918)	Novel Protein sim. GBank gi 2281983 emb CAB10860 - (Z98056) hypothetical protein [Schizosaccharomyces pombe]		ubiquitin	
1960	80308608 (3919, 3920)	Novel Protein sim. GBank gi 2274851 dbj BAA21515 - (D64159) 3-7 gene product [Homo sapiens]		struct	264805, 264806, 264907, 264908, 264909, 265006, 265007, 264910, 264595, 265017, 264804, 265018, 18108351, 264784, 264369, 264768, 264768, 21908765, 18108368, 264628, 18108379, 264635, 264636, 264637, 264638, 264486
1961	16292607 (3921, 3922)				264635
1962	91003385 (3923, 3924)			UNCLASSIFIED	65274572, 284592, 284593, 265019, 264691
1983	90936017 (3925, 3926)	Novel Protein sim. GBank gi 3721653 dbj BAA33581 - (AB012933) acyl-CoA synthetase 5 [Rattus norvegicus]		eph	65274572, 18108398, 35696286, 29331825, 60432288, 29331827, 264828, 265008, 265009, 60433356, 60433438, 21908754, 265020, 265021, 33657023, 33657109, 27486265, 35895855, 264555
1984	94317605 (3927, 3928)	Novel Protein sim. GBank gi 5262638 emb CAB45757.1 - (AL080169) hypothetical protein [Homo sapiens]		cadherin	284486, 284092, 264259, 264509, 264905, 264806, 264907, 264908, 264909, 264510, 264511, 265007, 265009, 264910, 264592, 264593, 264594, 264595, 264758, 264600, 264603, 264604, 264605, 264760, 264782, 264448, 264764, 264288, 264685, 264766, 264768, 264769, 21906766, 264691, 264692, 264693, 18108370, 264628, 264629, 18108374, 264630, 264631, 264634, 264636, 264637, 264638, 18108382, 83373044, 18108385, 264483, 264584, 264585, 264566, 264486, 264567
1965	94317445 (3929, 3930)	Novel Protein sim. GBank gi 4107017 dbj BAA36294 - (AB001773) PEM-8 [Clona savignyi]	Contains protein domain (PF01428) - ubiquitin AN1-like Zinc finger	ubiquitin	264488, 264510, 284780, 264768, 264486

1866	94192058 (3831, 3832)	Novel Protein sim. GBank gi 4929707 gb AAD34114.1 AF15187 - (AF151877) CGI-119 protein [Homo sapiens]	Contains protein domain (PF01027) - Uncharacterized protein family	glycoprotein	22278999, 264092, 264259, 29331828, 29331828, 29146498, 264595, 265011, 264448, 18108354, 264288, 264684, 264766, 264685, 264686, 265022, 264691, 264692, 18108370, 18108377, 264555, 18108381, 18108385, 264486, 264567
1867	87386123 (3933, 3934)	Novel Protein sim. GBank gi 2957270 (AF044576) - phospholipase C PLC210 [Caenorhabditis elegans]	Contains protein domain (PF00388) - Phosphatidylinositol-specific phospholipase C, X domain	esterase	28331824, 265010, 265017, 264288, 21906764, 263981, 56528486
1868	88095841 (3935, 3936)	Novel Protein sim. GBank gi 2584953 (AF030001) - unknown [Mus musculus]	Contains protein domain (PF00008) - EGF-like domain	oncogene	3588288, 264905, 264509, 264908, 264907, 264908, 264909, 264511, 264512, 265008, 264910, 265009, 264594, 264757, 264758, 264604, 264605, 264760, 264762, 264682, 264784, 264685, 264766, 264767, 264689, 264691, 264693, 264628, 264629, 35898423, 35895855, 264631, 264632, 264634, 264635, 264636, 264637, 18108380, 264564, 264565, 264566, 264567
1869	84328529 (3937, 3938)	Novel Protein sim. GBank gi 2911274 (U20329) - spidrolin 1 [Nephila clavipes]		UNCLASSIFIED	22278995, 22278996, 35696052, 264908, 264908, 18108351, 264482
1870	80596049 (3939, 3940)	Novel Protein sim. GBank gi 4050087 (AF109907) - S164 [Homo sapiens]		UNCLASSIFIED	264908, 264288, 264766, 264636
1871	94843914 (3941, 3942)	Novel Protein sim. GBank gi 134208 sp P09593 SANT_PLAFV - S-ANTIGEN PROTEIN PRECURSOR		collagen	284488, 264489, 22278998, 264259, 60432049, 68714117, 29331828, 60432289, 29331827, 35898052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 264910, 264591, 264592, 60432229, 60433358, 264595, 264596, 264600, 264604, 264605, 264760, 18108351, 264448, 264764, 264288, 264766, 264768, 264769, 21806765, 33657023, 264692, 18108370, 264629, 35898423, 65274791, 35895855, 264632, 264635, 264555, 264636, 264637, 264638, 264639, 18108385, 60432113, 22278000, 264563, 264564, 264565, 264566, 264486
1872	87645444 (3943, 3944)	Novel Protein sim. GBank gi 4519623 dbj BAA75671.1 - (AB017616) homologous to the yeast YGR163 gene [Mus musculus]	Contains protein domain (PF01462) - Leucine rich repeat N-terminal domain		22278999, 264259, 29331822, 56182181, 60432289, 29331827, 52644045, 264909, 265008, 264511, 265008, 52644296, 265018, 265019, 264761, 264689, 21906768, 21906769, 264691, 264693, 33657109, 33657182, 264556, 52644332, 264558, 60432113
1873	86385533 (3945, 3946)			UNCLASSIFIED	29331826, 264692, 35896423, 264631, 264555, 264556, 264557, 264558, 264559
1874	80396629 (3947, 3948)	Novel Protein sim. GBank gi 3309543 (AF036382) - MLL [Fugu rubripes]		UNCLASSIFIED	264682, 264764, 264563

1975	84316479 (3949, 3950)			UNCLASSIFIED	264488, 66714117, 28331826, 29331828, 56182435, 265008, 264757, 55812038, 265010, 265017, 284369, 55811957, 65274781, 35695855, 56182323, 60432113
1976	95358914 (3951, 3952)			UNCLASSIFIED	264259, 35696052, 265018, 265020, 265021, 33657109, 56526486
1977	94852684 (3953, 3954)	Novel Protein sim. GBank gi 2499526 sp Q07782 NASU_RAT - SODIUM/SULFATE COTRANSPORTER (NA(+)/SULFATE COTRANSPORTER)		homeobox	264908, 264598, 265021, 284566
1978	87447645 (3955, 3956)	Novel Protein sim. GBank gi 103421 pir A33471 - transcription factor NTF1 - fruit fly (Drosophila melanogaster) (fragment)		transcriptfactor	80170831, 264566
1979	87627708 (3957, 3958)	Novel Protein sim. GBank gi 2244815 emb CAB10238.1 - (Z97336) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	29331826, 29146498, 264905, 264907, 265007, 265009, 265010, 265018, 264688, 18108359, 21906768, 35695917, 265020, 60170615, 264693, 18108368, 18108370, 264631, 284635, 284556, 264558, 18108384, 22279000, 284585
1980	86577059 (3959, 3960)	Novel Protein sim. GBank gi 4759290 ref NP_004642.1 pUSP1 - Ubiquitin carboxyl- terminal hydrolase, X-linked		ubiquitin	284489
1981	87606974 (3961, 3962)	Novel Protein sim. GBank gi 4406683 gb AAD20060 - (AF131849) Unknown [Homo sapiens]		UNCLASSIFIED	22278995, 22278997, 22278999, 264259, 29331825, 29331828, 29146498, 29146499, 264107, 264908, 264910, 284595, 21908754, 265010, 265017, 265018, 265019, 284448, 284288, 21908767, 33657023, 27468264, 18108370, 18108374, 18108376, 264630, 284631, 264635, 18108385, 87188518, 22278000, 264482, 264584
1982	80995367 (3963, 3964)	Novel Protein sim. GBank gi 5689523 dbj BAA63045.1 - (AB028016) KIAA1093 protein [Homo sapiens]			65274572, 29331825, 35696052, 33656970, 284908, 265008, 55811386, 284760, 264686, 284691, 27488264
1983	95098668 (3965, 3966)	Novel Protein sim. GBank gi 3417297 (AC002310) - Unknown gene product [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	22278998, 35696288, 284259, 29331822, 20281099, 29331824, 60432289, 29331827, 284509, 284905, 264908, 264907, 66712502, 284908, 52844045, 264909, 284510, 284512, 264910, 265009, 284591, 284592, 60433356, 60433438, 264758, 265010, 264600, 264603, 264604, 264760, 264762, 264763, 264764, 264766, 264687, 264768, 264769, 21908765, 55811857, 35695917, 264690, 264692, 264693, 264628, 264629, 263978, 18108379, 35696423, 35895855, 20281071, 264632, 284634, 284635, 264555, 264636, 264637, 284638, 284639, 83373044, 18108385, 22279000, 22279002

1984	85760889 (3867, 3968)	Novel Protein sim. GBank gij2898895[embjCAA17174.1] - (AL021897) fadD14 [Mycobacterium tuberculosis]		synthase	284688, 21906766, 55811957, 56994075, 265020, 265021, 22278999, 265022, 284259, 29331822, 33657182, 29148499, 284628, 18108370, 284908, 264629, 55811576, 35695855, 265008, 265007, 284591, 21908754, 33657084, 285010, 285017, 265019, 284288
1985	85636897 (3969, 3970)	Novel Protein sim. GBank gij5712131[gbJAAD47378.1]AF12049 - (AF120499) DEM1 protein [Homo sapiens]		glycoprotein	284760, 284288, 263978, 55811578, 284637, 58182323, 18108385, 264584
1986	80200507 (3971, 3972)			UNCLASSIFIED	264488, 284629
1987	87011117 (3973, 3974)	Novel Protein sim. GBank gij4868443[gbJAAD31319.1]AF14457 - (AF144573) Mx-Interacting protein kinase PKM [Mesocricetus auratus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain		22278999, 29331830, 265007, 265018, 21906768, 33657023, 284692, 284693, 18108377, 284635, 60170394, 22279002
1988	94122106 (3975, 3976)			UNCLASSIFIED	284905, 284906, 284807, 284908, 284808, 284910, 284591, 264593, 264758, 264764, 284688, 284788, 285021, 284692, 284628, 284629, 35695855, 284630, 284635, 284636, 284637, 284638, 284639, 284483
1989	91225225 (3977, 3978)	Novel Protein sim. GBank gij2801701 (AF042379) - spindle pole body protein spc87 homolog GCP2 [Homo sapiens]		tubulin	60432049, 60432289, 52844045, 56182435, 284112, 265007, 33657402, 52844229, 21906765, 21906788, 21906769, 55811957, 33657023, 263987, 33657109, 18108370, 22279000, 22279002
1990	85698888 (3979, 3980)	Novel Protein sim. GBank gij5701727[dbjBAA83074.1] - (AB024729) alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV-homologue [Homo sapiens]			284508, 264757, 264764, 18108381
1991	95353114 (3981, 3982)	Novel Protein sim. GBank gij4240287[dbjBAA74822.1] - (AB020706) KIAA0898 protein [Homo sapiens]	Contains protein domain (PF01602) - Adaplin N terminal region	glycoprotein	18108394, 56182575, 22278994, 35688286, 56994075, 22278997, 22278999, 29331822, 29331824, 29331825, 80432289, 29331828, 284508, 284908, 284807, 284908, 56182435, 284510, 265007, 21906754, 33109954, 87168474, 265017, 265018, 265019, 284762, 18108351, 284763, 284683, 284369, 284288, 284685, 264766, 264687, 284769, 21906765, 21906768, 21906769, 55811957, 265020, 60431528, 283974, 18108379, 35695855, 284555, 264557, 284639, 83373044, 18108384, 87168518, 60432113, 22279000, 22279002, 284584, 284486
1992	95317232 (3983, 3984)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	struct	29331827, 264906, 284907, 264909, 265007, 284603, 264768, 284686, 284768, 21906768, 284628, 284635, 284636, 18108385, 56528486, 284566, 284567
1993	80054763 (3985, 3986)	Novel Protein sim. GBank gij2565091 (U80761) - CTG26 alternate open reading frame [Homo sapiens]		UNCLASSIFIED	284592, 35698423

1994	84329114 (3987, 3988)	Novel Protein sim. GBank gi 5630077 gb AAD45822.1 AC00601 - (AC006017) similar to ALR; similar to AAC51735 (PID:g2358287) [Homo sapiens]	Contains protein domain (PF00556) - SET domain	mapolymerase	264486, 22278997, 22278998, 22278999, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264907, 264908, 265008, 60432229, 33657402, 60433356, 264757, 60433438, 264758, 33109954, 265011, 265017, 265018, 265019, 264684, 264369, 264685, 264686, 264768, 21908765, 21908767, 21908768, 21908769, 265020, 264690, 18108362, 264693, 85274620, 18108370, 264635, 264555, 264556, 264557, 56182323, 83373044, 56526486, 22279000, 22279002, 264584 264486, 18108396, 22278994, 56984075, 22278996, 35696288, 22278997, 22278999, 264259, 29147620, 56182181, 29331824, 60432289, 29331828, 29331827, 35696052, 29148499, 284905, 284907, 86712502, 58182435, 265006, 265007, 265008, 265009, 60431735, 60433356, 33657402, 264595, 55812038, 33657084, 55811386, 85658542, 265010, 265011, 265017, 265018, 265019, 264761, 264762, 264448, 264683, 264764, 264288, 264766, 264686, 264768, 264769, 56181562, 264689, 21906765, 21906768, 21906767, 29148627, 21906768, 21906769, 29148629, 29148784, 265020, 265021, 264690, 18108361, 264693, 27486262, 27486264, 27488285, 18108370, 60431528, 18108374, 18108377, 35696423, 55811576, 65274791, 35695855, 264631, 264634, 264635, 264555, 264636, 60431850, 264557, 264558, 264559, 83373044, 20798451, 87188518, 264404, 60432113, 264567 264564
1995	85414353 (3989, 3990)	Novel Protein sim. GBank gi 4827040 ref NP_005110.1 pTRAP - thyroid hormone receptor-associated protein, 150 kDa subunit		UNCLASSIFIED	
1996	80254186 (3991, 3992)	Novel Protein sim. GBank gi 791146 emb CAA60020 - (X86028) extensin-like protein [Vigna unguiculata]		UNCLASSIFIED	
1997	87028423 (3993, 3994)	Novel Protein sim. GBank gi 2642034 (AF034547) - protein phosphatase M130 myosin binding subunit [Ovis aries]	Contains protein domain (PF00023) - Ank repeat	phosphatase	264908, 264909, 264592, 264593
1998	85262704 (3995, 3996)	Novel Protein sim. GBank gi 4589634 dbj BAA76839.1 - (AB023212) KIAA0995 protein [Homo sapiens]		UNCLASSIFIED	264113, 264685, 264555, 264567

1898	84324903 (3997, 3998)	Novel Protein sim. GBank gil5225312 gb AAD40846.1 AF07244 - (AF072441) calcineurin binding protein cabin 1 (Homo sapiens)	Contains protein domain (PF00515) - TPR Domain	UNCLASSIFIED	18108384, 18108397, 35698286, 60424269, 29331827, 29331828, 35696052, 265006, 264512, 55811386, 265010, 265018, 265019, 55811150, 18108351, 264763, 264682, 264369, 264685, 264686, 56181562, 265020, 264691, 33857023, 264693, 33857108, 27486284, 18108370, 18108379, 35695855, 264634, 264635, 264636, 264555, 264557, 58182323, 18108382, 264559, 83373044, 60432113, 22279000, 264563, 264564, 264566
2000	95413705 (3999, 4000)	Novel Protein sim. GBank gil1723232 sp Q10155 YATA_SCHPO - HYPOTHETICAL 90.6 KD PROTEIN C1D4.10 IN CHROMOSOME 1		UNCLASSIFIED	52646365, 52646842, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331826, 29331827, 29331828, 35696052, 264106, 29331830, 52644045, 265007, 265008, 60170831, 264592, 264593, 33657402, 60433438, 21906754, 52644286, 265017, 265018, 265019, 264761, 264369, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 60170815, 52644150, 33657023, 65274620, 52645129, 27486261, 27486262, 27486264, 35695763, 35696423, 35695855, 264631, 52644332, 56182323, 60170394, 83373044, 56526486, 22279002, 264566, 264567
2001	95072534 (4001, 4002)	Novel Protein sim. GBank gil107560 pir B38637 - Ras inhibitor (clone JC265) - human (fragment)		UNCLASSIFIED	264769, 52644228, 65274572, 21906768, 22278996, 35696286, 35695917, 265020, 22278999, 264534, 264490, 264259, 264692, 60432289, 33657109, 35696052, 264508, 264509, 18108370, 80431528, 18108374, 35696423, 65274781, 35695855, 264510, 264511, 264512, 265009, 264634, 264636, 264555, 264556, 264636, 264557, 264558, 264559, 60433438, 83373044, 264759, 18108385, 265011, 264600, 264601, 60432113, 264603, 264604, 264605, 264448, 264288, 264765
2002	80236368 (4003, 4004)	Novel Protein sim. GBank gil729433 sp P38657 ER60_BOVIN - PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (ERP60) (58 KD MICROSOMAL PROTEIN) (P58)	Contains protein domain (PF00085) - Thioredoxin	isomerase	264807, 265006, 264910, 264503, 264692, 264829, 18108374, 264556, 264557
2003	80074449 (4005, 4006)	Novel Protein sim. GBank gil86388 pir A27040 - neurofilament triplet M protein - chicken (fragment)		UNCLASSIFIED	264805, 264906, 264908, 264910, 264598, 265017, 18108351, 264692, 264628, 264634, 264565

2004	95317318 (4007, 4008)	Novel Protein sim. GBank gi 4684249 emb CAB43230.1 - (AL048998) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	52645158, 52646842, 52648365, 56182575, 22278994, 22278995, 56994075, 22278996, 3588286, 22278997, 22278998, 22278999, 60432049, 284259, 52645080, 29331824, 29331828, 29331827, 35888052, 29331828, 33658970, 29331830, 264908, 264592, 60433358, 33857402, 52646317, 21908754, 33657084, 52644296, 87188474, 87188559, 265017, 285018, 285019, 284763, 284683, 284288, 52644229, 21906785, 21908788, 21908787, 21906788, 21906789, 35895917, 265020, 265021, 265022, 52644150, 33657023, 52645129, 33857109, 33657182, 27486261, 27486262, 33857349, 27486265, 35895763, 18108374, 18108376, 18108377, 35896423, 35895855, 264631, 52644332, 284558, 18108385, 56528488, 87188518, 60432113, 284483, 284488, 264908
2005	87400864 (4009, 4010)	Novel Protein sim. GBank gi 3879501 emb CAA87795 - (Z47812) similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33386 comes from this gene; cDNA EST EMBL:D33965 comes from this gene; cDNA EST EMBL:D33822 comes from this gene; cDNA EST EMBL:D34547 comes from this ge...		ubiquitin	
2008	95351177 (4011, 4012)	Novel Protein sim. GBank gi 4108673 emb CAA22613 - (AL035064) queuine tma-ribosyltransferase [Schizosaccharomyces pombe]	Contains protein domain (PF01702) - Queuine (RNA-ribosyltransferase	UNCLASSIFIED	56182575, 56181688, 22278995, 22278996, 22278997, 22278998, 22278999, 264259, 56182181, 60424288, 86714117, 35896052, 264808, 66712502, 264909, 264510, 60433358, 85858542, 265010, 265018, 265019, 264882, 264448, 264288, 264768, 28148827, 21906789, 29148784, 35895917, 60170815, 264891, 33857023, 65274820, 33657109, 55810784, 55811578, 35895855, 87188518, 60432113, 284563, 264482, 284488, 263994, 35896052, 264508, 264905, 264806, 264907, 264908, 264909, 265007, 264910, 264592, 284595, 264758, 265011, 264760, 264762, 264784, 264788, 264885, 264787, 264788, 264789, 55811957, 35895917, 265020, 264691, 264693, 264628, 264628, 65274791, 35895855, 264631, 264632, 264634, 264635, 264637, 264638, 264639, 264586, 264909, 264768, 35895855
2007	94325558 (4013, 4014)	Novel Protein sim. GBank gi 2662161 dbj BAA23712 - (AB007900) HH0452 cDNA clone for KIAA0440 has a 438-bp insertion at position 1711 of the sequence of KIAA0440. [Homo sapiens]		UNCLASSIFIED	
2008	85084428 (4015, 4016)	Novel Protein sim. GBank gi 1550783 emb CAA69257 - (Y07860) homeodomain protein [Mus musculus]	Contains protein domain (PF00046) - Homeobox domain	homeobox	

2009	85749240 (4017, 4018)	Novel Protein sim. GBank gi 3882305 dbj BAA34512.1 - (AB018335) KIAA0792 protein [Homo sapiens]		UNCLASSIFIED	22278999, 264259, 284910, 284591, 265017, 264881, 264683, 21908788, 284691, 33657182, 33657349, 264631, 87168518, 264404, 22279002, 264563
2010	85422458 (4019, 4020)	Novel Protein sim. GBank gi 5262629 emb CAB45753.1 - (AL080164) hypothetical protein [Homo sapiens]	Contains protein domain (PF00057) - eph Low-density lipoprotein receptor domain class A		52844507, 52845158, 52846365, 52846842, 18108397, 85274572, 22278994, 58994075, 35898286, 22278998, 22278997, 22278999, 264259, 28331822, 52845080, 29331824, 28331825, 29331828, 29331827, 29331828, 284511, 265007, 284512, 265008, 265009, 80432228, 80433356, 21906754, 52846317, 33109954, 52844286, 87168474, 87168559, 265017, 265018, 265019, 284681, 284685, 284687, 52844229, 284689, 21906765, 21908768, 21908767, 21908768, 35895917, 265020, 52844150, 264691, 264692, 33657023, 263987, 52845129, 35895763, 18108376, 35898423, 85274791, 35895855, 264631, 264634, 80431850, 264637, 284638, 52844332, 80170394, 18108385, 87168518, 22279002, 284584, 284585, 284586, 284587, 58182575, 58994075, 22278999, 264259, 29331824, 29331826, 29331827, 29331828, 35898052, 284908, 66712502, 265006, 265007, 265008, 265010, 265011, 265017, 265019, 284681, 284448, 284683, 264369, 284288, 284685, 284766, 284687, 21908765, 21908767, 21908768, 21908769, 265020, 285022, 284691, 33657023, 65274620, 33657109, 284628, 284557, 264559, 83373044, 87168518, 80432113, 22279002
2011	94328149 (4021, 4022)	Novel Protein sim. GBank gi 3347953 (AF076183) - cytosolic sorting protein PACS-1a [Rattus norvegicus]		UNCLASSIFIED	264259, 29331822, 29331824, 29331825, 29146498, 87168558, 265019, 284682, 284288, 264686, 21908764, 265020, 265022, 33657023, 284693, 33657109, 55811576, 284632, 284558, 58182323, 284639, 18108383, 18108384, 18108388, 22279000, 22279002, 284587
2012	87772137 (4023, 4024)	Novel Protein sim. GBank gi 1086878 (U41020) - coded for by C. elegans cDNA yk100g4.5; coded for by C. elegans cDNA yk100g4.3; weakly similar to human SREBP-2 basic-helix-loop-helix-leucine zipper transcription factor [Caenorhabditis elegans]	Contains protein domain (PF00409) - Kinesin light chain repeat	UNCLASSIFIED	264259, 29331822, 29331824, 29331825, 29146498, 87168558, 265019, 284682, 284288, 264686, 21908764, 265020, 265022, 33657023, 284693, 33657109, 55811576, 284632, 284558, 58182323, 284639, 18108383, 18108384, 18108388, 22279000, 22279002, 284587
2013	94843842 (4025, 4026)	Novel Protein sim. GBank gi 4507985 ref NP_003427.1 pZNF1 - zinc finger protein 135 (clone p4Z-17)	Contains protein domain (PF00098) - Zinc finger, C2H2 type	dna_ma_bind	18108398, 264908, 265007, 265010, 265018, 265019, 264689, 21908767, 265020, 264692
2014	87347940 (4027, 4028)	Novel Protein sim. GBank gi 127720 sp P20938 MYO0_METFR - MYELIN P0 PROTEIN PRECURSOR		UNCLASSIFIED	284488, 29331826, 264907, 264636, 264555, 284639, 264558

2015	88094922 (4029, 4030)	Novel Protein sim. GBank gij 81286 pir S22697 - extensin - Volvox carterl (fragment)		UNCLASSIFIED	56182575, 35698288, 284259, 35898052, 284508, 284906, 284907, 284510, 284512, 87188474, 285010, 284681, 284288, 284689, 284628, 35698423, 35698555, 284639, 284563, 284584
2016	85298641 (4031, 4032)	Novel Protein sim. GBank gij 285046 pir S26413 - l-complex protein Tcp-10 - mouse		strud	284102, 284508, 284110, 285009, 33109954, 21906768, 285021, 33657109, 27488282, 283972, 18108374, 283976, 284555, 284584
2017	79464293 (4033, 4034)			UNCLASSIFIED	284685, 284636
2018	79637067 (4035, 4036)	Novel Protein sim. GBank gij 124735 sp P18175 INVQ_PIG - INVOLUCRIN			284693
2019	87787900 (4037, 4038)	Novel Protein sim. GBank gij 2143910 pir S68216 - phosphatase-1 glycogen-binding (GL)-chain - rat		phosphatase	264107, 264110, 264112, 265017, 263976
2020	94674476 (4039, 4040)	Novel Protein sim. GBank gij 2078483 (U43200) - antifreeze glycoprotein AFGP polypeptide precursor [Boreogadus saida]		UNCLASSIFIED	284259, 284508, 284591, 265018, 284682, 284288, 284688, 22278002
2021	86718818 (4041, 4042)	Novel Protein sim. GBank gij 585084 sp Q07803 EFGM_RAT - ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)			55994075, 284593, 33109954, 21908754, 21908788, 33857023, 33857109, 27488261, 87168518
2022	95295665 (4043, 4044)	Novel Protein sim. GBank gij 4218005 (AC006135) - putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]			284757, 284767, 60170615, 18108385
2023	87722976 (4045, 4046)	Novel Protein sim. GBank gij 5410230 gb AAD42992.1 AF07334 - (AF073344) ubiquitin specific protease 3 [Homo sapiens]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	18108394, 22278999, 284259, 284905, 284908, 284908, 284595, 284762, 284769, 284634, 284636, 87168518, 60432113, 22278000, 284482, 284565
2024	87886443 (4047, 4048)				60433438, 265017, 284886, 264692, 284693, 284636
2025	87858863 (4049, 4050)	Novel Protein sim. GBank gij 4755188 gb AAD29055.1 AC00701 - (AC007018) unknown protein [Arabidopsis thaliana]	Contains protein domain (PF00637) - 7-fold repeat in Clathrin and VPS	UNCLASSIFIED	22278997, 284509, 284906, 264909, 55812038, 285017, 265021, 285022, 60170615, 284556
2026	94122114 (4051, 4052)	Novel Protein sim. GBank gij 1655699 emb CAA69032 - (Y07752) perlecanin-S [Volvox carterl]		UNCLASSIFIED	56994075, 60432049, 284508, 66712502, 284112, 60170831, 87168559, 284288, 284688, 284689, 21908768, 33657109, 18108370, 284638, 18108385, 80432113, 22279000, 22279002, 284584, 284566, 284587
2027	80249001 (4053, 4054)			UNCLASSIFIED	263976, 284634, 284488

2028	94699884 (4055, 4056)	Novel Protein sim. GBank gl 1330345 (U58755) - coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....	Contains protein domain (PF00632) - HECT-domain (ubiquitin-transferase).	ubiquitin	52644507, 52645156, 52646842, 56182575, 56994075, 35696286, 22278997, 22278998, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 68714117, 29331825, 29331826, 29331827, 29331828, 35686032, 264906, 264907, 264908, 29331830, 52644045, 56182435, 265006, 265009, 60432229, 33657402, 264595, 264757, 55812038, 21908754, 52646317, 52644286, 265010, 265011, 67168559, 265017, 265018, 265019, 264448, 18108354, 264288, 264369, 264766, 52644229, 21908765, 21908766, 21908767, 21908768, 21908769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 65274620, 33657109, 52645129, 18108368, 27486281, 27486282, 27486284, 27486285, 35695763, 264629, 55811576, 35698423, 35695855, 264635, 264636, 52644332, 264556, 83373044, 56526486, 22278000, 22279002, 264563, 265009, 264595, 85658542, 264555, 264556, 264557, 264558, 264559, 83373044
2029	95362032 (4057, 4058)	Novel Protein sim. GBank gl 3599940 (AF017368) - faclogenicital dysplasia protein 2 [Mus musculus]	Contains protein domain (PF00621) - RhoGEF domain	UNCLASSIFIED	18108394, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 264108, 66712502, 264828, 265009, 265018, 265019, 264681, 264882, 264884, 264885, 56181562, 264689, 21906769, 265022, 264692, 264693, 264628, 18108370, 18108374, 264634, 264636, 264558, 18108385, 87168518, 22279002, 264565
2030	91213734 (4059, 4060)	Novel Protein sim. GBank gl 5630080[gb AAD45825.1 AC004890] similar to HUB1; similar to BAA24380 (PID:g2789430) [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	264558, 18108382, 18108384
2031	80245281 (4061, 4062)				65274572, 35696286, 29331824, 264908, 265009, 264593, 265018, 264288, 264686, 264769, 21906766, 21906767, 29148627, 264826, 35698423, 264634, 264556, 18108381, 60170394, 264559, 83373044, 18108385, 264482, 264484
2032	91232607 (4063, 4064)	Novel Protein sim. GBank gl 5689491[dbj BAA83029.1 (AB029000) KIAA1077 protein [Homo sapiens]	Contains protein domain (PF00884) - Sulfatase	hydrolase	56181562, 264628, 264632, 264555, 264558
2033	95000809 (4065, 4066)	Novel Protein sim. GBank gl 2464828[sp Q64886 CAG7_RAT - ALPHA-N-ACETYL GALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (ST6GALNACII) (STY)		synthase	
2034	91232529 (4067, 4068)	Novel Protein sim. GBank gl 4826984[ref NP_005147.1 PROD1 - UNKNOWN	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	22278998, 22278999, 264907, 29331830, 265008, 265018, 264681, 264682, 264684, 21906767, 21906768, 21906769, 33657109, 83373044, 56526486

2035	83553451 (4069, 4070)				264369, 264686, 265022, 56526486, 264567
2036	87115833 (4071, 4072)				29331827, 29331828, 264682, 264368, 29148627, 60432113
2037	94324833 (4073, 4074)	Novel Protein sim. GBank gi2734081 (AF000195) - similar to oxysterol-binding proteins [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 29331824, 60432289, 29331826, 29331828, 35696052, 264907, 29331830, 66712502, 56182435, 265008, 265009, 60170831, 264584, 55812038, 33109954, 21906754, 87168559, 265017, 265018, 265019, 264762, 264369, 264288, 21906765, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 33657182, 35695763, 35695855, 264632, 264634, 264636, 56182323, 83373044, 60432113, 22279000, 22279002, 264563
2038	95422384 (4075, 4076)	Novel Protein sim. GBank gi3880625[embjCAB07858] - (Z93785) predicted using GeneFinder; similar to RNA recognition motif (aka RRM, RBD, or RNP domain); cDNA EST EMBL: T01682 comes from this gene; cDNA EST EMBL: M75823 comes from this gene; cDNA EST EMBL: D27559 comes from this ge...	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	UNCLASSIFIED	22278995, 22278996, 56994075, 264259, 29331824, 35696052, 264905, 264906, 52644045, 265007, 265009, 87168559, 265017, 18108351, 264448, 264369, 264768, 264767, 264686, 18108358, 21906765, 21906769, 52644150, 33657023, 264692, 18108362, 33657109, 27486262, 18108370, 18108374, 18108379, 35696423, 65274791, 264632, 264636, 18108383, 63373044, 18108385, 87168518, 22279000, 22278002, 264563, 264564, 264566
2039	95514626 (4077, 4078)	Novel Protein sim. GBank gi2224653[dbjBAA20813] - (AB002354) KIAA0356 [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	22278997, 264259, 29331822, 264905, 264906, 264907, 264908, 264909, 264510, 265009, 264910, 264593, 264758, 265011, 265018, 264762, 264288, 264768, 264769, 21906766, 33657023, 264692, 264693, 33657109, 35696423, 264631, 264632, 264634, 264635, 264636, 264637, 264639, 87168518, 264486
2040	95308417 (4079, 4080)			UNCLASSIFIED	264592
2041	95071736 (4081, 4082)	Novel Protein sim. GBank gi2500825[spjP70700]RPA2_MOUSE - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135)	mapolymerase	UNCLASSIFIED	264488, 22278998, 35696052, 264905, 264907, 264908, 264910, 265018, 264605, 265019, 18108351, 264766, 264769, 21906766, 265021, 265022, 264692, 33657109, 264628, 264629, 35696423, 35695855, 264637, 264638, 264563, 264564, 264565, 264567

2042	95307447 (4083, 4084)	Novel Protein sim. GBank gi 4406590 gb AAD20040 - (AF131766) Similar to Ena-VASP like protein [Homo sapiens]	Contains protein domain (PF00566) - WH1 domain	UNCLASSIFIED	60424179, 35696286, 284259, 29331826, 35696052, 29331828, 264508, 264509, 264907, 264909, 264510, 264511, 265009, 264910, 264591, 60433356, 264595, 265017, 265018, 264681, 264784, 264369, 264765, 264684, 264288, 264766, 264686, 52644229, 264769, 21906765, 35695917, 264535, 52644150, 264691, 264692, 18108365, 27486261, 27486262, 27486265, 18108374, 35698423, 65274791, 35695855, 264555, 264558, 60170394, 18108385, 264404, 22279000, 22279002, 264482, 264563, 264584, 264586
2043	94328076 (4085, 4086)	Novel Protein sim. GBank gi 5052554 gb AAD38607.1 AF14563 - (AF145632) BcDNA. GH06032 [Drosophila melanogaster]	Contains protein domain (PF00122) - E1-E2 ATPase	transport	264488, 52644507, 52646385, 56994075, 22278997, 22278998, 20281171, 264259, 29331822, 29331824, 68714117, 29331826, 29331828, 33656970, 29146498, 264508, 264908, 52644045, 56182435, 265006, 33657402, 21906754, 52644296, 87168559, 265017, 265018, 265019, 264681, 264288, 264766, 264685, 264686, 21906768, 21906767, 21906768, 21906769, 265020, 265021, 60170615, 264691, 33657023, 264693, 65274620, 33657109, 33657182, 27486261, 27486262, 33657349, 35695763, 18108374, 55811576, 35695855, 18108380, 18108381, 60170394, 56182323, 264558, 83373044, 18108385, 56526486, 87168518, 60432113, 22279000, 264567
2044	87106927 (4087, 4088)	Novel Protein sim. GBank gi 2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	264093, 29331827, 264905, 66712502, 264592, 264689, 21906765, 21906769, 265020, 264692, 284482, 284586
2045	79835532 (4089, 4090)				264692
2046	87320849 (4091, 4092)	Novel Protein sim. GBank gi 4406698 gb AAD20062 - (AF131852) Unknown [Homo sapiens]			264259, 264806, 264683, 22279002
2047	84578801 (4083, 4094)	Novel Protein sim. GBank gi 4101720 (AF006466) - lymphocyte specific formin related protein [Mus musculus]			22278998, 29147620, 29331824, 29146498, 264508, 265007, 265008, 265019, 264605, 264681, 29146627, 29146629, 265021, 33657023, 18108365, 33657109, 33657182, 18108377, 264556, 264638, 264559, 18108388
2048	84606378 (4095, 4096)			UNCLASSIFIED	264909
2049	88094690 (4097, 4098)	Novel Protein sim. GBank gi 4589656 gb BAA76850.1 - (AB023223) KIAA1006 protein [Homo sapiens]		UNCLASSIFIED	264488, 264259, 29331824, 29331828, 35696052, 264906, 264907, 264908, 264909, 264910, 264603, 264783, 21906767, 21906768, 264628, 264634, 264637, 22279002, 264564, 264565, 264566, 264567

2050	79633835 (4089, 4100)			UNCLASSIFIED	264693	264488, 264259, 264509, 264908, 264907, 264769, 18108374, 35698423, 264563, 264566, 264488
2051	87780188 (4101, 4102)			UNCLASSIFIED		264488, 263994, 35698052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264113, 264511, 265008, 264910, 60170831, 264592, 264758, 265010, 265011, 264805, 264760, 264682, 264784, 264369, 264768, 264688, 264768, 264769, 52644229, 264689, 35695917, 33657023, 33657109, 264628, 18108374, 35698423, 55811576, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264556, 264638, 264639, 18108385, 56526486, 60432113, 264563, 264564, 264566, 264488, 264567, 264488, 263994, 35698052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264113, 264511, 265009, 264910, 60170831, 264592, 264758, 265010, 265011, 264605, 264760, 264682, 264764, 264369, 264768, 264688, 264768, 264769, 52644229, 264689, 35695917, 33657023, 33657109, 264628, 18108374, 35698423, 55811576, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264556, 264638, 264639, 18108385, 56526486, 60432113, 264563, 264564, 264566, 264488, 264567
2052	88096393 (4103, 4104)	Novel Protein sim. GBank gi 45298889 gb AAD21812.1 - (AF134728) G9A [Homo sapiens]	Contains protein domain (PF00856) - kinase SET domain			22278996, 22278997, 264259, 29331822, 264102, 264508, 35695917, 263972, 264482, 60424179, 264094, 264259, 29331825, 60424269, 264908, 60432229, 60433356, 87168559, 265019, 264760, 264288, 264686, 21906789, 33657023, 264693, 55810784, 55811576, 264635, 56182323, 60432113
2053	87763078 (4105, 4106)	Novel Protein sim. GBank gi 2995449 emb CAA75113 - (Y14848) midline 1 protein [Mus musculus]		UNCLASSIFIED		264488, 29331826, 60432289, 29331828, 60433356, 265019, 264883, 264684, 265021, 33657109, 18108374, 264637, 18108385, 87168518, 60432113, 22279000, 264564
2054	95358937 (4107, 4108)	Novel Protein sim. GBank gi 3876326 emb CAB02090 - (Z79754) similar to C2 domain [Caenorhabditis elegans]	Contains protein domain (PF00166) - C2 domain			
2055	88259449 (4109, 4110)	Novel Protein sim. GBank gi 5353748 gb AAD42226.1 AF15913 - (AF159133) SIR2-like protein [Oryza sativa subsp. indica]		UNCLASSIFIED		

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2061	95362204 (4121, 4122)	Novel Protein sim. GBank gi 2496947 sp Q09298 YQO9_CAEEL - HYPOTHETICAL 141.2 KO PROTEIN EEED8.8 IN CHROMOSOME II	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	22278997, 22278999, 264258, 29331822, 29331824, 29331826, 29331827, 35698052, 29331828, 264906, 66712502, 29331830, 264908, 264909, 264112, 264511, 265007, 265009, 264910, 264591, 33857402, 21908754, 85858542, 265017, 265019, 264448, 264683, 264288, 264684, 264369, 264686, 264687, 18108358, 264689, 21906765, 21908767, 21908768, 21906769, 265020, 265022, 264691, 33857023, 33857109, 20281149, 18108379, 35695855, 264634, 264556, 264557, 264558, 18108382, 264559, 83373044, 18108384, 56528486, 60432113
2062	87028440 (4123, 4124)	Novel Protein sim. GBank gi 4502091 ref NP_001139.1 pANK2 - ankyrin 2, neuronal	Contains protein domain (PF00023) - Ank repeat	struct	264905, 264628, 264907, 264629, 264908, 264909, 18108374, 263978, 35695855, 264512, 264635, 60431850, 264636, 264760, 264563, 18108351, 264762, 264565, 264764, 264487, 264766
2063	87601272 (4125, 4126)	Novel Protein sim. GBank gi 4589562 dbj BAA76803.1 - (AB023176) KIAA0959 protein [Homo sapiens]	Contains protein domain (PF00617) - RasGEF domain	oncogene	22278994, 22278999, 264259, 29331827, 264906, 264909, 52644045, 264686, 21906767, 55811957, 264682, 18108365, 263972, 55811576, 18108384, 22279002, 264482, 264563, 264584, 264484
2064	95317253 (4127, 4128)	Novel Protein sim. GBank gi 1754515 dbj BAA13413.1 - (D87515) amlinopeptidase-B [Rattus norvegicus]		hydrolase	264488, 52646365, 56994075, 35696286, 22278997, 22278998, 264259, 29331826, 60432289, 29331827, 29331828, 35696052, 264509, 265007, 265008, 60432229, 60433436, 21906754, 265010, 265011, 87168559, 265017, 265018, 264781, 18108351, 264682, 264369, 264288, 52644229, 21906765, 21906767, 21906768, 35695917, 33857109, 18108368, 18108374, 35698423, 35695855, 52644332, 264559, 60432113, 22279000, 22279002, 264566, 264486
2065	95092238 (4129, 4130)	Novel Protein sim. GBank gi 2507144 sp Q04205 TENS_CHICK - TENSIN		kinase	264569, 18108394, 56182181, 60432289, 29331828, 264905, 264906, 264908, 60431735, 60433356, 55811386, 85658542, 265018, 55811150, 264681, 264766, 264682, 60431528, 263974, 55810764, 35695855, 264631, 264634, 264635, 60431850, 264557, 83373044, 18108388, 22279000, 22279002, 56182575, 264259, 264906, 264764, 264288, 56182323, 264567
2066	85793402 (4131, 4132)	Novel Protein sim. GBank gi 160171 (M58285) - circumsporozoite protein [Plasmodium yoelii]	Contains protein domain (PF00096) - Zinc finger, C2-H2 type	UNCLASSIFIED	

2067	95303892 (4133, 4134)				35698288, 22278997, 22278998, 60432049, 264259, 60432289, 60433438, 264882, 264448, 264369, 264288, 18108355, 21906765, 21906768, 265022, 33657109, 35698423, 35695855, 264558, 264404, 264563, 264488
2068	84344754 (4135, 4136)			UNCLASSIFIED	264887
2069	94319177 (4137, 4138)	Novel Protein sim. GBank gij3152882 (AF084604) - KE03 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	transcript factor	60424179, 56182575, 22278995, 22278998, 56994075, 264259, 29331822, 29331824, 29331825, 35696052, 29331828, 33656970, 264509, 264905, 56182435, 265009, 60433358, 87188559, 265017, 265018, 264604, 265019, 264448, 264764, 264766, 21906765, 21906767, 21906768, 21906769, 285020, 265021, 33657023, 33657109, 263976, 264555, 264557, 56182323, 83373044, 87188518, 60432113, 22279000, 22279002
2070	85791380 (4139, 4140)	Novel Protein sim. GBank gi15712131 gb AAD47379.1 AF12049 - (AF120499) DEM1 protein [Homo sapiens]		UNCLASSIFIED	35695917, 264905, 264628, 264908, 264638
2071	86846116 (4141, 4142)	Novel Protein sim. GBank gi13551531 dbj BAA33016 - (AB017437) avana [Gallus gallus]	Contains protein domain (PF00588) - WH1 domain		18108398, 265006, 265007, 265008, 265009, 264594, 265010, 265011, 18108351, 18108354, 18108364, 18108365, 18108388, 264634, 18108381, 18108385, 18108388, 18108391
2072	81718429 (4143, 4144)		Contains protein domain (PF00184) - Neurohypophyseal hormones, C-terminal Domain		22278995, 35698288, 22278997, 22278998, 22278999, 264490, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 265008, 33657402, 21906754, 265011, 265019, 18108351, 264682, 264369, 21906765, 21906768, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264690, 264892, 35696423, 264555, 264556, 264558, 22279000
2073	27925664 (4145, 4146)	Novel Protein sim. GBank gi1504026 dbj BAA13212 - (D86976) similar to C.elegans protein (Z37093) [Homo sapiens]		UNCLASSIFIED	264556
2074	94324767 (4147, 4148)	Novel Protein sim. GBank gi14240317 dbj BAA74937.1 - (AB020721) KIAA0914 protein [Homo sapiens]			29331822, 264909, 264511, 285009, 264594, 264595, 265010, 265011, 265017, 265018, 265019, 264448, 264683, 265020, 265021, 18108370, 264632, 83373044, 264567

2075	94314886 (4149, 4150)	Novel Protein sim. GBank gi 5138930 gb AAD40382.1 - (AF093880) transcription factor IIB [Homo sapiens]			18108394, 22278994, 22278996, 35698286, 22278998, 22278999, 264259, 29331822, 29331825, 29331827, 35698052, 29331828, 264905, 264907, 264908, 264510, 265007, 264910, 265008, 33657084, 264760, 264448, 264288, 264766, 264767, 264689, 21908768, 21906767, 21906769, 265021, 265022, 60170615, 33657023, 27488282, 27486255, 35698423, 35698555, 264631, 264634, 264639, 87188518, 22279002, 264563, 264488, 18108391
2076	87594118 (4151, 4152)				264259, 29331826, 264508, 264908, 264510, 265007, 265011, 264288, 264637, 18108385
2077	11389877 (4153, 4154)			UNCLASSIFIED	264592
2078	87539384 (4155, 4156)	Novel Protein sim. GBank gi 4220590 db BAA74579 - (D87908) nuclear protein np85 [Mus musculus]	Contains protein domain (PF00628) - PHD-finger	ubiquitin	29331825, 265017, 265018, 264288, 265020, 265021, 264634, 56528488
2079	88085916 (4157, 4158)	Novel Protein sim. GBank gi 4240255 db BAA74906.1 - (AB020690) KIAA0883 protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, CCHC class	UNCLASSIFIED	264768, 22278997, 265021, 264690, 264259, 264692, 29331822, 264693, 29331824, 29331828, 264508, 264509, 264908, 264907, 264628, 20281089, 264909, 265007, 265009, 264632, 264636, 264591, 264592, 264639, 264758, 264759, 33109954, 264604, 265018, 265019, 22279002, 264563, 264564, 264448, 264684, 264567, 264685
2080	94136689 (4159, 4160)	Novel Protein sim. GBank gi 2408021 emb CAB16218.1 - (Z99162) putative vacuolar protein [Schizosaccharomyces pombe]	Contains protein domain (PF01363) - FYVE zinc finger	UNCLASSIFIED	56182575, 264082, 29331824, 29331826, 29331830, 265017, 265018, 265020, 83373044
2081	94847186 (4161, 4162)	Novel Protein sim. GBank gi 5524734 gb AAD44360.1 AF16635 - (AF166350) ST7 protein [Homo sapiens]	Contains protein domain (PF00431) - CUB domain	eph	22278998, 22278997, 22278999, 60432049, 29331822, 29331824, 33657402, 85858542, 265011, 265018, 265019, 21908767, 21908768, 264693, 18108385, 22279000, 22279002
2082	87628629 (4163, 4164)	Novel Protein sim. GBank gi 3880558 emb CAA94234 - (Z70271) predicted using GeneFinder, similar to collagen; cDNA EST yk308e7.3 comes from this gene; cDNA EST yk308e7.5 comes from this gene; cDNA EST yk385a8.3 comes from this gene; cDNA EST yk385a8.5 comes from this gene [Caeno...]		collagen	264907, 265019
2083	94141000 (4165, 4166)	Novel Protein sim. GBank gi 2352427 (AF004161) - peroxisomal Ca-dependent solute carrier [Oryctolagus cuniculus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	56182575, 22278998, 22278997, 264259, 29331822, 29331825, 264509, 264112, 265009, 264593, 21908754, 265018, 265019, 264448, 264288, 264685, 21908769, 265020, 265022, 264691, 18108370, 65274791, 264631, 264555, 264563
2084	95189298 (4167, 4168)	Novel Protein sim. GBank gi 728836 sp P39193 ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		UNCLASSIFIED	265018, 264763, 264683, 264691

2085	94889476 (4169, 4170)	Novel Protein sim. GBank gi 1655699 emb CAA69032 - (Y07752) pterophorin-S [Volvox carter]		UNCLASSIFIED	56182575, 60432289, 264908, 56182435, 87168474, 264763, 264369, 264688, 264693, 18108370, 56182323
2086	91234404 (4171, 4172)	Novel Protein sim. GBank gi 3875032 emb CAA88936 - (Z49125) similarity to Trichostrogylus colubriformis 11 kd secretory protein (Swiss Prot accession number P21937); cDNA EST EMBL:D33349 comes from this gene; cDNA EST EMBL:D37644 comes from this gene; cDNA EST EMBL:D38149 come...		UNCLASSIFIED	35696286, 264259, 35696052, 264906, 264907, 264908, 264909, 264910, 264759, 264604, 264762, 264768, 264769, 35695917, 263978, 35698423, 35695855, 264632, 264634, 264637, 264638, 264639, 56182323, 18108385, 264482, 264488
2087	21436337 (4173, 4174)			UNCLASSIFIED	264489
2088	94111527 (4175, 4176)	Novel Protein sim. GBank gi 3880930 emb CAA16334.1 - (AL021481) similar to Phosphoglucomutase and phosphomannomutase phosphoserine; cDNA EST EMBL:D36168 comes from this gene; cDNA EST EMBL:D70697 comes from this gene; cDNA EST yk373h9.5 comes from this gene; cDNA EST EMBL:T0080...		UNCLASSIFIED	264488, 22278994, 35696286, 22278996, 29331827, 35696052, 33657402, 21906754, 33109954, 87168474, 265017, 265018, 265019, 264448, 264683, 264369, 264685, 264687, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 264692, 33657023, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35698423, 35695855, 83373044, 87168518, 22279000, 264587
2089	95422801 (4177, 4178)	Novel Protein sim. GBank gi 4758118 ref NP_004623.1 pDAP3 - Death associated protein 3	cadherin		18108392, 264488, 52644507, 18108394, 18108397, 52646842, 18108398, 56182575, 22278994, 22278995, 35696286, 22278996, 56994075, 22278997, 22278998, 22278999, 264091, 264092, 264093, 264094, 60432049, 264259, 26331822, 20281099, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 29146498, 29146499, 264102, 264108, 264107, 264109, 264508, 264905, 264509, 264906, 264907, 264908, 66712502, 264828, 52844045, 264909, 56182435, 264110, 264112, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265009, 60170831, 264592, 264593, 60433356, 33657402, 60433438, 264595, 55812036, 264756, 21906754, 33657084, 55811386, 52844286, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264761, 55811150, 264762, 18108351, 264682, 264448, 264763, 264764, 264683, 264369, 18108354, 264288, 264685, 264768, 264686, 264687, 264768, 52844228, 264688, 18108358, 56181562, 264769, 18108359, 264689, 21906765, 21906768, 21906767, 21906768, 29148627, 21906769, 55811957, 29148529, 29148764, 35695917, 265020, 265021, 265022, 60170815, 264690,

2080	88222470 (4179, 4180)				22278995, 22278998, 22278999, 284259, 29331826, 35696052, 284910, 33657402, 60433438, 33109954, 87188474, 87188559, 265018, 265019, 284681, 284684, 284688, 284687, 284688, 284689, 21908765, 21908766, 21908767, 21908769, 35695917, 285022, 60170615, 33657023, 35696423, 35695855, 284952, 18108387, 22279000
2091	95309161 (4181, 4182)	Novel Protein sim. GBank gil4580997 gb AAD24571.1 AF12108 - (AF121081) cAMP inducible 2 protein [Mus musculus]		UNCLASSIFIED	263994, 284905, 284908, 284511, 284512, 265008, 284910, 55811386, 284288, 284768, 56181562, 21908765, 21908768, 21908769, 265022, 284628, 284563, 284567
2092	88223605 (4183, 4184)			homeobox	22278997, 22278999, 66712502, 87168559, 284683, 285021, 284486
2093	87406073 (4185, 4186)	Novel Protein sim. GBank gil2352427 (AF004181) - peroxisomal Ca-dependent solute carrier [Ornitholagus cuticulus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264905, 284908, 284907, 264908, 264510, 265008, 265007, 265009, 264910, 264598, 21906754, 87168474, 265011, 264603, 265018, 265019, 284760, 284766, 264768, 284769, 21908767, 21906768, 21908769, 265021, 284690, 33657023, 264693, 284628, 284634, 284636, 284637, 284557, 56182323, 284564
2094	91230929 (4187, 4188)	Novel Protein sim. GBank gil4929551 gb AAD34036.1 AF15178 - (AF151799) CGI-40 protein [Homo sapiens]		MHC	35696286, 265017, 265018, 265019, 18108388
2095	95351528 (4189, 4190)	Novel Protein sim. GBank gil1363238 pir A57284 - spermatid perinuclear RNA-binding protein Spnr - mouse	Contains protein domain (PF00035) - Double-stranded RNA binding motif	dna_ma_bind	35696286, 52844045, 265008, 265007, 265008, 87168559, 18108351, 21908769, 29148784, 265020, 33657023, 27486262, 18108374, 18108388
2096	94119760 (4191, 4192)	Novel Protein sim. GBank gil3834423 (AF070689) - cytoplasmic dynein intermediate chain isoform DIC1a [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	ATPase_associated	284488, 284489, 65274572, 56182575, 22278996, 22278997, 22278999, 284259, 60432289, 29331826, 35698052, 264107, 284508, 284509, 284905, 264906, 264907, 284908, 52844045, 264909, 264510, 264511, 284512, 265008, 264910, 265009, 264592, 60433356, 60433438, 284758, 264596, 55812038, 21908754, 284601, 284602, 284605, 284782, 284681, 18108351, 284764, 284683, 284288, 284687, 284768, 284769, 284689, 21908765, 21908768, 21908767, 35695917, 265020, 265022, 52844150, 284691, 284692, 33657023, 284693, 27486261, 35695783, 284628, 284629, 35696423, 35695855, 264631, 284632, 284634, 284635, 284555, 284637, 283981, 284638, 284639, 264563, 284483, 284565, 284566, 284486, 284567

2097	95322772 (4193, 4194)	Novel Protein sim. GBank gil5174501[ref]NP_008051.1 pLYF1 - zinc finger protein, subfamily 1A, 1 (Ikaros)	Contains protein domain (PF00086) - Zinc finger, C2H2 type	transcript factor	65274572, 264511, 265010, 264600, 265017, 264448, 264288, 265021, 80170815, 264892, 33657109, 18108370, 264838, 264483 56994075, 264259, 264288, 265020, 264563
2098	87780340 (4195, 4196)	Novel Protein sim. GBank gil4758208[ref]NP_004081.1 pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	phosphatase	
2099	95412927 (4197, 4198)	Novel Protein sim. GBank gil2695659 (AF026954) - pyruvate dehydrogenase phosphatase regulatory subunit precursor, PDP1 [Bos taurus]		phosphatase	85274572, 264905, 65274444, 264891, 264638, 264555
2100	95332856 (4199, 4200)	Novel Protein sim. GBank gil3881189[emb]CAB16514] - (Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:CO8179 comes from this gene; cDNA EST EMBL:CO8337 comes from this gene; cDNA EST EMBL:CO9829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4...	Contains protein domain (PF00025) - ADP-ribosylation factor family	nuc _rept	56182575, 22278995, 22278996, 22278997, 22278998, 60432048, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 29146498, 264909, 265008, 265009, 264910, 264591, 60432229, 60433356, 33657402, 264758, 21908754, 85658542, 87188474, 265017, 265018, 265019, 264681, 18108351, 264762, 264448, 264369, 264288, 18108355, 264688, 21908765, 21908767, 21908768, 21906769, 265020, 265021, 33657023, 18108374, 35896423, 264558, 83373044, 87188518, 60432113, 22279000, 22279002 264091, 29331824, 264105, 265007, 265010, 18108380
2101	87762604 (4201, 4202)	Novel Protein sim. GBank gil4589468[dbj]BAA76761.1] - (AB012808) mBOCT [Mus musculus]		UNCLASSIFIED	
2102	87770461 (4203, 4204)	Novel Protein sim. GBank gil3874149[emb]CAA97423.1] - (Z73103) predicted using Genefinder [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264489, 35696286, 264259, 35696052, 264508, 264905, 264907, 264908, 264909, 264511, 264512, 264591, 264593, 60433358, 264758, 264601, 264605, 264760, 18108351, 264448, 264764, 264288, 264767, 264768, 21908768, 35695917, 18108374, 264634, 264555, 264559, 264563, 264482, 264486
2103	95413576 (4205, 4206)	Novel Protein sim. GBank gil4240159[dbj]BAA74858.1] - (AB020842) KIAA0835 protein [Homo sapiens]	Contains protein domain (PF01530) - Zinc finger, C2HC type	transcript factor	65274572, 56994075, 22278999, 264259, 29331824, 29331825, 35696052, 29331828, 66712502, 265009, 80170831, 264595, 33109954, 85658542, 87188559, 265017, 265019, 264448, 21908765, 21908768, 265022, 33657023, 27488282, 33657349, 35695763, 60431528, 18108374, 55811576, 56182323, 18108387, 87188518, 60432113, 264564
2104	85776161 (4207, 4208)			UNCLASSIFIED	264592, 264604, 22278000

2105	94848080 (4209, 4210)	Novel Protein sim. GBank gi 1707032 (U80445) - coded for by C. elegans cDNA yk13g5.3; coded for by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA yk65h8....		UNCLASSIFIED	264488, 56182575, 22278994, 56994075, 22278998, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331828, 60432289, 29331827, 29331828, 264508, 264905, 264508, 264807, 29331830, 52644045, 264510, 264511, 265007, 264512, 265009, 60170831, 60432228, 33857402, 60433358, 264595, 60433438, 264758, 33857084, 87188474, 265010, 87188559, 265017, 265018, 265019, 264782, 18108351, 264684, 18108354, 264288, 264686, 52644229, 18108359, 21908785, 21908788, 21908787, 21908788, 21908789, 35695917, 265020, 265022, 60170615, 52644150, 264692, 33857023, 264693, 33857109, 60431528, 18108374, 65274791, 35695855, 264635, 60170394, 264639, 264558, 18108385, 18108387, 56526488, 87188518, 60432113, 264564, 264566, 264567, 265008, 265019, 264606, 264639
2106	83365475 (4211, 4212)	Novel Protein sim. GBank gi 3881524 emb CAA93883 - (Z70038) ZK1067.4 [Caenorhabditis elegans]			
2107	79822862 (4213, 4214)	Novel Protein sim. GBank gi 3176689 (AC003671) - Contains similarity to ubiquitin carboxyl-terminal hydrolase 14 gb Z35927 from S. cerevisiae. [Arabidopsis thaliana]		UNCLASSIFIED	264905, 264906, 264907, 264908, 264909, 264758, 265011, 264600, 264601, 264764, 264768, 264767, 264788, 264769, 264693, 264629, 35695855, 264632, 264634, 264635, 264638, 264639, 83373044, 264488
2108	94233978 (4215, 4216)				18108348, 264789, 18108370, 18108374, 264555, 264556, 264557, 264558
2109	80478719 (4217, 4218)			UNCLASSIFIED	264584
2110	87729075 (4219, 4220)	Novel Protein sim. GBank gi 481043 pir S37671 - bai2 protein - human		UNCLASSIFIED	
2111	87818419 (4221, 4222)	Novel Protein sim. GBank gi 2143639 pir I56542 - calmodulin-binding protein - rat		UNCLASSIFIED	264788, 35695917, 264630, 264567, 264488
2112	87293783 (4223, 4224)	Novel Protein sim. GBank gi 4426629 gb AAD20459 - (AF100980) protocadherin [Rattus norvegicus]	Contains protein domain (PF00069) - struct		264508, 264806, 264591, 264682, 22279002
2113	78941388 (4225, 4226)	Novel Protein sim. GBank gi 3327184 dbj BAA31660 - (AB014585) KIAA0885 protein [Homo sapiens]	Contains protein domain (PF00028) - cadherin		265008
2114	87889342 (4227, 4228)	Novel Protein sim. GBank gi 3327184 dbj BAA31660 - (AB014585) KIAA0885 protein [Homo sapiens]	Cadherin domain		66714117, 28331826, 29331827, 60433438, 55812038, 265017, 265019, 264689, 21908789, 55811957, 265020, 285021, 33857109, 60170394, 264558
2115	80893785 (4229, 4230)	Novel Protein sim. GBank gi 4757890 ref NP_004328.1 pC8OR - chromosome 8 open reading frame 1		UNCLASSIFIED	65274572, 284689, 284691, 284692, 60432113

2116	88259387 (4231, 4232)	Novel Protein sim. GBank gi 2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	35696286, 22278999, 56182181, 29331824, 29331825, 29331827, 35696052, 284907, 56182435, 265008, 264591, 55812038, 55811366, 87168559, 264288, 264369, 21908769, 29148629, 33857023, 35695763, 55811578, 35698423, 18108385
2117	87788904 (4233, 4234)	Novel Protein sim. GBank gi 2330021 (AF019250) - kinesin-related protein; KRP; Costal2 [Drosophila melanogaster]		struct	29331824, 284511, 265009, 33109954, 265017, 265018, 264288, 264689, 265020, 264692, 56526486, 264482
2118	87078894 (4235, 4236)	Novel Protein sim. GBank gi 1078307 pir B56573 - nuclear pore complex glycoprotein p62 - African clawed frog		glycoprotein	264259, 264805, 264907, 264908, 264510, 264511, 265009, 264910, 265010, 264602, 264288, 264768, 264693, 263967, 263972, 264638, 284559
2119	8699317 (4237, 4238)	Novel Protein sim. GBank gi 4321407 gb AAD15748 - (AF047890) ATP-binding cassette protein M-ABC1 [Homo sapiens]		UNCLASSIFIED	264693, 18108385
2120	87789395 (4239, 4240)	Novel Protein sim. GBank gi 4885527 ref NP_005480.1 pNSP3 - novel SH2-containing protein 3	Contains protein domain (PF00017) - eph Src homology domain 2		264091, 264259, 29331826, 29331828, 265017, 284804, 264288, 264685, 265020, 264691, 18108370, 55810764, 264555, 264636, 60432113
2121	80021375 (4241, 4242)	Novel Protein sim. GBank gi 4757728 ref NP_004886.1 pAGTA - angiotensin/vasopressin receptor AII/AVP-like		UNCLASSIFIED	264601, 284766, 263978
2122	91230831 (4243, 4244)	Novel Protein sim. GBank gi 4929551 gb AAD34036.1 AF15179 - (AF151799) CGI-40 protein [Homo sapiens]			18108384, 56182575, 22278997, 29331822, 29331824, 29331825, 29331826, 29331828, 264907, 56182435, 265007, 264910, 265010, 265018, 264686, 265020, 55811576, 264555, 264637, 18108382, 83373044, 18108383, 18108384, 56526486, 264565, 284567
2123	86787998 (4245, 4246)	Novel Protein sim. GBank gi 2224551 dbj BAA20764 - (AB002303) KIAA0305 [Homo sapiens]	Contains protein domain (PF01363) - struct FYVE zinc finger	struct	18108386, 264757, 265011, 18108351, 264691, 284634, 18108385
2124	83005951 (4247, 4248)	Novel Protein sim. GBank gi 5689455 dbj BAA83011.1 - (AB028982) KIAA1059 protein [Homo sapiens]	Contains protein domain (PF00801) - transport PKD domain	transport	29331822, 264906, 264907, 264591, 264639, 284563
2125	95354041 (4249, 4250)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - !!! ALU SUBFAMILY J WARNING ENTRY !!!		UNCLASSIFIED	264259, 284509, 264907, 264511, 85658542, 264763, 21908765, 35695917, 264636, 264488
2126	95084231 (4251, 4252)	Novel Protein sim. GBank gi 4539284 emb CAB38853.1 - (AL049495) conserved hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	264488, 264489, 29331827, 35696052, 264905, 264509, 264908, 264909, 264510, 265009, 264591, 264592, 264593, 33857402, 264594, 264585, 264598, 264758, 264601, 264603, 265018, 264604, 264605, 264760, 264681, 264762, 264683, 264764, 264684, 264288, 264685, 264689, 60170615, 33857023, 33857109, 55810764, 264635, 264636, 264637, 264638, 264639, 83373044, 264564, 264566

2127	81118652 (4253, 4254)	Novel Protein sim. GBank gi 4868435 gb AAD31315.1 AF14323 - (AF143236) apoptosis related protein APR-2 [Homo sapiens]			35698288, 29331828, 35698052, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264510, 265008, 264511, 264512, 265007, 265009, 264910, 264758, 265011, 264800, 264801, 264804, 264762, 264763, 264766, 264887, 264768, 264769, 264889, 35695917, 264690, 264691, 264692, 264693, 264629, 18108374, 35695855, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264567, 56182575, 35698288, 56182181, 29331824, 60432289, 35698052, 264905, 264907, 66712502, 264908, 264909, 264510, 264512, 265009, 264910, 264591, 55812038, 265018, 264764, 264288, 264389, 264687, 264768, 55811957, 264692, 18108368, 264628, 264632, 264634, 264635, 264637, 56182323, 264639, 18108384, 18108388, 264563, 264567
2128	87414262 (4255, 4256)				66714117, 264628, 264595, 55812038, 55811150, 55811957, 264693, 18108374, 263976, 65274791, 18108381, 83373044, 22279000 263981
2129	95102089 (4257, 4258)		UNCLASSIFIED		
2130	95417144 (4259, 4260)	Novel Protein sim. GBank gi 2649255 (AE001012) - conserved hypothetical protein [Archaeoglobus fulgidus]	UNCLASSIFIED		
2131	85723085 (4261, 4262)	Novel Protein sim. GBank gi 1086886 (U41276) - Similar to potassium channel protein. [Caenorhabditis elegans]		Contains protein domain (PF00805) - Pentapeptide repeats (8 copies)	35698052, 264909, 264768, 35695917
2132	95361096 (4263, 4264)	Novel Protein sim. GBank gi 5689373 dbj BAA82973.1 - (AB028944) KIAA1021 protein [Homo sapiens]		Contains protein domain (PF00122) - E1-E2 ATPase	264488, 22278999, 264259, 29331827, 29331828, 35698052, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 265007, 264910, 264591, 264592, 264595, 264758, 21906754, 33109954, 87168474, 265011, 264600, 264801, 264605, 265019, 264760, 18108351, 264681, 264762, 264764, 264288, 264684, 264766, 264686, 264687, 264768, 264769, 264688, 21908769, 264690, 52644150, 264691, 264693, 18108370, 264628, 264629, 18108372, 18108374, 35698423, 35695855, 264631, 264634, 264635, 264636, 264555, 264637, 18108380, 264639, 264558, 56182323, 56526486, 264564, 264565, 264566, 264567

2133	95351539 (4265, 4266)	Novel Protein sim. GBank gi 4220489 (AC006069) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	60424179, 52646385, 52646842, 56994075, 35696286, 22278997, 22278998, 60432049, 56182181, 66714117, 60424269, 29331826, 29331828, 35696052, 264905, 264908, 264907, 66712502, 29331830, 56182435, 265006, 264512, 265008, 60431735, 60433358, 33657402, 55812038, 33109954, 21908754, 55811386, 265010, 264603, 265017, 265018, 265019, 55811150, 18108351, 264682, 264368, 264288, 52644229, 56181562, 21906765, 21906768, 21906767, 21906768, 21906769, 55811857, 35895917, 265020, 265021, 60170615, 33657023, 33657109, 60431528, 18108374, 35896423, 65274791, 35695855, 264634, 60431850, 18108380, 56182323, 83373044, 18108385, 18108387, 60432113, 22279002, 264583, 264588
2134	95412697 (4267, 4268)	Novel Protein sim. GBank gi 3875351 emb CAB09415 - (Z96047) DY3.6 [Caenorhabditis elegans]			56181688, 35696286, 21906754, 55811388, 265011, 265017, 18108351, 264765, 264768, 264688, 21906768, 35895917, 265020, 33657023, 264628, 35695855, 264632, 264555, 264556, 264557, 264558, 18108382, 22279002
2135	86079813 (4269, 4270)	Novel Protein sim. GBank gi 5689559 dbj BAA83063.1 - (AB029034) KIAA1111 protein [Homo sapiens]	Contains protein domain (PF00628) - PHD-finger	UNCLASSIFIED	22278998, 29331828, 35696052, 264906, 264908, 264910, 265009, 264591, 264758, 52646317, 265011, 87188559, 264601, 18108351, 264448, 264683, 264684, 264689, 18108358, 264691, 33657023, 264682, 35695763, 264629, 35695855, 264631, 264635, 264636, 264637, 56182323, 264639, 22279002, 264564
2136	84346479 (4271, 4272)	Novel Protein sim. GBank gi 2662167 dbj BAA23715 - (AB007803) KIAA0443 [Homo sapiens]		UNCLASSIFIED	264639
2137	87637716 (4273, 4274)	Novel Protein sim. GBank gi 4884110 emb CAB43262.1 - (AL050090) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264568, 264809, 33109854, 264763, 21908768, 60170394, 18108385, 264563
2138	87385446 (4275, 4276)	Novel Protein sim. GBank gi 5174779 gb AAD40696.1 - (U87804) 50 kDa protein [Caulobacter crescentus]		ATPase_associated	264259, 29331828, 35696052, 264909, 265006, 265017, 265018, 18108351, 264288, 21908768, 33657023, 33657109, 264628, 18108374, 35695855, 264634, 264555, 264556, 264557, 264558, 264559
2139	94843882 (4277, 4278)	Novel Protein sim. GBank gi 3850821 emb CAA77135 - (Y18350) U2 snRNP auxiliary factor, large subunit [Nicotiana glauca]			264905, 264910, 264591, 55812038, 55811386, 85858542, 264760, 18108351, 18108359, 55811857, 265020, 265021, 33657023, 18108384, 55811576, 83373044, 18108385, 56528486, 264482

2140	87645655 (4279, 4280)	Novel Protein sim. GBank gi 4417293 gb AAD20418 - (AC007019) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 264259, 29331824, 264104, 264109, 264509, 265006, 264759, 265018, 264448, 264288, 21906768, 55811957, 265021, 33657023, 27486265, 35698423, 264638, 264556, 264557, 264559, 264566
2141	79623986 (4281, 4282)			UNCLASSIFIED	265020, 264893
2142	80041222 (4283, 4284)			UNCLASSIFIED	263978
2143	94140051 (4285, 4286)	Novel Protein sim. GBank gi 2135766 pir S53362 - muchn 5AC (clone JER47) - human (fragment)		UNCLASSIFIED	22278987, 29331827, 264907, 265020, 60432113
2144	94320114 (4287, 4288)	Novel Protein sim. GBank gi 2078483 (U43200) - antifreeze glycopeptide AFGP polypeptide precursor [Boreogadus salda]		UNCLASSIFIED	65274572, 264259, 29331824, 29331827, 264906, 264908, 264591, 265011, 87168559, 264800, 265018, 264288, 264768, 21906765, 21906767, 55811576, 35698423, 65274791, 22279002
2145	20564305 (4289, 4290)			UNCLASSIFIED	263978
2146	87010515 (4291, 4292)	Novel Protein sim. GBank gi 1255871 (U53341) - short region of weak similarity to bovine membrane receptor p63 (PIR:S28503) [Caenorhabditis elegans]		UNCLASSIFIED	264908, 60433358, 264686
2147	80432911 (4293, 4294)	Novel Protein sim. GBank gi 3080398 emb CAA18718.1 - (AL022603) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	264907, 264768, 264769, 18108385
2148	80048811 (4295, 4296)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - III ALU SUBFAMILY SQ WARNING ENTRY III		UNCLASSIFIED	264593
2149	87362022 (4297, 4298)	Novel Protein sim. GBank gi 19863 sp P20693 FCE2_MOUSE - LOW AFFINITY IMMUNOGLOBULIN EPSILON FC RECEPTOR (LYMPHOCYTE IGE RECEPTOR) (FC-EPSILON-RII) (CD23)	Contains protein domain (PF00059) - Lectin C-type domain	glycoprotein	29331824, 29331826, 35698052, 264758, 87168474, 265018, 52844150, 33657109
2150	94140059 (4299, 4300)	Novel Protein sim. GBank gi 5420387 emb CAB46678.1 - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	22278988, 29331822, 29331824, 29331828, 264764, 264769, 21906768, 264488
2151	95353241 (4301, 4302)	Novel Protein sim. GBank gi 5689407 dbj BAA82987.1 - (AB028958) KIAA1035 protein [Homo sapiens]			22278996, 56994075, 22278999, 60432049, 264259, 29331822, 29331824, 29331828, 35698052, 29331828, 264508, 284511, 80433358, 264758, 264596, 33109954, 60174638, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264288, 264689, 21906765, 21906768, 21906768, 265020, 60170615, 33657109, 33657182, 33657349, 18108370, 264635, 264557, 60170394, 18108385, 87168516, 22279000
2152	79321640 (4303, 4304)	Novel Protein sim. GBank gi 3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]		kinase	18108397, 18108398, 265007, 264591, 265011, 18108351, 18108368, 18108374, 18108388

2153	88313371 (4305, 4308)	Novel Protein sim. GBank gil4758704 refNP_004218.1 pMASL - MFH-amplified sequences with leucine-rich tandem repeats 1	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264488, 263994, 52646842, 22278896, 22278898, 22278988, 264258, 29331822, 3588052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 264512, 264758, 87188474, 87188559, 265017, 265019, 264760, 264288, 264369, 264766, 264687, 264769, 52644229, 21906766, 21908768, 35695917, 33857023, 33857109, 35695855, 264631, 264632, 264635, 264636, 264639, 18108385, 264483, 264584, 264486
2154	87408034 (4307, 4308)	Novel Protein sim. GBank gil225150 prfj1209265U - chorion protein B11 [Bombyx mori]		UNCLASSIFIED	56994075, 264094, 265009, 265019, 264288, 21908767, 35695917
2155	87424072 (4309, 4310)			UNCLASSIFIED	18108392, 18108398, 22278896, 264259, 29331824, 265008, 265010, 265011, 265017, 265019, 264288, 264688, 265020, 264693, 264628, 56182323
2156	84285205 (4311, 4312)	Novel Protein sim. GBank gil3970966 (AC004974) - spa-1- like; similar to AF026504 (PID:g2555183) [Homo sapiens]			265007, 264684
2157	87316344 (4313, 4314)				264591
2158	86444218 (4315, 4316)	Novel Protein sim. GBank gil1076211 prfjS50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	264596
2159	80083729 (4317, 4318)	Novel Protein sim. GBank gil4650844 dbj BAA77027.1 - (AB026180) Kelch motif containing protein [Homo sapiens]	Contains protein domain (PF00551) - BTB/POZ domain	dna_ma_bind	29331822, 264112, 265009, 264691, 33857023, 264634
2160	16283674 (4319, 4320)	Novel Protein sim. GBank gil2879825 dbj BAA24826 - (AB007897) KIAA0437 [Homo sapiens]			264634
2161	87739131 (4321, 4322)			UNCLASSIFIED	265008
2162	94319526 (4323, 4324)	Novel Protein sim. GBank gil1504006 dbj BAA13202 - (D86866) similar to human ZFY protein. [Homo sapiens]		UNCLASSIFIED	65274572, 264508, 264905, 264906, 264907, 264908, 52644045, 264909, 265007, 264910, 264591, 264592, 264593, 55812038, 264598, 264758, 265011, 264600, 264762, 264763, 264683, 264764, 264288, 264766, 264686, 264768, 264769, 264689, 265020, 264691, 264628, 264629, 263978, 264632, 264634, 264557, 264638, 264639, 18108385, 264563, 264586, 264587
2163	95417158 (4325, 4326)	Novel Protein sim. GBank gil3876537 emb CAA98270 - (Z73974) cDNA EST yk291f5.3 comes from this gene; cDNA EST yk291f5.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	56182575, 22278988, 264093, 264683, 33857023, 65274820, 80432113
2164	80569456 (4327, 4328)		Contains protein domain (PF01006) - Hepatitis C virus non-structural protein NS4a	collagen	264603, 264637, 264565

2165	94329169 (4329, 4330)	Novel Protein sim. GBank gjl1086794 (U41107) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	56994075, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264908, 29331830, 56182435, 265009, 21906754, 33657084, 265011, 265019, 264448, 264288, 264369, 21906765, 21906768, 21906769, 265020, 265021, 264691, 264692, 33657023, 65274620, 35695855, 264556, 60170394, 83373044, 60432113, 22278002, 264567, 52645156, 22278994, 22278998, 66714117, 29331828, 52644045, 265018, 265019, 264369, 21906765, 21906767, 21906768, 21906769, 265021, 265022, 264693, 27486262, 35695763, 18108376, 56526488, 67168518, 264567
2166	87618934 (4331, 4332)	Novel Protein sim. GBank gjl2706522[embjCAA75816] - (Y15895) ubiquitin activating enzyme [Drosophila melanogaster]	ubiquitin		56182575, 35696286, 29331824, 29331826, 29148498, 56182435, 265008, 265009, 264592, 264593, 33657402, 33109854, 265011, 265017, 265018, 18108351, 264369, 21906764, 21906765, 21906768, 29148627, 21906769, 52644150, 33657109, 35698423, 18108381, 18108384, 18108385, 60432113, 264567
2167	87718864 (4333, 4334)	Novel Protein sim. GBank gjl2224713[dbjBAA20840] - (AB002384) KIAA0386 [Homo sapiens]	UNCLASSIFIED		66714117, 29331827, 264907, 264511, 264591, 265018, 264764, 264663, 264766, 264768, 264566
2168	86989334 (4335, 4336)	Novel Protein sim. GBank gjl4321407[gbjAAD15748] - (AF047690) ATP-binding cassette protein M-ABC1 [Homo sapiens]	transport	Contains protein domain (PF00664) - ABC transporter transmembrane region.	264829, 264555, 264559
2169	87869937 (4337, 4338)	Novel Protein sim. GBank gjl5106521[gbjAAD39741.1]AF10536 - (AF105365) K-CI cotransporter KCC4 [Homo sapiens]	UNCLASSIFIED		65274572, 56182575, 22278997, 22278998, 264259, 29331825, 264509, 264908, 56182435, 60433438, 55812036, 264598, 55811388, 265019, 264762, 264763, 264448, 264764, 264684, 264288, 264766, 264685, 56181562, 264689, 55811957, 265020, 264535, 264691, 33657109, 60431528, 18108374, 35698423, 55811576, 65274791, 264634, 264639, 264558, 67168518, 60432113, 264584
2170	94141033 (4339, 4340)	Novel Protein sim. GBank gjl2493778[spIQ09456]YQ35_CAEEL - PUTATIVE CUTICLE COLLAGEN C09G5.5	UNCLASSIFIED		264369, 265020, 264558
2171	80194050 (4341, 4342)	Novel Protein sim. GBank gjl4308681[gbjAAD15478] - (AC006930) R33423.1 [Homo sapiens]	UNCLASSIFIED		264259, 264558
2172	85452460 (4343, 4344)	Novel Protein sim. GBank	UNCLASSIFIED		264369
2173	87036740 (4345, 4346)	Novel Protein sim. GBank			264906, 35695855, 264555, 264557

2175	84325850 (4348, 4350)	Novel Protein sim. GBank gij1263287 (U47855) - fibroin-3 (Araneus diadematus)		UNCLASSIFIED	264488, 35686286, 20281099, 29331826, 60432289, 35696052, 264109, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265008, 264910, 264591, 264594, 264595, 264596, 264758, 55812038, 265011, 264600, 264603, 264760, 264762, 264448, 264764, 264288, 264766, 264686, 264687, 21806768, 55811957, 35695917, 265020, 265022, 264691, 264692, 33657023, 264693, 264628, 264629, 55811576, 35696423, 65274791, 35695855, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264558, 18108385, 60432113, 264563, 264564, 264565, 264566, 264486, 264567
2176	88223392 (4351, 4352)	Novel Protein sim. GBank gij126837[sp P39184 ALU7_HUMAN - !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!	Contains protein domain (PF00805) - Pentapeptide repeats (8 copies)	oncogene	52844507, 52646842, 22278994, 35696286, 22278996, 22278998, 29331826, 29331827, 35696052, 29331828, 33656970, 29331830, 264910, 33657402, 264758, 52644296, 87168559, 265018, 264689, 21906765, 21906767, 21906769, 35695917, 52644150, 264690, 33657023, 33657109, 52645129, 33657162, 27486261, 27486262, 33657349, 18108376, 18108377, 35695855, 87168518, 60432113, 264404, 22279000, 264486
2177	84128842 (4353, 4354)	Novel Protein sim. GBank gij15454072[ref NP_008416.1 pSLU7 - step II splicing factor SLU7		kinase	18108392, 22278997, 22278999, 284093, 33657402, 265019, 264448, 264766, 264689, 21906767, 21906768, 21906769, 265021, 33657023, 18108370, 18108374, 60432113, 22279002
2178	87601557 (4355, 4356)	Novel Protein sim. GBank gij1473407 (U08215) - NST-1 (Mus musculus)	Contains protein domain (PF00012) - Hsp70 protein	eph	264488, 22278996, 22278999, 29331824, 29331825, 29331826, 29331827, 52644296, 87168474, 18108370, 35695855, 22279002
2179	87316275 (4357, 4358)			UNCLASSIFIED	60424269, 264760, 264628, 264632

2180	85351397 (4359, 4360)	Novel Protein sim. GBank gi 3122317 sp P90848 KMH8_DICD1 - MYOSIN HEAVY CHAIN KINASE B (MHCK B)	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	52644507, 22278994, 35698286, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331828, 33656970, 264508, 264509, 264908, 264908, 29331830, 264909, 264510, 265006, 265007, 33657402, 55812038, 21908754, 87188474, 87188559, 265017, 265018, 265019, 264763, 264682, 264683, 264684, 264288, 264686, 21906765, 21906766, 21906769, 265020, 265021, 265022, 52644150, 33657023, 33657109, 27486265, 33657349, 18108374, 35698423, 35695855, 263981, 60170394, 18108385, 56526466, 87188518, 60432113, 22279000, 264482, 264566, 264567, 264488, 29331827, 264369, 18108376, 264564
2181	85764930 (4361, 4362)	Novel Protein sim. GBank gi 3024689 sp Q15542 T2D4_HUMAN - TRANSCRIPTION INITIATION FACTOR TFIID 100 KD SUBUNIT (TAFII100)		kinase	
2182	87637731 (4363, 4364)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	22278996, 22278997, 22278999, 264259, 29331822, 56182435, 264112, 264764, 264288, 21908767, 21906768, 21908769, 33657109, 18108376, 60170394, 22279000, 22279002
2183	85460649 (4365, 4366)	Novel Protein sim. GBank gi 3873408 gb AAC77482.1 - (U17129) unknown [Rhodococcus erythropolis]			264760
2184	87760690 (4367, 4368)	Novel Protein sim. GBank gi 3114713 (AF081346) - Edp1 protein [Mus musculus]		inf	29331822, 29331825, 29331826, 56182435, 265011, 264685, 264686, 21906768, 18108370, 264629, 264631, 264636, 264557
2185	87826463 (4369, 4370)	Novel Protein sim. GBank gi 5106956 gb AAD39906.1 AF11361 - (AF113615) FH1/FH2 domain-containing protein FHOS [Homo sapiens]			29331824, 264907, 66712502, 264757, 265019, 264288, 264692, 56526486
2186	87739227 (4371, 4372)	Novel Protein sim. GBank gi 2884625 emb CAA16972 - (AL021811) putative protein [Arabidopsis thaliana]		ATPase associated	264259, 29331822, 29331824, 29331826, 56182435, 264592, 55812038, 264760, 264768, 55811957, 33657023, 55811576, 56182323, 264563
2187	87386173 (4373, 4374)			UNCLASSIFIED	35698052, 264905, 264906, 264907, 264908, 264510, 264511, 265008, 264910, 264758, 265019, 264762, 264681, 264766, 264769, 35695917, 264692, 35698423, 264631, 264635, 264637, 18108388, 264566, 264488
2188	87771708 (4375, 4376)	Novel Protein sim. GBank gi 5107816 gb AAD40129.1 AF14941 - (AF149413) contains similarity to histone deacetylases; Pfam PF00850, Score=13.3, E=5e-10, N=1 [Arabidopsis thaliana]		histone	18108388, 56994075, 264259, 29331824, 29331825, 66714117, 29331827, 264908, 29331830, 265018, 265020, 265021, 56182323, 264559, 22279000, 22279002
2189	85693573 (4377, 4378)	Novel Protein sim. GBank gi 3452357 (AF075724) - unknown [Legionella pneumophila]	Contains protein domain (PF01596) - O-methyltransferase		22278996, 264259, 29331826, 21906754, 264369, 264288, 263987

2190	87639197 (4379, 4380)	Novel Protein sim. GBank gij132575[sp]P29315[RINI_RAT - RIBONUCLEASE INHIBITOR]		nucleaseinhib	22278998, 22278999, 29331822, 29331824, 29331826, 265008, 264910, 60170831, 55812038, 52644298, 265010, 265018, 264685, 264686, 56181582, 21908769, 35695917, 265022, 60170394, 22279000
2191	95198928 (4381, 4382)	Novel Protein sim. GBank gij5327002[emb]CAB46272.1] - (Y18503) XAP-5-like protein [Homo sapiens]			29331825, 29331828, 29331830, 264510, 264511, 264910, 264593, 264594, 264556, 264559
2192	11126316 (4383, 4384)	Novel Protein sim. GBank gij462600[sp]P34400[M10_CAEEL - MIG-10 PROTEIN]	Contains protein domain (PF00169) - PH domain		264558
2193	94140073 (4385, 4386)	Novel Protein sim. GBank gij5420389[emb]CAB46880.1] - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	56181686, 29331825, 29331827, 264508, 264909, 285008, 264592, 60432229, 264288, 264684, 264766, 35695917, 33657023, 60431602, 60431528, 55810764, 55811578, 65274791, 35695855, 60431850, 56182323, 60432113
2194	21418714 (4387, 4388)	Novel Protein sim. GBank gij2773341 (AF040954) - putative protein phosphatase 1 nuclear targeting subunit [Rattus norvegicus]			264592
2195	88083023 (4389, 4390)	Novel Protein sim. GBank gij2832763[emb]CAA15685.1] - (AL009191) /prediction=(method:: /prediction=(method:: /match=(desc:: /match=(desc:: /motif=(desc: [Drosophila melanogaster]		UNCLASSIFIED	22278998, 22278999, 35696052, 265006, 21908754, 265017, 35695917, 265021, 265022, 35695855
2196	85091631 (4391, 4392)	Novel Protein sim. GBank gij5262487[emb]CAB45699.1] - (AL080076) hypothetical protein [Homo sapiens]		collagen	56182575, 35696286, 22278997, 22278999, 264259, 29331822, 66714117, 60432288, 29331827, 35698052, 29331828, 264508, 52644045, 56182435, 264510, 265007, 265008, 265009, 60433438, 55812038, 265010, 265011, 264448, 264288, 264686, 264687, 52644229, 21908765, 21908768, 21908767, 35695917, 265022, 264691, 33657023, 264693, 18108370, 18108376, 35698423, 55811576, 65274791, 35695855, 264636, 56182323, 18108385
2197	95073813 (4393, 4394)	Novel Protein sim. GBank gij4928567[gb]AAD34044.1]AF15180 - (AF151807) CGI-49 protein [Homo sapiens]			264768, 264769, 21908765, 21908766, 21908767, 29148827, 55811857, 35696286, 265020, 22278998, 265021, 264259, 33657023, 264683, 29331824, 35696052, 29331828, 18108370, 35695855, 264113, 265008, 264910, 60432228, 56182323, 33657402, 264768, 83373044, 21908754, 265018, 265019, 22279002, 264482, 264448, 264565, 264288, 264369
2198	88060814 (4395, 4396)	Novel Protein sim. GBank gij3548787 (AC005622) - R30953_1 [Homo sapiens]		UNCLASSIFIED	

2188	68054355 (4397, 4398)	Novel Protein sim. GBank gi 2739372 (AC002505) - hypothetical protein [Arabidopsis thaliana]				284105, 284110, 284112, 284688, 55811957, 33857023, 284692, 283987, 20281071, 56526486
2200	67405385 (4399, 4400)	Novel Protein sim. GBank gi 3043634[dbj BAA25481] - (AB011127) KIAA0555 protein [Homo sapiens]	struc			29331824, 284763, 284788
2201	94316872 (4401, 4402)	Novel Protein sim. GBank gi 3913470[sp O57314 DHBX_ANAPL - PUTATIVE STEROID DEHYDROGENASE SPM2	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase		29331824, 35696052, 284905, 284907, 33857402, 55811388, 285017, 285018, 285019, 284288, 21906768, 35695917, 285020, 285022, 33857023, 33857109, 27486261, 18108370, 35698423, 35695855, 284555, 284556, 83373044, 87188518, 60432113
2202	91672385 (4403, 4404)	Novel Protein sim. GBank gi 5262665[emb CAB45767.1] - (AL080186) hypothetical protein [Homo sapiens]	UNCLASSIFIED			284489, 284259, 29331824, 60432289, 35696052, 284905, 284909, 284592, 285017, 285018, 285019, 18108351, 284762, 284448, 284368, 284288, 264766, 21906765, 21906768, 284890, 264891, 264692, 33857109, 284634, 284636, 284555, 284639, 284558, 284559, 83373044, 18108385, 264404, 22279002, 264482
2203	87761832 (4405, 4406)	Novel Protein sim. GBank gi 1172845[sp P48629 RB25_RABIT - RAS-RELATED PROTEIN RAB-25	Contains protein domain (PF00071) - Ras family	glycoprotein		52646365, 56994075, 284259, 29331822, 29331828, 29331827, 29331828, 284910, 285010, 285011, 87168559, 285018, 285019, 284605, 284288, 21906768, 35695917, 33857023, 284692, 33857109, 35695763, 18108376, 284638, 22279000, 284568, 264567
2204	88088671 (4407, 4408)	Novel Protein sim. GBank gi 121036[sp P28348 GBT3_RAT GUANINE NUCLEOTIDE-BINDING PROTEIN G(7), ALPHA-3 SUBUNIT (GUSTDUCIN ALPHA-3 CHAIN)	Contains protein domain (PF00503) - G-protein alpha subunit	UNCLASSIFIED		
2205	94147589 (4409, 4410)	Novel Protein sim. GBank gi 4589480[dbj BAA76768.1] - (AB023141) KIAA0924 protein [Homo sapiens]	Contains protein domain (PF00096) - dna_ma_bind Zinc finger, C2H2 type			18108394, 18108397, 56182575, 60432049, 284259, 29331822, 29331824, 29331825, 29331828, 29331827, 284806, 265007, 285008, 285009, 80432228, 265010, 265011, 285018, 284883, 284288, 284369, 284686, 21906768, 21906768, 21906769, 284690, 284891, 284693, 18108388, 55811576, 65274791, 284634, 18108381, 18108384, 60432113, 22279002, 284563, 284566, 264591
2206	20820008 (4411, 4412)		UNCLASSIFIED			
2207	87787870 (4413, 4414)	Novel Protein sim. GBank gi 4557753[ref NP_000372.1 pMID1 - midline 1 protein	Contains protein domain (PF00622) - SPRY domain			29331822, 56182181, 29331827, 35696052, 52644045, 285008, 285019, 56181562, 55811957, 265021, 33857023, 35695763, 35695855, 60170394, 60432113, 264568, 284906, 285019, 18108351, 21906769, 284112, 285009, 284891, 18108385, 18108374, 284634, 20281166
2208	86100830 (4415, 4416)					
2209	87800420 (4417, 4418)	Novel Protein sim. GBank gi 3986746 (AF105228) - tuftelin [Bos taurus]		struc		

2210	57152407 (4419, 4420)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		Kinase	264603
2211	87341720 (4421, 4422)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		oncogene	264665, 264686, 18108365, 22278002, 264482
2212	91223924 (4423, 4424)	Novel Protein sim. GBank gi 3776027 emb CAA09214 - (AJ010475) RNA helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) - helicase DEAD/DEAH box helicase		22278995, 22278997, 22278999, 264092, 264094, 29331822, 66714117, 29331828, 29331828, 284907, 52844045, 265009, 60170831, 21906754, 87168559, 265017, 265019, 18108351, 264683, 18108354, 264369, 284766, 264687, 52644229, 21906765, 21906766, 21906767, 21906768, 265021, 33657108, 18108370, 18108374, 284638, 56182323, 18108384, 18108387, 87168518, 264565
2213	91219309 (4425, 4426)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]			56182575, 22278996, 22278997, 35696052, 264905, 66712502, 264908, 264828, 56182435, 284112, 265008, 60431735, 60433438, 21906754, 265010, 265011, 265017, 265018, 265019, 18108351, 264765, 21906765, 21906766, 21906769, 265020, 265021, 264693, 264629, 263974, 263976, 18108378, 55811576, 264556, 264637, 284558, 83373044, 22278002, 264482, 264483

2214	85361453 (4427, 4428)	Novel Protein sim. GBank gil504325[refNP_000173.1]pHADH - hydroxyacyl- Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha su	Contains protein domain (PF00725) - 3-hydroxyacyl-CoA dehydrogenase	- dehydrogenase	264468, 52644507, 18108394, 56182575, 22278994, 22278995, 35696288, 56994075, 22278997, 22278998, 22278999, 264490, 60432049, 264259, 52645080, 29331822, 29147620, 29331824, 66714117, 29331825, 60432288, 29331826, 29331827, 35698052, 29331828, 20281100, 264509, 264907, 66712502, 264908, 29331830, 52644045, 56182435, 264510, 265006, 264511, 264512, 265007, 265008, 265009, 60170831, 264593, 60433358, 60433438, 33109954, 33657084, 52644298, 87168474, 265010, 265011, 87168559, 264601, 265017, 265018, 265019, 18108351, 264448, 264682, 264763, 264288, 264687, 52644229, 264689, 21908765, 21908766, 21908767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 264532, 60170815, 264690, 52644150, 264691, 33657023, 264692, 18108364, 33657109, 33657182, 27486262, 27486264, 27486265, 35695763, 18108370, 264629, 60431528, 18108374, 18108376, 55810764, 35696423, 35695855, 264634, 264636, 52644332, 264638, 264558, 60170394, 18108381, 56182323, 83373044, 18108385, 18108387, 18108388, 56526486, 87168518, 60432113, 22279002, 264482, 264584, 264585, 264586, 264909, 265006, 264555, 264558, 87168518
2215	95419206 (4429, 4430)	Novel Protein sim. GBank gil1947160 (AF000288) - weak similarity to collagens; glycine- and proline-rich [Caenorhabditis elegans]			
2216	87614046 (4431, 4432)	Novel Protein sim. GBank gil1572802 (U70854) - similar to Enterococcus faecalis TRAB (GI:388268) [Caenorhabditis elegans]		UNCLASSIFIED	264683
2217	80589404 (4433, 4434)	Novel Protein sim. GBank gil5031707[refNP_005503.1]pGARP - glycoprotein A repetitions predominant	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264288, 33657109, 264556
2218	85518254 (4435, 4436)	Novel Protein sim. GBank gil3878638[emb]CAA88953] - (Z49128) similar to cAMP-dependant protein kinase; cDNA EST EMBL:TD0719 comes from this gene; cDNA EST yk465d8.3 comes from this gene; cDNA EST yk485d8.5 comes from this gene; cDNA EST yk492f4.3 comes from this gene; cDNA EST y...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain		35696423, 264563
2219	87614048 (4437, 4438)	Novel Protein sim. GBank gil1572802 (U70854) - similar to Enterococcus faecalis TRAB (GI:388268) [Caenorhabditis elegans]	Contains protein domain (PF01963) - TraB family		264682, 264683, 264688, 264689, 264693, 18108370, 18108376

2220	95354185 (4439, 4440)	Novel Protein sim. GBank gi 4507261 ref NP_003145.1 pSTAT - statherin			264486, 18108384, 18108385, 35696286, 264259, 284097, 60432289, 284509, 284905, 284906, 284907, 29331830, 284908, 284909, 284510, 284511, 265007, 284512, 284910, 285008, 284593, 284594, 60433356, 284595, 55812038, 284758, 85858542, 265010, 264601, 264803, 265019, 284605, 284760, 284762, 284448, 284784, 284389, 284786, 18108357, 284788, 284687, 18108358, 264769, 55811957, 284690, 284691, 33857023, 264692, 18108362, 18108368, 264628, 284629, 18108374, 263978, 284634, 284635, 284638, 284637, 284638, 18108385, 284483, 284568, 284488, 284587
2221	88060927 (4441, 4442)	Novel Protein sim. GBank gi 3549154 (AC005625) - R27328_1 [Homo sapiens]			
2222	84425892 (4443, 4444)			UNCLASSIFIED	264908, 265020, 35895855
2223	85091849 (4445, 4446)			UNCLASSIFIED	265010, 284685, 284690, 284693, 284628, 263974, 263976, 55811576, 264555, 284638, 83373044, 284483
2224	87388515 (4447, 4448)	Novel Protein sim. GBank gi 3876005 emb CAA84799 - (Z35719) cDNA EST EMBL:D67419 comes from this gene; cDNA EST EMBL:C13853 comes from this gene; cDNA EST EMBL:C11578 comes from this gene; cDNA EST yk234a7.3 comes from this gene; cDNA EST yk234a7.5 comes from this gene; cDNA ES...	Contains protein domain (PF01958) - Domain of unknown function	UNCLASSIFIED	284259, 284509, 56182435, 265008, 265008, 285009, 284757, 21908754, 18108351, 284693, 18108374, 18108385
2225	85748484 (4449, 4450)	Novel Protein sim. GBank gi 1255847 (U53338) - C05E11.1 gene product [Caenorhabditis elegans]		transport	22278894, 22278895, 22278999, 52844045, 284600, 265019, 21908765, 21908769
2226	86978953 (4451, 4452)	Novel Protein sim. GBank gi 4826524 emb CAB42852.1 - (AL049848) hypothetical protein [Homo sapiens]			264259, 29331822, 29331824, 28331825, 29331827, 264508, 264906, 265007, 264691, 284634, 284486
2227	87721135 (4453, 4454)			UNCLASSIFIED	22278999, 265008, 265008, 18108354, 29148629, 29148784, 27486261, 18108374, 284637, 18108384
2228	91227337 (4455, 4456)	Novel Protein sim. GBank gi 806976 (U16800) - ribonucleoprotein [Xenopus laevis]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	284091, 284092, 284094, 29331822, 29331825, 68714117, 284693, 263972, 284638, 83373044, 284583
2229	88060931 (4457, 4458)	Novel Protein sim. GBank gi 3549155 (AC005625) - R27328_2 [Homo sapiens]		UNCLASSIFIED	

2230	95342915 (4459, 4460)	Novel Protein sim. GBank gij226154 prfj 1412350A - DNA polymerase [Human adenovirus type 2]		UNCLASSIFIED	264488, 264768, 52644507, 264769, 21906765, 21906766, 21906767, 21906769, 22278995, 35695917, 22278998, 22278997, 22278998, 22278999, 265021, 264259, 52645129, 29331827, 264508, 264509, 264907, 18108370, 18108374, 35696423, 35695855, 265007, 264910, 264555, 33657402, 21906754, 18108387, 265010, 265018, 265019, 264760, 264288, 264567, 264563
2231	88060937 (4461, 4462)	Novel Protein sim. GBank gij3549154 (AC005625) - R27328_1 [Homo sapiens]		UNCLASSIFIED	
2232	87762581 (4463, 4464)	Novel Protein sim. GBank gij5281316 gb AAD41476.1 AF133124 - transcription factor IIC63 [Homo sapiens]		transcriptfactor	18108394, 56182575, 22278995, 35696286, 22278997, 22278999, 264259, 29331827, 35696052, 264907, 56182435, 265006, 265007, 265008, 264910, 264758, 55812038, 264603, 265018, 265019, 18108351, 264682, 264764, 264683, 264369, 264288, 264688, 264687, 264689, 21906765, 21906766, 21906767, 21906769, 29148629, 35695917, 264690, 52644150, 264691, 33657023, 264693, 18108370, 18108374, 55811576, 35695855, 264639, 18108385, 264584, 264906, 33657402, 265018, 264288, 264688, 265020, 264635, 18108385
2233	87755292 (4465, 4466)	Novel Protein sim. GBank gij4249733 gb AAD13780 - (AF109377) IdBp [Mus musculus]			kinase
2234	87771817 (4467, 4468)	Novel Protein sim. GBank gij1706559 sp P54352 EAS_DROME - ETHANOLAMINE KINASE (EASILY SHOCKED PROTEIN)			265020, 264693, 264556, 58526486
2235	91012316 (4469, 4470)	Novel Protein sim. GBank gij4972734 gb AAD34762.1 - (AF132174) unknown [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	22278997, 264563
2236	88003131 (4471, 4472)	Novel Protein sim. GBank gij1082675 prfj B53814 - p20 protein - human	Contains protein domain (PF00011) - Hsp20/alpha crystallin family	eph	264569, 264687, 264769, 265022, 264259, 60432049, 264691, 29331828, 60432289, 20281149, 264908, 264907, 264511, 265008, 285009, 264634, 264635, 264636, 264555, 264556, 264557, 264558, 60433358, 264595, 264559, 60433438, 60432113, 264761, 264762, 264763, 264764
2237	91012318 (4473, 4474)	Novel Protein sim. GBank gij4972734 gb AAD34762.1 - (AF132174) unknown [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	264488, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 22278995, 22278996, 22278997, 22278998, 265020, 265021, 22278998, 264259, 29331824, 29331826, 29331827, 35695763, 18108376, 35695855, 265007, 60432228, 33657402, 60433358, 60433438, 83373044, 18108385, 21906754, 18108387, 60432113, 22279000, 265019, 22279002, 264482, 18108351, 264288

2238	94998857 (4475, 4476)			Contains protein domain (PF00286) - Viral coat protein		264508, 264907, 264629, 264634, 264564
2239	87798688 (4477, 4478)					29331825, 265009, 264368, 33657109, 18108370, 18108374, 264557, 264559
2240	94121471 (4479, 4480)	Novel Protein sim. GBank gi 2982311 (AF051240) - probable ubiquitin-conjugating enzyme E2 [Picea mariana]		Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	264468, 65274572, 56182575, 35698286, 22278987, 22278999, 264259, 29331827, 35696052, 264508, 52644045, 56182435, 264511, 265007, 265008, 265009, 60433356, 60433438, 55812038, 21908754, 33857084, 55811388, 265018, 265019, 18108351, 264683, 264288, 264768, 264687, 264688, 264769, 21908765, 21908768, 21906769, 35695917, 265021, 265022, 60170615, 52644150, 33657023, 33657182, 33657349, 35695763, 18108370, 35698423, 35695855, 67168518, 22279000
2241	80091951 (4481, 4482)				UNCLASSIFIED	264693, 264629
2242	91228075 (4483, 4484)	Novel Protein sim. GBank gi 2484312 sp P70541 E2BG_RAT - TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR)			synthase	22278995, 22278996, 22278997, 22278998, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 264509, 265007, 265009, 264586, 21906754, 265010, 265011, 265017, 265018, 265019, 264448, 264369, 264288, 52644229, 21906765, 21906768, 21906767, 21906768, 21906769, 265020, 265021, 33657109, 27488282, 27486264, 18108374, 35695855, 264634, 264637, 56182323, 63373044, 56528486, 67168518, 264564
2243	78902026 (4485, 4486)				UNCLASSIFIED	265008
2244	85723527 (4487, 4488)	Novel Protein sim. GBank gi 2291143 (AF016417) - Similar to BZIP transcription factor [Caenorhabditis elegans]			UNCLASSIFIED	264604
2245	95318545 (4489, 4490)	Novel Protein sim. GBank gi 470340 (U00043) - similar to beta-mannosyltransferase [Caenorhabditis elegans]		Contains protein domain (PF00534) - Glycosyl transferases group 1	UNCLASSIFIED	52645156, 22278995, 22278996, 22278997, 22278999, 29331822, 29331824, 29331827, 264907, 264512, 60433438, 264758, 21908754, 265011, 264603, 264764, 264687, 21908767, 21906768, 21906769, 55811957, 265022, 264691, 264629, 35698423, 264638, 18108387, 60432113, 22278000, 22279002, 264568

2246	84648710 (4481, 4492)	Novel Protein sim. GBank gi 4996096 dbj BAA78326.1 - (AB028069) activator of S phase Kinase [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	65274572, 22278995, 35696286, 22278996, 22278997, 22278999, 264259, 35696052, 264106, 264905, 264907, 265008, 265007, 265008, 60433438, 33108854, 87168559, 265018, 265019, 264288, 21906765, 21906767, 21906768, 21906769, 55811857, 35695917, 265020, 265022, 27486284, 18108370, 18108374, 65274791, 35695855, 60432113
2247	87862542 (4493, 4494)	Novel Protein sim. GBank gi 654065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	52845156, 52846385, 52845080, 35696052, 33656970, 52846317, 33657084, 265017, 21908768, 21908769, 35695917, 33657108, 52845129, 33657182, 27486261, 27486262, 33657349, 27486285, 18108387
2248	95412886 (4485, 4496)	Novel Protein sim. GBank gi 4758502 ref NP_004123.1 phABP - hyaluronan-binding protein 2	Contains protein domain (PF00089) - Trypsin	cathepsin	284488, 284259, 284907, 29331830, 264909, 265007, 265009, 264595, 21908754, 65274444, 264603, 265019, 264762, 264448, 264288, 264688, 21906768, 55811957, 265021, 264691, 18108374, 264634, 264635, 264636, 264555, 264638, 264557, 264558, 264559, 18108383, 83373044, 18108385, 284488
2249	94685662 (4497, 4498)	Novel Protein sim. GBank gi 4038461 (AF107772) - TcST11 [Trypanosoma cruzi]	Contains protein domain (PF00515) - TPR Domain	eph	284786, 264628, 264636, 264637
2250	79827508 (4499, 4500)	Novel Protein sim. GBank gi 3738140 emb CAA21241 - (AL031852) valyl-tRNA synthetase, mitochondrial precursor [Schizosaccharomyces pombe]		UNCLASSIFIED	264908, 18108374
2251	87385863 (4501, 4502)	Novel Protein sim. GBank gi 3218467 emb CAA07090.1 - (A1008529) putative phosphatase [Gallus gallus]		UNCLASSIFIED	284259, 35696052, 264508, 56182435, 265009, 264592, 264593, 264760, 264448, 264684, 264288, 264690, 264628, 55811576, 264555, 264556, 264557, 264558, 264559, 264566
2252	87735867 (4503, 4504)	Novel Protein sim. GBank gi 4929325 gb AAD33953.1 AF14531 - (AF145316) vacuolar proton pump delta polypeptide [Homo sapiens]	Contains protein domain (PF01813) - ATP synthase subunit D	synthase	264092, 264094, 264259, 29331822, 66714117, 26331828, 264102, 264103, 264104, 264105, 264109, 264112, 264511, 265007, 60433356, 265010, 18108351, 21906767, 21906768, 264691, 263974, 263977, 264488, 264567
2253	91010703 (4505, 4506)			UNCLASSIFIED	65274572, 265019

2254	95320031 (4507, 4508)	Novel Protein sim. GBank g 4502847 ref NP_001271.1 pCIRB - cold inducible RNA- binding protein	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	284569, 18108394, 18108398, 56182575, 5694075, 35698286, 22278999, 284084, 60432049, 284259, 29331822, 29331824, 29331825, 29331826, 60432288, 29331827, 29331828, 35696052, 284108, 284508, 284509, 284906, 284907, 29331830, 66712502, 284908, 284909, 284510, 265006, 284511, 265007, 265008, 265009, 60170831, 60432229, 60433356, 60433438, 284758, 85858542, 265010, 265011, 67168559, 265017, 265018, 265019, 284448, 284764, 284288, 284369, 284768, 284686, 284768, 284769, 21908765, 21908767, 55811957, 264691, 33857023, 264692, 18108362, 65274620, 263969, 284628, 18108370, 60431528, 283972, 284629, 18108372, 18108377, 18108378, 55811576, 35696423, 35695855, 284630, 284634, 284635, 284636, 284556, 263981, 284638, 56182323, 60170394, 284558, 18108381, 18108382, 83373044, 18108385, 87168518, 60432113, 22279002, 284482, 284584, 284585, 284486, 284587, 18108391
2255	91010546 (4508, 4510)	Novel Protein sim. GBank g 5541865 emb CAB51072.1 - (AL096858) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	strud	65274572, 56182575, 22278997, 22278999, 284258, 29331822, 29331825, 29331826, 29331827, 29331828, 284508, 284905, 284906, 284907, 66712502, 284908, 56182435, 284510, 284511, 265008, 284593, 284595, 21908754, 33109954, 87168474, 265011, 265017, 265018, 284682, 284764, 284369, 284288, 284768, 284685, 284686, 284768, 21908765, 21908768, 21908768, 21908769, 265020, 60170615, 52844150, 284690, 284692, 284693, 33857109, 33857349, 284632, 284636, 52844332, 56182323, 22279000, 22279002
2256	87020531 (4511, 4512)	Novel Protein sim. GBank g 3327174 dbj BAA31655 - (AB014580) KIAA0680 protein [Homo sapiens]		UNCLASSIFIED	284768, 284689, 18108374
2257	80088235 (4513, 4514)			UNCLASSIFIED	22278996, 22278999, 284681, 21908765, 21908768, 284587
2258	88090516 (4515, 4516)	Novel Protein sim. GBank g 3025446 (AC004528) - R32184_2 [Homo sapiens]	Contains protein domain (PF00080) - Ligand-gated ion channel	misc_channel	284908, 284582, 284764

2259	95384155 (4517, 4518)	Novel Protein sim. GBank gi 4884140 emb CAB43278.1 - (AL050110) hypothetical protein [Homo sapiens]		UNCLASSIFIED	18108386, 65274572, 58182575, 22278997, 22278998, 264259, 29331822, 29331827, 264805, 66712502, 264908, 264909, 58182435, 265007, 265008, 60432229, 33657084, 87168559, 18108351, 264448, 264683, 264288, 264369, 58181562, 265021, 60170815, 264690, 33657109, 60431528, 18108374, 52644332, 58182323, 18108385, 22279000, 22279002, 284482
2260	88084119 (4519, 4520)	Novel Protein sim. GBank gi 3080663 (AC004614) - similar to f-spondin proteins AB008086 (PID:g2529225) [Homo sapiens]	Contains protein domain (PF00090) - Thrombospondin type 1 domain	oxidase	58182575, 265020, 264905, 264906, 264908, 35698423, 264511, 264635, 55812038, 264758, 265018, 265019, 264805, 284760, 264583
2261	88074157 (4521, 4522)	Novel Protein sim. GBank gi 3334528 emb CAA16138 - (AL021308) predicted using FGENEH [Homo sapiens]		UNCLASSIFIED	
2262	91639282 (4523, 4524)	Novel Protein sim. GBank gi 487759 gb AAD31421.1 AF12444 - (AF124440) MAGE tumor antigen D1 [Homo sapiens]			58182575, 22278999, 29331822, 29331825, 60432289, 29331827, 35698052, 264508, 66712502, 52644045, 58182435, 265008, 265008, 265009, 60433358, 55812038, 265010, 265017, 265019, 264288, 264369, 21908765, 21908767, 55811957, 35695917, 52644150, 33657023, 33657109, 55811576, 65274791, 58182323
2263	87602495 (4525, 4526)	Novel Protein sim. GBank gi 3341697 (AC003672) - hypothetical protein [Arabidopsis thaliana]			22278994, 22278997, 264907, 264628, 52644150, 18108361, 284693, 18108374
2264	87756525 (4527, 4528)	Novel Protein sim. GBank gi 1657601 (U66220) - unknown [Nannocystis exedens]		UNCLASSIFIED	264686, 284488, 264768, 284769, 264691, 264508, 284905, 264509, 264906, 264907, 264908, 284908, 35695855, 284510, 284511, 284512, 265007, 265009, 264638, 264639, 264757, 264758, 18108385, 285011, 284760, 264584, 264585, 264764, 264586, 264488, 264768
2265	86818663 (4529, 4530)	Novel Protein sim. GBank gi 477072 pir A48018 - mucin 7 precursor, salivary - human	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	264689, 264910, 264764
2266	87773458 (4531, 4532)	Novel Protein sim. GBank gi 3150479 (AF067212) - partial CDS [Caenorhabditis elegans]	Contains protein domain (PF01305) - Ribosomal protein L15 amino terminal region	ribosomal prot	22278995, 22278997, 22278999, 264259, 265008, 265007, 265009, 60433438, 21908754, 265010, 265011, 265017, 284448, 264683, 264288, 264689, 21908785, 21908788, 35695917, 265021, 18108374, 264638, 22279000, 22279002, 264586, 284487

2267	87395838 (4533, 4534)	Novel Protein sim. GBank gj 3560229 emb CAA20697.1 - (AL031530) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	35698286, 284259, 29331824, 29331825, 35698052, 29331828, 284805, 284509, 284907, 284908, 284909, 284512, 285009, 284910, 284593, 33857402, 285010, 285018, 284782, 284448, 284288, 264389, 264768, 52844229, 35695917, 284691, 33657023, 18108382, 33657109, 35698423, 284634, 18108381, 87188518, 284568
2268	85893867 (4535, 4536)	Novel Protein sim. GBank gj 728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII		cadherin	284488, 284259, 284509, 284595, 285010, 265017, 284768, 18108385, 284488
2269	88177977 (4537, 4538)	Novel Protein sim. GBank gj 103418 pir S17885 - Tcd37 protein - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	56182575, 60432049, 265007, 265009, 264591, 87188559, 284605, 18108351, 21908784, 265020, 264629, 60431528, 264638, 18108385, 18108387, 60432113
2270	80410327 (4539, 4540)				264763
2271	91010392 (4541, 4542)			cyto-450	284909, 56182435, 265008, 55812038, 55811957, 33657023, 284693, 33657109, 55810784, 55811576, 56182323
2272	84208220 (4543, 4544)			UNCLASSIFIED	284905, 284908
2273	95014271 (4545, 4546)	Novel Protein sim. GBank gj 4176370 (AC005058) - similar to calcium-independent phospholipase A2; similar to AC004392 (PID:g3387519) [Homo sapiens]	Contains protein domain (PF00462) - Glutaredoxin		52845156, 22278997, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35698052, 284909, 285008, 284593, 60433438, 21908754, 285018, 284689, 21908765, 21908768, 21908767, 21908769, 265021, 265022, 60170615, 284691, 33657023, 284693, 33657109, 27486264, 18108376, 35698423, 3569855, 284630, 52844332, 284558, 58182323, 22278902
2274	91840217 (4547, 4548)	Novel Protein sim. GBank gj 1480112 emb CAA67961 - (X99642) HP1-BP74 protein [Mus musculus]	Contains protein domain (PF00538) - linker histone H1 and H5 family	histone	52845156, 22278997, 22278999, 52645080, 29331824, 29331825, 29331826, 29331827, 29331828, 284905, 284908, 52644045, 284511, 265008, 265009, 60170831, 264591, 21908754, 33109954, 265011, 265018, 18108351, 284448, 284288, 284684, 284786, 21908765, 21908768, 21908767, 21908768, 52844150, 284693, 18108384, 35695783, 18108374, 35698423, 284634, 284557, 284638, 52844332, 83373044, 18108385, 58528488, 87188518, 22279002
2275	88082501 (4549, 4550)	Novel Protein sim. GBank gj 3165406 (AC004755) - fos37502_2 [Homo sapiens]	Contains protein domain (PF00122) - E1-E2 ATPase	transport	
2276	11287447 (4551, 4552)			UNCLASSIFIED	284555, 284558

2277	88084123 (4553, 4554)	Novel Protein sim. GBank gi 2880079 (AC004142) - similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D49802 (PID:gi1369906) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	22278999, 35696052, 265008, 265019, 264369, 265020, 265022, 55810764, 264404, 22278002
2278	84133079 (4555, 4556)	Novel Protein sim. GBank gi 2618702 (AC002510) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	18108394, 22278997, 29331826, 60433356, 60433438, 21908754, 265018, 33657023, 264639, 83373044, 264565
2279	80419375 (4557, 4558)	Novel Protein sim. GBank gi 119714 sp P13983 EXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)		UNCLASSIFIED	264766, 264565
2280	94239723 (4559, 4560)				
2281	95293048 (4561, 4562)	Novel Protein sim. GBank gi 4240299 dbj BAA74928.1) - (AB020712) KIAA0905 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transport	265008, 33109954, 265010, 265019, 265020, 264092, 264259, 29331822, 29331824, 29331826, 35696052, 264107, 264906, 264909, 52644045, 265006, 33657402, 60433356, 264758, 265011, 265019, 264881, 264683, 264684, 264686, 21908765, 21908767, 21908768, 21908769, 60170615, 264690, 52644150, 18108382, 264692, 18108388, 18108374, 263978, 264631, 18108381, 264559, 18108385, 56526486, 22279000, 264566, 264567
2282	87602829 (4563, 4564)	Novel Protein sim. GBank gi 1537070 (U83840) - nucleoporin p54 [Rattus norvegicus]		UNCLASSIFIED	264486, 264259, 29331822, 29331824, 29331827, 29331828, 29331830, 33657402, 60433438, 87168474, 265019, 18108351, 21908767, 21908769, 55811957, 33657023, 52645129, 33657109, 33657182, 27486262, 263972, 55811576, 87168516, 20281169, 60424179, 56182575, 22278994, 35696286, 22278997, 22278999, 29331822, 29331824, 56182181, 29331825, 29331827, 35696052, 29148499, 264905, 66712502, 264908, 265007, 265009, 60432229, 264593, 60431735, 60433356, 33109954, 33657084, 55811386, 87168474, 265010, 265011, 265018, 265019, 55811150, 264683, 264369, 264286, 264686, 21906765, 21908767, 21908768, 29148627, 21908769, 55811957, 265020, 265022, 33657182, 27486261, 18108370, 264628, 18108374, 55810764, 18108379, 55811576, 35696423, 35695855, 264630, 60431850, 263981, 18108382, 83373044, 18108385, 18108387, 60432113, 22279000, 264482, 264567
2283	95362386 (4565, 4566)	Novel Protein sim. GBank gi 2495728 sp Q92556 Y281_HUMAN - HYPOTHETICAL PROTEIN KIAA0281 (HA6725)		UNCLASSIFIED	

2284	95414955 (4567, 4568)	Novel Protein sim. GBank gij2498797 sp Q84311 PNAD_MOUSE - PROTEIN N- TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN- AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNAA)			60424179, 52644507, 18108394, 52648842, 22278994, 35698286, 22278998, 22278997, 22278999, 284259, 60432049, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35698052, 29331830, 52644045, 56182435, 33657402, 60433438, 33109954, 21906754, 85658542, 87188559, 265018, 265019, 55811150, 264682, 264368, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 33657023, 33657162, 27486262, 27486264, 27486265, 18108376, 55810784, 35698423, 35695855, 60431850, 87188518, 60432113, 284482, 264584
2285	87781484 (4569, 4570)	Novel Protein sim. GBank gij3342234 (U93909) - nuclear antigen EBNA-1 [Cercopithecus herpesvirus 15]		collagen	35698052, 284905, 284907, 264808, 284909, 284512, 265009, 284910, 284595, 264760, 18108351, 264682, 264763, 264885, 264766, 264686, 264768, 264693, 264629, 35695855, 264631, 264634
2286	87737825 (4571, 4572)	Novel Protein sim. GBank gij3873414 (U00043) - similar to D. melanogaster trithorax protein [Caenorhabditis elegans]		kinase	35698286, 58182435, 60170831, 264591, 60432229, 264592, 264593, 264594, 264595, 55812038, 264596, 87188474, 35695917, 264692, 55811576, 264555, 264557
2287	82986696 (4573, 4574)	Novel Protein sim. GBank gij630905 pir S42731 - collagen alpha 1 chain - sea urchin (Hemicentrotus pulcherrimus) (fragment)	Contains protein domain (PF01391) - Collagen triple helix repeat (20 copies)	UNCLASSIFIED	264682
2288	94133083 (4575, 4576)	Novel Protein sim. GBank gij728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII		tm7	22278995, 56994075, 22278997, 22278999, 284259, 60432289, 284508, 284512, 265008, 33657402, 265017, 265018, 265019, 18108351, 264448, 21908765, 21908766, 21908767, 21908768, 33657023, 264557, 22279000, 22279002
2289	88084133 (4577, 4578)	Novel Protein sim. GBank gij2887497 (AC004144) - R34001_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	
2290	88084137 (4579, 4580)	Novel Protein sim. GBank gij2887497 (AC004144) - R34001_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264683
2291	84295281 (4581, 4582)	Novel Protein sim. GBank gij3253120 (AC005175) - R31449_3 [Homo sapiens]		struct	18108394, 284807, 265006, 265009, 33109954, 52646317, 265010, 18108351, 264681, 264686, 264692, 18108370, 18108374, 18108385

2292	94328834 (4583, 4584)	Novel Protein sim. GBank gi 4803672 emb CAB42643.1 - (AJ133769) nuclear transport receptor [Homo sapiens]		UNCLASSIFIED	56182575, 35698286, 56994075, 29331824, 29331825, 35698052, 56182435, 60433438, 55812038, 33109954, 87188474, 87188559, 265018, 18108351, 284763, 284448, 284389, 284288, 56181562, 284769, 21908765, 21908766, 21908767, 21906769, 265021, 265022, 33857023, 284693, 65274620, 33857109, 27486264, 284629, 55810764, 55811576, 35695855, 56182323, 56528486, 87188518, 22279000, 284587
2293	87759213 (4585, 4586)	Novel Protein sim. GBank gi 3252981 (AF068921) - Ras-binding protein SUR-8 [Mus musculus]	Contains protein domain (PF00560) - struct Leucine Rich Repeat		264488, 18108397, 35696286, 264092, 284259, 29331822, 29331826, 264906, 284908, 264511, 284512, 265009, 284910, 18108351, 264764, 284369, 284288, 264685, 264766, 265020, 265022, 264534, 35698423, 264631, 284637, 18108381, 56182323, 284639, 18108385, 264404, 284563, 264585, 22278997, 22278998, 22278999, 284259, 29331822, 60432289, 29331828, 35698052, 265018, 264684, 284288, 264686, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 264692, 33657109, 18108376, 35696423, 35695855, 284634, 22279000, 22279002, 264563, 264488, 22278998, 60432289, 264662, 264663, 264689, 18108374
2294	86693580 (4587, 4588)	Novel Protein sim. GBank gi 2062680 (U88964) - HEM45 [Homo sapiens]	Contains protein domain (PF00929) - Exonuclease	nuclease	263974, 263978
2295	95312200 (4589, 4590)			UNCLASSIFIED	264488, 65274572, 56182575, 22278997, 22278998, 264259, 29331822, 29331824, 29331826, 29331828, 35698052, 264907, 284908, 52844045, 56182435, 284112, 265006, 265007, 284910, 265009, 60433356, 33857402, 264595, 55812038, 21908754, 265011, 265018, 265019, 264448, 284784, 284288, 284768, 21906765, 21906767, 21908768, 21906769, 55811857, 265020, 265021, 264690, 264691, 33657023, 264692, 264693, 33657109, 55811576, 56182323, 60170394, 83373044, 18108385, 56528486, 264584, 264488
2296	80030781 (4591, 4592)				
2297	94321251 (4593, 4594)	Novel Protein sim. GBank gi 5689501 dbj BAA83034.1 - (AB028005) KIAA1082 protein [Homo sapiens]		transcriptfactor	

2288	95312207 (4595, 4598)	Novel Protein sim. GBank gij3875051[emb]CAB02849] - (Z81050) predicted using Genefinder; similar to collagen; cDNA EST EMBL:D85564 comes from this gene; cDNA EST EMBL:D69046 comes from this gene; cDNA EST yk366b12.3 comes from this gene; cDNA EST yk366b12.5 comes from this gene ...		collagen	60424179, 56181586, 22278995, 35696288, 22278998, 22278998, 22278999, 284490, 284259, 29331822, 29331824, 66714117, 60424289, 35698052, 29331826, 66712502, 56182435, 284510, 265006, 60433438, 21906754, 33109954, 55811388, 285010, 265018, 55811150, 264762, 18108351, 284882, 284883, 284288, 284684, 284686, 284688, 56181562, 284689, 21906768, 21906767, 29148629, 55811957, 29148784, 35895917, 265020, 18108362, 33657023, 18108384, 33657109, 60431602, 18108370, 60431528, 18108374, 55810784, 35698423, 35895855, 284630, 284634, 60431850, 18108380, 56182323, 284558, 83373044, 18108385, 60432113, 22278000, 284482, 284567, 284486
2299	80193720 (4597, 4598)			UNCLASSIFIED	284389
2300	94124346 (4599, 4600)	Novel Protein sim. GBank gij2443886 (AC002284) - Unknown protein [Arabidopsis thaliana]			284488, 22278998, 22278999, 284259, 29331824, 66714117, 35698052, 284509, 284905, 284908, 284907, 284908, 284909, 285008, 284910, 265009, 284758, 265010, 67168559, 284600, 265018, 284760, 284762, 18108351, 284764, 284766, 284768, 284769, 21906766, 21906767, 35895917, 285021, 284691, 33657023, 35695783, 18108370, 18108374, 35698423, 35895855, 284631, 284636, 284638, 18108385, 22279002, 284563
2301	91235725 (4601, 4602)	Novel Protein sim. GBank gij2143637[pir]84505 - calcium-dependent actin-binding protein - rat		struct	284908, 284758, 265017, 21906765, 83373044, 284563
2302	68084141 (4603, 4604)	Novel Protein sim. GBank gij2887497 (AC004144) - R34001_1 [Homo sapiens]		UNCLASSIFIED	52844045, 265019, 264288, 33657023, 18108370, 18108385
2303	94141439 (4605, 4606)	Novel Protein sim. GBank gij4884194[emb]CAB43220.1] - (AL049946) hypothetical protein [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	struct	284259, 60432049, 284907, 284909, 284910, 60432229, 33657402, 265011, 265018, 284762, 284448, 284769, 284637, 284638, 83373044, 284486
2304	94840434 (4607, 4608)	Novel Protein sim. GBank gij2494162[sp]Q10005[YRY1_CAEEL - HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR		UNCLASSIFIED	284259, 29331824, 21906767, 33657182, 33657348
2305	90935911 (4609, 4610)	Novel Protein sim. GBank gij4972686[jb]AAD34738.1] - (AF132150) unknown [Drosophila melanogaster]			65274572, 22278996, 284908, 265006, 21906769, 284691, 284486

2306	85334840 (4611, 4612)	Novel Protein sim. GBank gi 4929585 gb AAD34043.1 AF15180 - (AF151806) CGI-48 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	264488, 22278995, 22278998, 35698286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35698052, 284508, 284905, 284907, 29331830, 284908, 284909, 284510, 285006, 284511, 265007, 264512, 285008, 265009, 33857402, 21908754, 85658542, 265010, 265011, 284801, 265017, 285018, 284604, 285019, 18108351, 284448, 284288, 284766, 284769, 21906765, 21906766, 21906767, 21906768, 29148629, 29148784, 35695917, 265020, 265021, 265022, 33657023, 284692, 18108370, 18108374, 18108376, 35698423, 35695855, 264630, 264634, 264635, 284636, 284637, 264638, 264639, 18108382, 18108385, 18108387, 264563, 264566, 284488 284828
2307	78415283 (4613, 4614)			UNCLASSIFIED	
2308	87608409 (4615, 4616)	Novel Protein sim. GBank gi 4758732 ref NP_004522.1 pMOCS - molybdenum cofactor synthesis 2		synthase	35698286, 264259, 29331822, 29331824, 264112, 264512, 284757, 21908754, 284288, 284690, 27486284, 284631, 284634, 284404
2309	95357218 (4617, 4618)	Novel Protein sim. GBank gi 3878058 emb CAB17070 - (Z99942) cDNA EST EMBL:D73444 comes from this gene; cDNA EST EMBL:D70905 comes from this gene; cDNA EST EMBL:D72208 comes from this gene; cDNA EST EMBL:D75030 comes from this gene; cDNA EST EMBL:D72844 comes from this gene; cDN...		glycoprotein	18108397, 22278998, 22278997, 22278998, 22278999, 60432049, 29331822, 29331826, 60432289, 68712502, 60432229, 60433356, 60433438, 65274444, 265010, 264600, 284681, 264448, 284683, 264288, 21908766, 21908768, 265020, 284691, 284692, 284693, 65274620, 65274791
2310	78601668 (4619, 4620)			UNCLASSIFIED	264508
2311	87721189 (4621, 4622)	Novel Protein sim. GBank gi 2137337 pir j46281 - gene mCBP protein - mouse	Contains protein domain (PF00013) - KH domain	transcriptfactor	18108397, 56182575, 22278996, 56994075, 264259, 29331824, 29331827, 264508, 284907, 56182435, 284510, 284511, 265006, 284512, 265007, 265008, 265009, 60433438, 33109954, 265010, 265011, 284603, 265017, 18108351, 284762, 284663, 284288, 284389, 284688, 33857023, 20281149, 20281069, 284628, 283972, 55811576, 35698423, 20281071, 284632, 284636, 18108385, 18108387, 87185518, 22279000, 264563, 284488

2312	87549881 (4623, 4624)	Novel Protein sim. GBank gij2911284 (AC002550) - Unknown gene product [Homo sapiens]			56182575, 56994075, 35696286, 22278998, 22278997, 22278999, 284259, 29331822, 29331824, 29331825, 29331826, 29331827, 52644045, 60432229, 60433356, 55812038, 33109954, 21906754, 87168474, 265018, 18108351, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265022, 60170815, 33857023, 27486281, 27486284, 35696423, 35695855, 18108385, 22279000, 22279002
2313	80042533 (4625, 4626)	Novel Protein sim. GBank gij3043626[dbj][BAA25477] - (AB011123) KIAA0551 protein [Homo sapiens]			263981
2314	94313401 (4627, 4628)	Novel Protein sim. GBank gij5596714[emb][CAB51401.1] - (AL035398) dJ786117.2 (CGI-51) [Homo sapiens]	UNCLASSIFIED		52644507, 52846365, 52646842, 22278996, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 60432229, 29331826, 29331827, 29331828, 35696052, 33658970, 52644045, 265008, 264593, 60433356, 60433438, 264758, 33108954, 265010, 265017, 265018, 265019, 264288, 264369, 21906765, 21906766, 21906768, 35695917, 52844150, 33657023, 33857109, 52845129, 33857349, 35695763, 18108374, 35696423, 35695855, 52644332, 22279000, 22279002, 264563, 264567
2315	80430119 (4629, 4630)		UNCLASSIFIED		264905, 284906, 284767, 264768, 264693, 55811576, 284635, 56182323, 18108385
2316	94312191 (4631, 4632)	Novel Protein sim. GBank gij5531827[gb][AAD44488.1] - (AF078856) p47 [Homo sapiens]	Contains protein domain (PF00789) - UBX domain	glycoprotein	52644507, 52645156, 52646365, 22278994, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 52645080, 29331824, 29331825, 29331826, 29331827, 35696052, 29331828, 264908, 264907, 29331830, 52644045, 56182435, 284511, 265007, 265008, 265009, 60170831, 60433438, 21906754, 52646317, 33109954, 33657084, 52644296, 87168474, 265010, 87168559, 265017, 265018, 265019, 264661, 264763, 264448, 264683, 264369, 52644229, 21906764, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 52644150, 33657023, 18108362, 52645129, 33657182, 33657349, 35695763, 18108370, 18108378, 35696423, 35695855, 264631, 264556, 52644332, 83373044, 18108385, 18108387, 87168518, 60432113, 22279000, 284568, 264567

2317	87020571 (4633, 4634)				UNCLASSIFIED	22278998, 60432049, 264910, 60432229, 264686, 264687, 264688, 264689, 264558, 18108385
2318	79959879 (4635, 4636)				UNCLASSIFIED	265006, 264910
2319	95101781 (4637, 4638)			Novel Protein sim. GBank gi 5262613 emb CAB45746.1 - (AL080155) hypothetical protein [Homo sapiens]		264486, 264569, 18108396, 52646365, 22278994, 22278995, 22278996, 58994075, 35696286, 22278997, 22278998, 264259, 52645080, 29331825, 29331826, 29331827, 29331828, 29331830, 56182435, 60170831, 60432229, 60431735, 33657402, 21908754, 52644296, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264448, 18108354, 264288, 264369, 52644228, 21908764, 21908765, 21908766, 21908767, 21908768, 21908769, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 27486264, 33657349, 35695763, 18108370, 18108376, 18108379, 35698423, 264558, 83373044, 18108385, 56528486, 87168518, 264584, 264585, 264586
2320	91622426 (4639, 4640)			Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	kinase	22278994, 60432049, 60432289, 29331827, 264511, 265008, 52646317, 265017, 265018, 21908765, 18108372, 18108387, 22279002
2321	94320377 (4641, 4642)			Novel Protein sim. GBank gi 3873837 emb CAB02700 - (Z81029) Similarity to S.pombe hypothetical protein C1D4.09C (SW:Q10154); cDNA EST EMBL:T00543 comes from this gene; cDNA EST EMBL:T01062 comes from this gene; cDNA EST EMBL:T01321 comes from this gene; cDNA EST EMBL:T02288 com...	UNCLASSIFIED	264486, 264687, 18108394, 264689, 21908765, 18108397, 18108398, 21908767, 21908768, 85274791, 22278995, 35695855, 22278998, 265021, 265022, 264510, 285008, 264511, 264512, 265008, 60170815, 264555, 264636, 264556, 18108361, 264259, 60432229, 33657023, 264557, 264558, 264693, 60433356, 264559, 60433438, 29331824, 18108365, 18108348, 18108384, 29331825, 18108385, 33109954, 29331827, 56526486, 29148499, 265011, 60432113, 265017, 265018, 264508, 264563, 264482, 264509, 18108351, 264448, 264907, 264682, 18108370, 264683, 264908, 264288, 264909, 18108354, 264486, 264567
2322	87803165 (4643, 4644)			Novel Protein sim. GBank gi 5678957 emb CAB51685.1 - (AL109630) BACR7A.y [Drosophila melanogaster]	Contains protein domain (PF00106) - short chain dehydrogenase	22278996, 264907, 264511, 264757, 18108351, 264768, 264638

2323	94840445 (4645, 4646)	Novel Protein sim. GBank gi 2494162 sp Q10005 YRY1_CAEEL - HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR	Contains protein domain (PF00228) - eph DnaJ domain	22278984, 22278995, 22278997, 60432049, 264259, 29331822, 33655970, 264509, 58182435, 264511, 265008, 60433358, 60433438, 55812038, 33109954, 21906754, 85858542, 87168474, 285011, 87168559, 265017, 265019, 264760, 264681, 18108351, 264369, 264288, 18108355, 264687, 264688, 21906765, 21906767, 21906768, 55811957, 35695917, 265021, 33657023, 18108362, 27486262, 55811578, 264631, 264555, 83373044, 87168518, 60432113, 22279002 264592, 264593, 265020
2324	86633607 (4647, 4648)	Novel Protein sim. GBank gi 5419865 emb CAB46377.1 - (AL086732) hypothetical protein [Homo sapiens]	ATPase-associated	265020
2325	88165074 (4649, 4650)	Novel Protein sim. GBank gi 231885 sp P29981 CP4C_BLADI - CYTOCHROME P450 4C1 (CYP1VC1)	Contains protein domain (PF00067) - Cytochrome P450	265006, 264759, 35695855, 56182323
2326	84390962 (4651, 4652)	Novel Protein sim. GBank gi 231885 sp P29981 CP4C_BLADI - CYTOCHROME P450 4C1 (CYP1VC1)	UNCLASSIFIED	
2327	88081648 (4653, 4654)	Novel Protein sim. GBank gi 4240227 dbj BAA74892.1 - (AB020678) KIAA0869 protein [Homo sapiens]	UNCLASSIFIED	264259, 264508, 264905, 264906, 264907, 264908, 265007, 264512, 264910, 264758, 265010, 264768, 264769, 33657023, 264693, 264628, 264631, 264634, 264636, 264638, 264486
2328	83388428 (4655, 4656)	Novel Protein sim. GBank gi 1245105 (U45463) - glutamine repeat protein-1 [Mus musculus]	UNCLASSIFIED	60433438, 264595, 265017, 264766, 264692, 264629, 264635, 264638, 264638, 56182323, 60432113, 264566
2329	87604478 (4657, 4658)	Novel Protein sim. GBank gi 1169343 sp P42209 DIF6_MOUSE - DIFF6 PROTEIN	UNCLASSIFIED	265017, 264685, 60432113, 264088
2330	87335396 (4659, 4660)	Novel Protein sim. GBank gi 5678136 gb AAD46874.1 AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]	transport	265009
2331	86980463 (4661, 4662)	Novel Protein sim. GBank gi 2104452 emb CAB08778 - (Z95397) unknown [Schizosaccharomyces pombe]	ATPase-associated	35696286, 22278998, 29331824, 60424269, 285008, 265008, 265018, 264448, 264764, 21908765, 35695917, 35695855, 264636, 22279000, 264566
2332	87784182 (4663, 4664)	Novel Protein sim. GBank gi 2104452 emb CAB08778 - (Z95397) unknown [Schizosaccharomyces pombe]	UNCLASSIFIED	56182575, 56994075, 29331826, 29331828, 264107, 33657402, 87168559, 264683, 35695917, 265021, 33657023, 263976
2333	88206958 (4665, 4666)	Novel Protein sim. GBank gi 3879985 emb CAA92691.1 - (Z88318) cDNA EST CEMSD62F comes from this gene; cDNA EST EMBL:C07930 comes from this gene; cDNA EST EMBL:C08493 comes from this gene; cDNA EST yk415e8.3 comes from this gene; cDNA EST yk415e8.5 comes from this gene; cDNA EST...	UNCLASSIFIED	
2334	84319788 (4667, 4668)	Novel Protein sim. GBank gi 4966270 gb AAB52261.2 - (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh). Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (Hydrolase). Score=57.4, E- value=1e-13, N=1 [C...	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	56182575, 29331825, 21906768, 264636, 83373044

2335	80048103 (4669, 4670)	Novel Protein sim. GBank gi 3283350 (AF062378) - calmodulin-binding protein SHA1 [Mus musculus]	Contains protein domain (PF00612) - IQ calmodulin-binding motif	struct	18108351, 21906769, 264555
2336	95196121 (4671, 4672)	Novel Protein sim. GBank gi 1929056 emb CAA72805 - (Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]		Kinase	264907, 35895917, 18108379
2337	95345810 (4673, 4674)	Novel Protein sim. GBank gi 4495063 emb CAB38181.1 - (Z85986) dJ108K11.3 (similar to yeast suppressor protein SRP40) [Homo sapiens]		UNCLASSIFIED	35696286, 22278998, 56182181, 29331825, 60424269, 56182435, 33657402, 55812038, 55811388, 265017, 265018, 265019, 21906768, 35695917, 264691, 33657023, 33657109, 263872, 35696423, 35695855, 60432113
2338	87634045 (4675, 4676)	Novel Protein sim. GBank gi 2224689 dbj BAA20829 - (AB002372) KIAA0374 [Homo sapiens]	Contains protein domain (PF00323) - Mammalian defensin	UNCLASSIFIED	18108394, 29331822, 66714117, 60432289, 284908, 56182435, 265009, 60433438, 284598, 265010, 265019, 18108354, 264288, 284368, 55811957, 265021, 33657023, 263976, 55811576, 264632, 56182323, 264639
2339	85663319 (4677, 4678)	Novel Protein sim. GBank gi 3873550 emb CAA22127 - (AL033534) serine-rich protein [Schizosaccharomyces pombe]		UNCLASSIFIED	35696286, 264592, 264369, 264691, 264558
2340	80937716 (4679, 4680)				65274572, 22278994, 35696286, 22278997, 22278999, 264259, 29331822, 60432289, 29331826, 29331830, 265009, 33657402, 33109954, 265017, 265018, 264768, 264685, 21906769, 35695917, 264691, 264692, 35696423, 87168518, 22279000
2341	87775281 (4681, 4682)				284259, 284908, 284909, 284682, 22279000
2342	95334986 (4683, 4684)	Novel Protein sim. GBank gi 3874563 emb CAB02797 - (Z81042) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk208h5.3 comes from this gene; cDNA EST yk208h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ...	Contains protein domain (PF00400) - WD domain, G-beta repeat	Kinase	264488, 65274572, 22278995, 22278996, 22278997, 22278998, 22278999, 60432049, 284259, 29331822, 29331824, 29331825, 66714117, 29331826, 60432289, 35696052, 284905, 284509, 29331830, 265006, 60170831, 60432229, 60433358, 87168474, 265017, 265018, 265019, 284448, 264369, 284288, 21906765, 21906766, 55811957, 35695917, 265020, 265022, 52644150, 33657023, 65274620, 33657109, 18108370, 18108376, 55810764, 35696423, 55811576, 284556, 284558, 18108385, 60432113, 284563, 284564, 284565, 284566, 284567, 284907, 264512, 265011, 284683
2343	87775448 (4685, 4686)	Novel Protein sim. GBank gi 4929741 gb AAD34131.1 AF15189 - (AF151894) CGI-136 protein [Homo sapiens]		UNCLASSIFIED	
2344	79953198 (4687, 4688)			UNCLASSIFIED	284758
2345	94319789 (4689, 4690)	Novel Protein sim. GBank gi 2506307 sp P13944 CA1C_CHICK - COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR (FIBROCHIMERIN)	Contains protein domain (PF00092) - von Willebrand factor type A domain	collagen	284488, 264259, 66712502, 264759, 83373044, 284566

2346	94131820 (4691, 4692)	Novel Protein sim. GBank gl 1255411 (U53153) - one short region of weak similarity to S. cerevisiae protease A Inhibitor 3 (SP:P01094) and another short region of weak similarity to S. cerevisiae glucose repression mediator protein (SP:P14922) (Caenorhabditis elegans)	Contains protein domain (PF00515) - TPR Domain	proteaseinhib	35696286, 22278998, 264259, 35698052, 29331828, 33657402, 60433356, 33109954, 87188559, 264603, 265019, 18108351, 264681, 264685, 21906788, 265021, 33657109, 55811576, 35695855, 264637, 52644332, 264557, 83373044, 22279000, 22279002
2347	85330367 (4693, 4694)				22278997, 264511, 264683, 264684, 264768, 264687, 264688, 264691, 264692, 55811576
2348	95186133 (4695, 4696)	Novel Protein sim. GBank gl 1929056[emb CAA72805] - (Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopodium obscurum]		kinase	18108394, 35696286, 264259, 35698052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265008, 265007, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264757, 264595, 264596, 264758, 265011, 264601, 264762, 18108351, 264764, 264288, 264768, 264768, 264689, 35695917, 264693, 264628, 18108370, 264628, 18108374, 35698423, 264631, 264635, 264636, 264637, 264638, 264639, 83373044, 18108385, 264567, 264486
2349	87776502 (4697, 4698)	Novel Protein sim. GBank gl 4884106[emb CAB43254.1] - (AL050062) hypothetical protein [Homo sapiens]			35698052, 29146499, 264909, 264369
2350	88260594 (4699, 4700)				22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 33109954, 21906754, 265010, 87188559, 265018, 265019, 264761, 264681, 264288, 18108357, 21906788, 21906767, 264691, 264692, 35695855, 87168518, 22278000, 22279002, 264482
2351	86988042 (4701, 4702)	Novel Protein sim. GBank gl 728832[sp P39189]ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII		kinase	56182575, 264909, 265006, 264558
2352	87337196 (4703, 4704)	Novel Protein sim. GBank gl 731637[sp P38760]YHH5_YEAST - HYPOTHETICAL 75.9 KD PROTEIN IN SPO13-ARG4 INTERGENIC REGION	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264259, 264448
2353	91638784 (4705, 4706)	Novel Protein sim. GBank gl 1346955[sp P48809]RB27_DROME - HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (HNRNP 48) (HRP48.1)	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	29331826, 55812038, 265019, 264692, 264638
2354	87337189 (4707, 4708)	Novel Protein sim. GBank gl 731637[sp P38760]YHH5_YEAST - HYPOTHETICAL 75.9 KD PROTEIN IN SPO13-ARG4 INTERGENIC REGION	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	29331824, 264909, 265006, 265008

2355	81638786 (4709, 4710)	Novel Protein sim. GBank gij4938503[embjCAB43861.1] - (AL078465) hnRNP-like protein [Arabidopsis thaliana]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	56994075, 22278996, 35686286, 22278999, 264259, 29331825, 29331826, 29331828, 29148498, 264905, 264908, 265008, 264758, 87168474, 265010, 265017, 264687, 21908765, 21908767, 21906769, 264691, 264692, 263987, 18108370, 87168518, 22279000
2356	85327688 (4711, 4712)	Novel Protein sim. GBank gij5138920[gbjAAD40377.1] - (AF092135) PTD014 [Homo sapiens]			52644507, 22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 284259, 29331824, 66714117, 29331825, 60432289, 35896052, 29331828, 264908, 66712502, 264512, 265007, 265008, 60170831, 60432229, 60433358, 60433438, 264758, 52646317, 33109954, 21906754, 55811386, 87168474, 265017, 265018, 264605, 265019, 264681, 264682, 264448, 264389, 264288, 264686, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 60170815, 33857109, 27486284, 35895763, 55810764, 18108379, 35896423, 55811576, 35895855, 60170394, 58182323, 83373044, 18108385, 56528486, 264404, 60432113, 22279000, 264482, 264563, 264566, 264486, 264567
2357	8775458 (4713, 4714)	Novel Protein sim. GBank gij4928741[gbjAAD34131.1] [AF15189 - (AF151894) CGI-136 protein [Homo sapiens]		UNCLASSIFIED	264488, 264768, 18108394, 264259, 29331822, 18108370, 18108374, 264510, 265017, 264482, 264563, 264762, 264565, 264586, 264389, 18108354
2358	8777078 (4715, 4716)	Novel Protein sim. GBank gij4218005 (AC006135) - putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]		UNCLASSIFIED	22278997, 22278999, 264509, 264905, 264592, 18108351, 264681, 264682, 264769, 32833986, 18108374, 264556, 18108385, 264482
2359	87755859 (4717, 4718)	Novel Protein sim. GBank gij1086830 (U41264) - coded for by C. elegans cDNA yk2018.5; coded for by C. elegans cDNA yk4491.5; coded for by C. elegans cDNA yk12b7.5; coded for by C. elegans cDNA yk36g6.5; coded for by C. elegans cDNA yk2018.5; coded for by C. elegans cDNA yk16g12....		UNCLASSIFIED	35696286, 22278998, 264905, 264511, 265007, 265008, 60433438, 264288, 264686, 21906769, 265020, 264692, 35895855, 264558, 56528486, 264583
2360	80046125 (4718, 4720)	Novel Protein sim. GBank gij3881545[embjCAA93779] - (Z69804) cDNA EST yk428d5.3 comes from this gene; cDNA EST yk428d5.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	22278997, 29331826, 263981, 22279000
2361	84232191 (4721, 4722)	Novel Protein sim. GBank gij746487 (U23514) - No definition line found [Caenorhabditis elegans]			22278995, 22278999, 264512, 265009, 264757, 21906765, 65274620, 18108370, 60431528, 18108374, 264635, 60170394, 264482

2362	91721193 (4723, 4724)	Novel Protein sim. GBank gil1171083 sp P19706 MYSB_ACACA - MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL)		UNCLASSIFIED	22278998, 284259, 29331822, 29331824, 60432289, 284509, 284512, 60432229, 60433356, 284448, 284682, 284683, 264369, 21906765, 21906768, 21906769, 60432113, 22279000, 22279002
2363	95006635 (4725, 4726)	Novel Protein sim. GBank gil1854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264907, 264629, 264635
2364	94827104 (4727, 4728)	Novel Protein sim. GBank gil5639830 gb AAD45888.1 AF14601 - (AF146018) hydroxypyruvate reductase [Homo sapiens]	Contains protein domain (PF00389) - D-isomer specific 2-hydroxyacid dehydrogenases	reductase	264488, 18108394, 284887, 18108398, 22278998, 56994075, 35696288, 22278997, 22278998, 264259, 66714117, 29331825, 35696052, 284509, 284905, 284906, 264907, 284908, 68712502, 284909, 284511, 285008, 284512, 265007, 285008, 33657402, 284758, 21906754, 87168474, 265010, 87168559, 264803, 285017, 265018, 265019, 264760, 264762, 18108351, 284448, 284784, 284683, 264684, 264288, 18108355, 284766, 18108358, 284689, 18108359, 21906765, 21906766, 21906767, 35695917, 265020, 265021, 265022, 60170615, 52644150, 264691, 33657023, 284892, 18108364, 33657109, 18108368, 18108370, 18108374, 35698423, 35695855, 284635, 284556, 284557, 284639, 60170394, 83373044, 18108383, 18108384, 18108385, 18108388, 56528486, 264482, 264564, 264488
2365	94140746 (4729, 4730)	Novel Protein sim. GBank gil1840045 (U48082) - transporter protein [Homo sapiens]		transport	22278998, 22278998, 22278999, 264907, 284909, 264910, 33657402, 284758, 284600, 264766, 264687, 264689, 21906765, 21906767, 21906768, 21906769, 265021, 33657023, 33657109, 83373044, 264566
2366	94312388 (4731, 4732)			UNCLASSIFIED	52644507, 284259, 29331824, 29331825, 29331826, 29331827, 29331828, 264907, 29331830, 284909, 284511, 265008, 33657402, 284595, 52646317, 265017, 265018, 265019, 264605, 264685, 264766, 264689, 21906766, 21906769, 35695917, 265020, 265021, 265022, 52644150, 35695855, 52644332, 18108385, 18108387, 264564, 264566
2367	94140910 (4733, 4734)	Novel Protein sim. GBank gil1065457 (U40410) - C54G7.4 gene product [Caenorhabditis elegans]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	35696288, 21906768, 55810764, 65274791, 284567
2368	94322190 (4735, 4736)				284628

2369	84314334 (4737, 4738)	Novel Protein sim. GBank gij5360901[dbj]BAA82158.1 - (AB028343) a-helix coiled-coil rod homologue [Homo sapiens]		struct	52644507, 52646842, 35696286, 264092, 264094, 52645080, 35696052, 264107, 29331830, 52644045, 265006, 265007, 265008, 52644296, 52644229, 264689, 21908765, 21906766, 35695917, 265020, 52644150, 263987, 33657109, 27486285, 35695763, 18108370, 263974, 18108374, 18108376, 52644332, 263981, 18108385, 264508, 264909, 264596
2370	79804120 (4739, 4740)			UNCLASSIFIED	264389
2371	57280406 (4741, 4742)			UNCLASSIFIED	263967, 263981
2372	87642413 (4743, 4744)	Novel Protein sim. GBank gij4589582[dbj]BAA76813.1 - (AB023186) KIAA0989 protein [Homo sapiens]		UNCLASSIFIED	29331826, 265010, 265019, 35695917, 264634, 60432113
2373	87418611 (4745, 4746)	Novel Protein sim. GBank gij5105131[dbj]BAA80445.1 - (AP000061) 246aa long hypothetical ribonuclease PH [Aeropyrum pernix]	Contains protein domain (PF01138) - 3' exoribonuclease family	UNCLASSIFIED	265006, 265007, 265008, 265009, 265011, 264766, 35695917, 35695655, 263981, 264557, 264585
2375	87731355 (4749, 4750)	Novel Protein sim. GBank gij1351115[sp]P47758[SRPB_MOUSE - SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA)]		UNCLASSIFIED	60432049, 28331824, 264907, 52644045, 264512, 60433356, 21906754, 52644288, 87168559, 264448, 21906765, 21908768, 21908769, 33657023, 18108368, 55811576, 52644332
2376	87613744 (4751, 4752)	Novel Protein sim. GBank gij2845435 (AF007780) - CHD3 [Drosophila melanogaster]	Contains protein domain (PF00628) - PHD-finger	ATPase-associated	284259, 29331830, 264909, 264910, 265009, 60433438, 21906754, 265017, 265018, 265019, 264682, 264288, 264685, 21908767, 263972, 35695855, 87168518, 60432113
2377	95319689 (4753, 4754)	Novel Protein sim. GBank gij5257005[gb]AAD41239.1 - (AF083248) Rb binding protein homolog [Homo sapiens]	Contains protein domain (PF01368) - ARID DNA binding domain	UNCLASSIFIED	18108394, 65274572, 22278997, 22278999, 264095, 29331822, 29147620, 29331824, 66714117, 29331825, 29331826, 29331828, 33656970, 29146498, 29146499, 264509, 265008, 265007, 265008, 265009, 60170631, 265010, 265011, 265016, 55811150, 18108351, 264764, 264288, 21908767, 21908768, 29148627, 29148629, 265021, 33657023, 33657109, 18108370, 18108374, 18108379, 35696423, 264558, 83373044, 18108385, 18108388, 55526486, 22279000, 22279002, 264563
2378	94137032 (4755, 4756)	Novel Protein sim. GBank gij1072198 (U40942) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 56182575, 35696286, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 60432289, 29331827, 56182435, 264510, 265009, 60433356, 87168474, 265011, 265016, 264288, 21908765, 33657023, 264557, 56182323, 83373044, 18108385, 22279002, 264482
2379	65444324 (4757, 4758)	Novel Protein sim. GBank gij3337357 (AC004481) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	265017, 264288, 21908768

2380	88923052 (4759, 4760)	Novel Protein sim. GBank gi 4502939 ref NP_001845.1 pCOL.1 - collagen, type XI, alpha 1	Contains protein domain (PF01410) - Fibrillar collagen C-terminal domain	collagen	264908, 264910, 265011
2381	87808241 (4761, 4762)	Novel Protein sim. GBank gi 4455609 emb CAB36555 - (AL031846) dJ742C19.5 (novel Chromobox protein) [Homo sapiens]	Contains protein domain (PF00385) - 'chromo' (CHR) domain Organization Modifier domain	helicase	56182575, 264091, 264093, 264258, 29331825, 264105, 264806, 60433356, 21906754, 265017, 265019, 264883, 264288, 264685, 264688, 264887, 264891, 264892, 264693, 55811576, 264636, 264567
2382	91225982 (4763, 4764)	Novel Protein sim. GBank gi 4325130 gb AAD17276 - (AF119716) dMi-2 protein [Drosophila melanogaster]	Contains protein domain (PF00628) - PHD-finger	transport	29331824, 60432289, 264805, 264596, 21906754, 264768, 265022, 264693, 263867, 33657109, 264629, 264631, 264558, 83373044, 60432113, 264482
2383	87442841 (4765, 4766)	Novel Protein sim. GBank gi 1902882 dbj BAA19005 - (D89049) lectin-like oxidized LDL receptor [Bos taurus]	Contains protein domain (PF00059) - Lectin C-type domain	glycoprotein	265008, 21906765, 21906766
2384	95354766 (4767, 4768)	Novel Protein sim. GBank gi 2462851 (AF016252) - Spinophilin [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	struct	264488, 52644507, 52645156, 52646365, 35896286, 22278999, 52645080, 29331824, 29331826, 35696052, 29331828, 264908, 264828, 52644045, 265006, 265008, 265009, 33109954, 33657084, 52644296, 265011, 265017, 265018, 264683, 52644229, 21906765, 21906767, 21906768, 265020, 52644150, 33657023, 264693, 65274820, 52645126, 33657108, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 18108374, 35695855, 264634, 264555, 264556, 264557, 52644332, 264558, 264559, 18108385, 22279000, 22279002
2385	95419485 (4769, 4770)			UNCLASSIFIED	264488, 52644507, 52645156, 264887, 52646365, 22278995, 22278998, 22278997, 22278999, 264259, 52645080, 29331822, 29331826, 35696052, 52644045, 265006, 265007, 265008, 265009, 264910, 60432229, 60433356, 52646317, 21906754, 265019, 264448, 264683, 264686, 264687, 264689, 21906765, 21906766, 21906767, 21906769, 55811957, 265021, 265022, 264690, 264691, 264692, 65274620, 33657109, 18108370, 264631, 52644332, 22279000, 22279002, 264563, 264565, 264567
2386	94742649 (4771, 4772)	Novel Protein sim. GBank gi 4928698 gb AAD34110.1 AF15187 - (AF151873) CGI-115 protein [Homo sapiens]		glycoprotein	264488, 22278995, 22278998, 22278997, 264259, 29148498, 264112, 264511, 60170831, 60432229, 264595, 60433438, 87188474, 87188559, 264682, 21906765, 21906766, 21906767, 21906769, 29148629, 35695917, 265021, 264690, 33657109, 264628, 18108376, 83373044, 60432113, 22279000, 264564, 264566, 264487

2387	14987990 (4773, 4774)			UNCLASSIFIED	284634
2388	11424804 (4775, 4776)			UNCLASSIFIED	284595
2389	95310650 (4777, 4778)	Novel Protein sim. GBank gi 4758058 refNP_004372.1 pCREB - cAMP responsive element binding protein-like 1	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED - dna_ma_bind	284488, 22278998, 22278999, 284509, 284905, 284906, 284907, 284908, 284909, 285006, 284511, 284512, 284910, 284591, 21908754, 284601, 284604, 284761, 18108351, 284764, 284288, 284766, 284768, 284769, 21908765, 21908766, 284892, 284893, 35896423, 284635, 284636, 284555, 83373044, 22278000, 284486
2380	84320912 (4779, 4780)	Novel Protein sim. GBank gi 1644239 dbj BAA12223 - (D84103) mitochondrial DNA polymerase gamma [Homo sapiens]	Contains protein domain (PF00476) - DNA polymerase family A	- polymerase	52844507, 56182575, 22278995, 35896286, 22278996, 22278997, 22278998, 29331822, 29331825, 29331826, 35896052, 284905, 52844045, 285009, 284758, 284759, 33109954, 52844296, 85658542, 265011, 265017, 265018, 284605, 52844229, 21908765, 21908787, 21908788, 21908789, 35895917, 52844150, 33657023, 33657109, 33657349, 35895763, 18108370, 18108374, 18108376, 35896423, 35895855, 284555, 52844332, 56182323, 60170394, 83373044, 56526486
2391	80036194 (4781, 4782)			UNCLASSIFIED	283978
2392	84245016 (4783, 4784)	Novel Protein sim. GBank gi 4240189 dbj BAA74863.1 - (AB020647) KIAA0840 protein [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	- nuclease	35896286, 35896052, 284508, 284905, 284509, 284906, 284907, 284908, 284909, 284510, 284511, 284512, 284910, 285009, 284591, 284758, 284600, 284604, 284762, 284448, 284764, 284389, 284768, 284769, 284769, 284689, 35895917, 284629, 18108374, 283978, 35896423, 35895855, 284631, 284634, 284635, 284636, 284637, 284638, 60170394, 284639, 284555, 284486

2393	95302633 (4785, 4786)	Novel Protein sim. GBank gi 4506667 ref NP_000983.1 pRPLP - ribosomal protein, large, P0	Contains protein domain (PF00466) - Ribosomal protein L10	- ribosomal prot	18108392, 60424179, 264489, 18108394, 18108397, 22278995, 58994075, 35896286, 22278996, 22278997, 22278999, 284093, 60432049, 264259, 28331822, 29147620, 20281099, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 35896052, 29146499, 284508, 284509, 284905, 284907, 284908, 66712502, 52844045, 284828, 284909, 58182435, 264112, 264113, 284510, 265006, 264511, 265007, 265008, 285009, 284910, 284591, 284593, 60433356, 284595, 60433438, 52846317, 33109954, 21906754, 55811388, 265010, 265011, 265017, 265018, 265019, 284681, 264762, 18108351, 264763, 284682, 284764, 284683, 284369, 284288, 18108354, 284766, 284686, 284687, 284688, 284689, 18108359, 21906765, 21906766, 21906767, 21906768, 21908769, 55811957, 29148629, 29148784, 35895917, 265021, 265022, 33857023, 284692, 284693, 18108384, 33857109, 18108388, 27486261, 27486262, 33857349, 35895763, 18108370, 263972, 284629, 18108374, 263977, 18108376, 263978, 55810764, 35896423, 35895855, 284634, 60431850, 264555, 264637, 264557, 263981, 284558, 18108381, 60170394, 35896286, 22278997, 22278998, 56182181, 35896052, 265006, 284592, 55811388, 265010, 265011, 265017, 265019, 284448, 284683, 284288, 21906765, 21906768, 21908769, 55811957, 35895917, 33857023, 65274620, 33857182, 33857349, 35895763, 18108374, 18108376, 55810764, 55811576, 35896423, 60170394, 18108385, 284584, 284586, 284567
2394	94323268 (4787, 4788)	Novel Protein sim. GBank gi 4159888 (AC004908) - zinc finger protein from gene of uncertain exon structure; similar to Q99878 (PID:g3025333) [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	- dna_ma_bln	
2395	95287212 (4789, 4790)	Novel Protein sim. GBank gi 5712756 gb AAD47836.1 AF16079 - (AF160798) calcium transporter CaT1 [Rattus norvegicus]		- dna_ma_bln	284259, 29331824, 264910, 264288, 265021, 83373044, 18108387, 284563, 284566

2396	85096700 (4791, 4792)	Novel Protein sim. GBank gi 106322 pir B34087 - hypothetical protein (L1H 3' region) - human	Contains protein domain (PF00560) - nuclease Leucine Rich Repeat	52846365, 18108387, 56182575, 35696286, 22278997, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264106, 264807, 29331830, 66712502, 264110, 60170831, 264591, 33657402, 60433438, 55812038, 33109954, 21908754, 33657084, 87168474, 265017, 265018, 265019, 264760, 264448, 264288, 264768, 52644229, 21908768, 21908767, 265020, 265021, 60170615, 264692, 33657023, 65274620, 52845129, 33657182, 27486262, 27486264, 27486265, 264629, 18108374, 35698423, 35695855, 264631, 264556, 52644332, 264558, 83373044, 18108388, 87168518, 22278002, 264482
2397	87280854 (4793, 4794)			52844507, 52645156, 56182575, 264259, 29147620, 264805, 264907, 264908, 264809, 284910, 264758, 52644296, 264803, 264804, 284762, 264681, 264764, 18108357, 264769, 21908768, 264693, 264628, 264635, 264638, 264639, 264584
2398	88047689 (4795, 4796)	Novel Protein sim. GBank gi 3258609 (AC005178) - H53_GS1 [Homo sapiens]	UNCLASSIFIED	
2399	87738965 (4797, 4798)	Novel Protein sim. GBank gi 786117 (L41834) - nuclear protein [Ensis minor]	UNCLASSIFIED	56994075, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 66714117, 60432289, 264906, 29331830, 56182435, 264112, 264810, 33109954, 21906754, 87168474, 264600, 265017, 265018, 265019, 264764, 264765, 21906765, 21906768, 21908767, 21908769, 35695917, 265020, 265022, 60170815, 33657023, 18108370, 18108374, 264556, 60170394, 284558, 87168518, 22279000, 22279002, 264564, 264566, 264487
2400	81214116 (4799, 4800)	Novel Protein sim. GBank gi 2352822 gb AAB69285.1 - (AF008945) glucose-6-phosphatase [Haplochromis nubilus]	phosphatase	21908766, 52646842, 56994075, 33657182, 27486262, 52644296, 265017

2401	91214118 (4801, 4802)	Novel Protein sim. GBank gi 2352822 gb AAB69285.1 - (AF008845) glucose-6-phosphatase [Haplochromis nubilus]		phosphatase	52844507, 52845156, 52844229, 284688, 21908784, 21908765, 52846385, 52846842, 21908786, 21908767, 21908768, 22278995, 35895917, 56994075, 35896286, 22278996, 22278997, 265020, 22278998, 22278999, 284259, 33857023, 52845080, 284693, 29331824, 33857109, 52845129, 29331826, 33857182, 29331827, 35896052, 27486261, 27486262, 33856970, 33857349, 27486285, 35895763, 284106, 264905, 35896423, 35895855, 265006, 265007, 265008, 265009, 284637, 52844332, 55812038, 52846317, 18108385, 52844286, 87188474, 265010, 87188559, 60432113, 265017, 265018, 265019, 284583, 284288, 284907, 284908, 284909, 284566
2402	91221408 (4803, 4804)	Novel Protein sim. GBank gi 4689258 gb AAD27832.1 AF12185 - (AF121859) sorting nexin 8 [Homo sapiens]			
2403	94135432 (4805, 4806)	Novel Protein sim. GBank gi 4929575 gb AAD34048.1 AF15181 - (AF151811) CGI-53 protein [Homo sapiens]	Contains protein domain (PF00062) - C-type lysozyme/alpha-lactalbumin family		22278999, 35896052, 265018, 284686, 284693, 83373044, 284567
2404	95312605 (4807, 4808)	Novel Protein sim. GBank gi 2315796 (AF016685) - similar to short chain-type dehydrogenases [Caenorhabditis elegans]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	35896286, 29331826, 35896052, 265008, 265018, 21908769, 284584
2405	94311851 (4809, 4810)	Novel Protein sim. GBank gi 464178 dbj BAA03581 - (D14853) polyprotein [Hepatitis C virus]		UNCLASSIFIED	35896286, 29331822, 265007, 21906754, 285017, 265018, 285019, 284763, 284369, 21906765, 35895917, 265020, 265021, 52844150, 284693, 35895855, 284632, 52844332, 22279002
2406	88094501 (4811, 4812)	Novel Protein sim. GBank gi 2773363 (AF041382) - microtubule binding protein D-CLIP-190 [Drosophila melanogaster]	Contains protein domain (PF01302) - CAP-Gly domain	struct	52846842, 22278994, 22278996, 35896286, 22278997, 22278998, 22278999, 284092, 284093, 60432049, 284259, 29331822, 29331824, 29331825, 29331827, 35896052, 29331828, 284102, 284106, 284908, 52844045, 265007, 265008, 265009, 284910, 284592, 60433358, 60433438, 33109954, 285010, 265011, 285018, 285019, 284369, 264685, 284686, 21908768, 21908769, 52844150, 284693, 52845129, 284628, 35896423, 284632, 56182323, 284639, 22278000, 22278002, 284563, 284685, 284686
2407	79465005 (4813, 4814)	Novel Protein sim. GBank gi 423442 pir S33513 - gene Fif		UNCLASSIFIED	
2408	87391503 (4815, 4816)	Novel Protein sim. GBank gi 423442 pir S33513 - gene Fif protein - mouse		UNCLASSIFIED	284910, 285010, 264448, 284557

2409	94741770 (4817, 4818)	Novel Protein sim. GBank gij1176801 sp P45966 YNZ8_CAEEL - HYPOTHETICAL 20.8 KD PROTEIN T09A5.8 IN CHROMOSOME III		UNCLASSIFIED	22278995, 22278996, 22278997, 264097, 29331822, 29331824, 29331827, 29148498, 52644045, 60433438, 33657084, 87168474, 264780, 21906767, 29148627, 29148629, 52644150, 33657023, 263967, 20281089, 18108374, 20281071, 56182323, 83373044, 18108385, 87168518 22278998, 264259
2410	87604860 (4819, 4820)	Novel Protein sim. GBank gij4966262 gb AAC48052.2 - (UB4849) Contains similarity to Pfam domain: PF00646 (F- box). Score=28.7, E-value=4.3e-05, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00080) - Copper/zinc superoxide dismutase (SODC)		
2411	87534633 (4821, 4822)	Novel Protein sim. GBank gij3114713 (AF061346) - Edp1 protein [Mus musculus]		tnf	29331824, 29331827, 29331828, 264764, 284388, 33657109, 56182323
2412	87778332 (4823, 4824)	Novel Protein sim. GBank gij5410336 gb AAD43038.1 - (AF106685) myelin gene expression factor 2 [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	22278998, 29331827, 264807, 265011, 265017, 265018, 265019, 18108351, 21906768, 265020, 33657109, 284559, 18108385
2413	94133820 (4825, 4826)	Novel Protein sim. GBank gij5262705 emb CAB45778.1 - (AL080214) hypothetical protein [Homo sapiens]	Contains protein domain (PF00038) - Intermediate filament proteins	struct	284488, 284259, 29331826, 264508, 264905, 264509, 284908, 284907, 264908, 264510, 264511, 264512, 265008, 265009, 264910, 265011, 264882, 264764, 264768, 264886, 264768, 264889, 265021, 33657023, 18108370, 264628, 35695855, 284632, 284634, 264635, 264636, 83373044, 264563, 264564, 264565, 264566, 264567, 264486, 52645156, 52646842, 52646385, 18108398, 56182575, 22278994, 22278995, 56994075, 22278998, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 29331830, 284909, 60433356, 33657402, 284594, 52646317, 21906754, 33657084, 265010, 87168559, 265017, 265018, 265019, 264369, 264684, 264687, 264688, 56181562, 21906764, 264689, 21906765, 21906766, 21906767, 29148627, 21906769, 265020, 265021, 60170615, 33657023, 264693, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 18108370, 60431528, 264629, 18108374, 18108376, 55810764, 264636, 52644332, 264638, 284558, 56182323, 83373044, 18108385, 87168518, 22279002
2414	94312590 (4827, 4828)	Novel Protein sim. GBank gij1082340 pir S52863 - DNA- binding protein R kappa B - human		ubiquitin	

2415	88089002 (4829, 4830)	Novel Protein sim. GBank gij423915 pir A45439 - myosin I heavy chain - rat	Contains protein domain (PF00063) - Myosin head (motor domain)	struct	284259, 284908, 60433356, 33657402, 21906754, 265018, 264687, 264689, 21906769, 55811957, 285021, 264690, 264691, 33657023, 264693, 35698423, 58182323, 56526486
2416	94118356 (4831, 4832)	Novel Protein sim. GBank gij3025445 (AC004528) - R32184_1 [Homo sapiens]			264638
2417	87733334 (4833, 4834)	Novel Protein sim. GBank gij1084944 pir S54495 - hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00153) - Mitochondrial carrier proteins		264094, 29331822, 29331824, 29331827, 264369
2418	94234349 (4835, 4836)	Novel Protein sim. GBank gij1176572 sp P45895 YNA4_CAEEL - HYPOTHETICAL 91.0 KD PROTEIN PAR2.4 IN CHROMOSOME III	Contains protein domain (PF00411) - Ribosomal protein S11	UNCLASSIFIED	56994075, 264091, 264259, 29331824, 29331825, 60432289, 29331828, 264905, 264907, 264511, 265009, 60432229, 21908754, 87188559, 285019, 264682, 21908768, 21906769, 265020, 285021, 33657023, 65274620, 18108370, 55811576, 264834, 60170394, 18108385, 22279000, 22279002, 264588
2419	82374249 (4837, 4838)	Novel Protein sim. GBank gij284006 pir S18732 - autoantigen, 64K - human		struct	264569, 264762, 264448, 264691, 264631, 264634, 264555, 264556, 264636, 264558
2420	94844244 (4839, 4840)	Novel Protein sim. GBank gij1076211 pir S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	29331824, 29331825, 29331828, 60432229, 33109954, 55658542, 87168474, 265018, 264288, 265020, 264584
2421	87805345 (4841, 4842)			UNCLASSIFIED	264909, 264768, 264638
2422	88084714 (4843, 4844)	Novel Protein sim. GBank gij2224567 dbj BAA20772 - (AB002311) KIA0313 [Homo sapiens]	Contains protein domain (PF00617) - RasGEF domain	transport	18108392, 18108394, 18108398, 264906, 265006, 265010, 18108351, 18108374, 18108385
2423	88056390 (4845, 4846)	Novel Protein sim. GBank gij4505153 ref NP_002392.1 pMEKK - MAP/ERK kinase kinase 3	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 60432049, 29331822, 29331826, 60432289, 29331828, 265008, 265009, 60433356, 21906754, 265017, 285018, 265019, 21906768, 21906769, 265020, 285021, 20281149, 263971, 60432113
2424	94854047 (4847, 4848)	Novel Protein sim. GBank gij2988398 (AC004381) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	56182575, 35686286, 22278997, 60432049, 264259, 29331826, 29331828, 264905, 66712502, 29331830, 60433356, 265011, 265019, 264768, 21906768, 55811957, 264692, 33657023, 33657109, 55811576, 58182323, 63373044, 18108385, 18108388, 60432113, 22279000
2425	87415981 (4849, 4850)	Novel Protein sim. GBank gij2077832 dbj BAA19879 - (D88556) Protein Kinase [Rattus norvegicus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264634
2426	87613945 (4851, 4852)	Novel Protein sim. GBank gij2039388 gb AAB53003.1 - (U94619) circulating cathodic antigen [Schistosoma mansoni]		UNCLASSIFIED	22278986, 22278998, 264259, 264102, 264512, 265008, 21908767, 18108370, 18108374, 263976

2427	87622693 (4853, 4854)	Novel Protein sim. GBank gil4680695[gblAAD27737.1]AF13296 - (AF132962) CGI-28 protein [Homo sapiens]	Contains protein domain (PF00573) - Ribosomal protein L4/L1 family	ribosomalprot	264259, 20281099, 35696052, 265008, 264594, 265011, 264760, 18108351, 264682, 264683, 264369, 264684, 264686, 264687, 264689, 21908766, 264691, 264692, 18108374, 18108377, 264557, 264639, 18108385
2428	85732889 (4855, 4856)	Novel Protein sim. GBank gil1537070 (U63840) - nucleoporin p54 [Rattus norvegicus]			22278998, 22278999, 35696052, 21906754, 264288, 21908765, 21908768, 21908769, 35695917, 265020, 263972, 22279002
2429	87769276 (4857, 4858)	Novel Protein sim. GBank gil601931 (M94316) - neurofilament-H [Oryctolagus cuniculus]	Contains protein domain (PF00711) - Beta defensins	UNCLASSIFIED	22278999, 29331824, 264906, 264909, 264511, 265009, 21908754, 265017, 265018, 265019, 264448, 264683, 264288, 21908765, 21908768, 265021, 264693, 18108381
2430	86948927 (4859, 4860)			UNCLASSIFIED	264112, 264691
2431	87649884 (4861, 4862)	Novel Protein sim. GBank gil3860729[emb CAA14630] - (AJ235270) CELL DIVISION PROTEIN FTSJ (ftsJ) [Rickettsia prowazekii]	Contains protein domain (PF01728) - FtsJ cell division protein		29331826, 29331827, 35696052, 29148499, 264905, 264906, 264691, 264288, 264689, 21908765, 264692, 35696423
2432	80083033 (4863, 4864)	Novel Protein sim. GBank gil3876367[emb CAA93287] - (Z69360) Weak similarity to Elmeria thrombospondin (PIR Acc. No. A45517); cDNA EST EMBL:M89266 comes from this gene; cDNA EST yk295b9.5 comes from this gene [Caenorhabditis elegans]		protease	264634, 264558
2433	80055092 (4865, 4866)	Novel Protein sim. GBank gil2224593[db JBAA20784] - (AB002324) KIAA0326 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	264569, 264905, 265018, 264762, 264683, 264691, 264556, 264557, 264639, 264558
2434	19520148 (4867, 4868)				264563
2435	20759044 (4869, 4870)			UNCLASSIFIED	264555
2436	88044008 (4871, 4872)	Novel Protein sim. GBank gil1263289 (U47856) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	265008, 264758, 265010, 264689, 27486261, 263972, 18108374, 18108381
2437	83363424 (4873, 4874)	Novel Protein sim. GBank gil3641352 (AF091234) - putative transcription factor [Mus musculus]		UNCLASSIFIED	29331828, 265007, 265009, 265017, 264760, 264685, 264693, 264565
2438	94143473 (4875, 4876)	Novel Protein sim. GBank gil3860014 (AF091088) - unknown [Homo sapiens]	Contains protein domain (PF01256) - Uncharacterized protein family UPF0031	UNCLASSIFIED	29331826, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 265008, 264512, 264910, 265009, 264591, 33657402, 21908754, 265011, 264760, 264764, 264885, 264686, 264768, 35695917, 33657023, 264693, 264631, 264632, 56182323, 264558, 83373044, 264583, 264584, 264585, 264586, 264587

2439	94850650 (4877, 4878)	Novel Protein sim. GBank gi 4263519 gb AAD15345 - (AC004044) small nuclear riboprotein Sm-D1 (Arabidopsis thaliana)	Contains protein domain (PF01423) - Sm protein	UNCLASSIFIED	60424179, 18108397, 56182575, 56181888, 56994075, 22278986, 35698286, 22278997, 22278989, 264259, 52645080, 29331822, 56182181, 29331824, 60424268, 66714117, 29331825, 60432288, 29331826, 29331827, 29331828, 35698052, 29148498, 264509, 264905, 264908, 52644045, 60431735, 33109954, 21908754, 33657084, 55811388, 52644296, 87168474, 265017, 265018, 265019, 18108351, 264448, 264288, 264768, 52644229, 56181562, 21906764, 21908765, 21908768, 21908767, 21908768, 21908769, 35695917, 33657023, 33657109, 33657182, 27486282, 27486284, 33657349, 27486285, 35695763, 18108370, 60431528, 263977, 55810764, 35696423, 65274791, 35695855, 60431850, 56182323, 60432113, 22278000, 22279002, 264567
2440	87641733 (4878, 4880)			UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264907, 264510, 265018, 265019, 264448, 264369, 265020, 265021, 56182323, 264639, 22279002
2441	87623914 (4881, 4882)	Novel Protein sim. GBank gi 3024889 sp P56524 Y288_HUMAN - HYPOTHETICAL PROTEIN KIAA0288 (HA6116)		UNCLASSIFIED	264488, 264628, 18108374, 264564
2442	87273590 (4883, 4884)	Novel Protein sim. GBank gi 4506013 ref NP_002703.1 pPPP1 - protein phosphatase 1, regulatory subunit 7	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	22278986, 22278989, 29331822, 264768, 264693
2443	84305949 (4885, 4886)	Novel Protein sim. GBank gi 1170658 sp Q02975 KID1_RAT - RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17)	Contains protein domain (PF01352) - KRAB box	transcriptfactor	264906
2444	88086345 (4887, 4888)	Novel Protein sim. GBank gi 4758824 ref NP_004280.1 pNRF3 - nuclear factor (erythroid-derived 2)-like 3	Contains protein domain (PF00170) - bZIP transcription factor	transcriptfactor	264259, 18108382, 18108383, 18108385, 22279000
2445	87338636 (4889, 4890)	Novel Protein sim. GBank gi 2135950 pir [S58222 - PQ-rich protein - human			264259, 35698052, 264369, 18108361
2446	88059293 (4891, 4892)	Novel Protein sim. GBank gi 4753887 emb CAA05408.2 - (AJ002424) p85 protein [Rattus norvegicus]	Contains protein domain (PF00095) - WAP-type (Whey Acidic Protein) 'four-disulfide core'	proteaseinhib	265011, 264689, 33657023, 263981, 18108385
2447	94845149 (4893, 4894)	Novel Protein sim. GBank gi 4885613 ref NP_005409.1 pST5 - suppression of tumorigenicity 5		cadherin	56182575, 264259, 29331824, 29331825, 29331827, 60433356, 60433438, 264758, 265018, 264692, 65274620, 60431528, 65274791, 56182323

2448	87749680 (4895, 4898)			UNCLASSIFIED	22278998, 22278997, 22278999, 29331826, 35896052, 264107, 264110, 87188474, 87188559, 18108351, 21906767, 21906769, 27486262, 263976
2449	87869075 (4897, 4898)	Novel Protein sim. GBank gij728837 sp P39194 ALU7_HUMAN - III! ALU SUBFAMILY SQ WARNING ENTRY III!		cadherin	264259, 264828, 265007, 264595, 265021, 58528488
2450	86597784 (4899, 4900)			UNCLASSIFIED	264908
2451	91014563 (4901, 4902)	Novel Protein sim. GBank gij1710021 sp P35290 RB24_MOUSE - RAS-RELATED PROTEIN RAB-24 (RAB-16)	Contains protein domain (PF00071) - Ras family	glycoprotein	264093, 29331822, 29331824, 29331825, 86714117, 29331826, 29331828, 35896052, 264907, 86712502, 29331830, 264910, 265009, 264758, 265017, 265018, 264762, 264448, 264288, 21906767, 265021, 33857023, 264693, 33857109, 263969, 83373044, 18108385
2452	91230509 (4903, 4904)	Novel Protein sim. GBank gij1504034 dbj BAA13216 - (D86980) KIAA0227 [Homo sapiens]		isomerase	264102, 264112, 264688, 263972, 18108374, 83373044, 264563
2453	84201088 (4905, 4906)	Novel Protein sim. GBank gij2880079 (AC004142) - similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D49802 (PID:g1369906) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	ngfrecep	264509, 264512, 18108385
2454	95310691 (4907, 4908)	Novel Protein sim. GBank gij1076802 pir S49915 - extensin like protein - maize	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	263994, 86714117, 29331827, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 265009, 264910, 264591, 264758, 264759, 265010, 265011, 264603, 264604, 264760, 264761, 264762, 18108351, 264764, 264765, 264766, 264686, 264768, 264769, 264534, 264691, 264692, 33857023, 264693, 33857109, 264628, 263978, 35895855, 264634, 264635, 264637, 264638, 264639, 83373044, 18108385, 264563, 264564, 264488
2455	95288301 (4909, 4910)	Novel Protein sim. GBank gij543817 sp P35585 AP47_MOUSE - CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN)	Contains protein domain (PF00928) - Adaptor complexes medium subunit family	glycoprotein	264488, 22278998, 264259, 35896052, 264905, 264906, 264907, 264908, 264909, 264510, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264758, 265019, 264760, 264681, 18108351, 264683, 264764, 18108354, 264766, 264768, 264769, 264689, 21906766, 21906767, 21906769, 29148629, 35895917, 265020, 265022, 33857023, 33857109, 18108370, 264628, 264629, 264631, 264632, 264635, 58182323, 60170394, 18108385, 264563, 264564, 264568, 264567
2456	88166700 (4911, 4912)	Novel Protein sim. GBank gij2588630 (AC003079) - Ankyrin- like; 54% similar to 2022340A (NID:g1092123) in exons spanning 43974 to 11551 of clone. [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	kinase	264693

2457	94118375 (4913, 4914)	Novel Protein sim. GBank gi 3025447 (AC004528) - R32184_3 [Homo sapiens]		UNCLASSIFIED	58181888, 284905, 284907, 284511, 284598, 55811388, 284682, 284684, 284685, 284687, 284691, 33857023, 284693, 35895855, 284636, 284555, 56182323, 284558, 58528488, 284563
2458	85875304 (4915, 4916)	Novel Protein sim. GBank gi 2384942 (AF022885) - Similar to collagen [Caenorhabditis elegans]		UNCLASSIFIED	284691, 284693, 284634, 284559
2459	87551913 (4917, 4918)	Novel Protein sim. GBank gi 5441942 gb AAD43187.1 AC004997 supported by mouse EST AA538043 (NID:g2284036) [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	transport	27486265
2460	94315289 (4919, 4920)	Novel Protein sim. GBank gi 4929701 gb AAD34111.1 AF15187 - (AF151874) CGI-116 protein [Homo sapiens]		kinase	65274572, 35898286, 22278996, 22278997, 60432049, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 33856970, 29148499, 284102, 284109, 60433438, 285017, 285018, 285019, 284288, 21908785, 21908788, 21908789, 35895917, 285020, 284691, 33857023, 27486281, 18108374, 35895855, 87188518, 60432113
2461	87645147 (4921, 4922)	Novel Protein sim. GBank gi 4426862 gb AAD20633 - (AF126062) Arf-like 2 binding protein BART1 [Homo sapiens]		UNCLASSIFIED	264259, 29331828, 284910, 18108351, 18108370, 18108374
2462	86998002 (4923, 4924)	Novel Protein sim. GBank gi 5420387 emb CAB46678.1 - (AJ243459) proteophosphoglycan [Leishmania major]			284909, 284758, 284684, 18108374, 284637, 18108385
2463	84388543 (4925, 4926)	Novel Protein sim. GBank gi 5052516 gb AAD38588.1 AF14561 - (AF145613) BcDNA.GH03108 [Drosophila melanogaster]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	264681, 264556
2464	91218957 (4927, 4928)	Novel Protein sim. GBank gi 5410300 gb AAD43021.1 - (AF100757) COP9 complex subunit 4 [Homo sapiens]	Contains protein domain (PF01399) - PCI domain	protease	284489, 52848842, 22278995, 35896286, 22278996, 22278997, 22278999, 284259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35896052, 29331828, 284509, 52844045, 284510, 284511, 284512, 285008, 60170831, 284593, 52846317, 33109954, 33657084, 285017, 285018, 285019, 284762, 284448, 284764, 264288, 284766, 21906765, 21906766, 21906767, 21906768, 21906769, 285021, 33857023, 33857109, 18108370, 18108381, 60170394, 18108385, 22279002, 284486

2465	85357483 (4828, 4930)	Novel Protein sim. GBank gij4508401refNP_002871.1 pRAF1 - v-raf-1 murine leukemia viral oncogene homolog 1	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	oncogene	18108392, 52644507, 52645156, 52646365, 22278994, 22278995, 35696286, 22278996, 22278998, 264259, 29331822, 29331824, 29331825, 60424289, 60432289, 29331827, 35696052, 29331828, 264907, 29331830, 52644045, 264909, 56182435, 264511, 265007, 265008, 265009, 264910, 33657402, 60433438, 55812038, 21908754, 33109954, 265010, 265011, 87168559, 264600, 265017, 265018, 265019, 18108351, 264389, 264288, 264685, 264767, 21908765, 21908767, 21908768, 55811957, 35695917, 265020, 265021, 60170615, 52644150, 33657023, 52645129, 33657109, 27486261, 27486264, 35695763, 264628, 263972, 18108374, 35695855, 264636, 264637, 60170394, 56526486, 87168518, 60432113, 264563, 264564, 264566, 264487 264369
2466	85681386 (4931, 4932)	Novel Protein sim. GBank gij4321618 gb AAD15788.1 - (AF051088) seven transmembrane domain orphan receptor [Mus musculus]			
2467	86059485 (4933, 4934)	Novel Protein sim. GBank gij3513300 (AC005595) - F16801_1, partial CDS [Homo sapiens]		UNCLASSIFIED	56994075, 264908, 21908768, 33657023
2468	87614696 (4935, 4936)	Novel Protein sim. GBank gij2143455 pir 58106 - gene DMR-N9 protein - mouse (fragment)	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	29331824, 52644045, 265008, 264910, 265019, 21908765, 21908769, 265021 264288, 264628
2470	86294397 (4937, 4938)	Novel Protein sim. GBank gij5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264592, 264692, 264555, 264556, 264557, 264558, 264559, 18108385, 264482
2471	91013681 (4941, 4942)	Novel Protein sim. GBank gij5419882 emb CAB46424.1 - (AL096749) DKFZp434G153 [Homo sapiens]		UNCLASSIFIED	65274572, 35696286, 29331827, 265007, 264592, 33109954, 265018, 265019, 264288, 55811957, 265020, 264693, 55811576, 56182323
2472	95060811 (4943, 4944)	Novel Protein sim. GBank gij4929747 gb AAD34134.1 AF15189 - (AF151897) CGI-139 protein [Homo sapiens]		UNCLASSIFIED	264092, 60432049, 29331825, 60433356, 265010, 265011, 18108351, 264784, 264288, 264692, 65274620, 18108370, 18108372, 18108374, 264634, 18108385
2473	95421509 (4945, 4946)	Novel Protein sim. GBank gij4539009 emb CAB39630.1 - (AL049481) putative protein [Arabidopsis thaliana]			60424179, 65274572, 22278999, 60424269, 29331826, 265008, 60433358, 60433438, 265010, 18108351, 264448, 264288, 264687, 264689, 265021, 264692, 65274620, 60431528, 65274791, 264556, 56182323, 60432113
2474	94315616 (4947, 4948)	Novel Protein sim. GBank gij3252827 (AC004382) - Unknown gene product [Homo sapiens]			65274572, 56994075, 264259, 29331826, 60170831, 265017, 265018, 265019, 264683, 264369, 265020, 264693, 264563, 264564

2475	94321693 (4949, 4950)	Novel Protein sim. GBank gj1216486 (U48852) - HT protein [Crictetus griseus]	Contains protein domain (PF00008) - EGF-like domain	tgf	284259, 29331822, 285008, 285007, 285010, 285011, 284448, 284288, 284389, 284685, 284686, 18108357, 264768, 18108362, 284693, 18108370, 18108374, 18108379, 35698423, 83373044, 18108383, 18108385, 284564, 284565, 284567
2476	94315618 (4951, 4952)	Novel Protein sim. GBank gj3252827 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	284259, 60424269, 66714117, 284905, 285006, 284511, 265008, 285009, 284758, 285010, 285011, 18108351, 264681, 264369, 284288, 264689, 21906767, 265020, 18108374, 264638, 18108382, 83373044, 18108385, 87168518
2477	20718974 (4953, 4954)			UNCLASSIFIED	263978
2478	17659165 (4955, 4956)			UNCLASSIFIED	265017
2479	94314569 (4957, 4958)	Novel Protein sim. GBank gj1644232 [dbj BAA11082] - (D67066) N-WASP [Bos taurus]		tm7	56994075, 22278999, 21906754, 264682, 21906765
2480	95285605 (4959, 4960)			UNCLASSIFIED	284905, 284907, 284765
2481	94718481 (4961, 4962)	Novel Protein sim. GBank gj5689469 [dbj BAA83018.1] - (AB028989) KIAA1066 protein [Homo sapiens]		collagen	65274572, 56182575, 22278997, 284094, 284259, 29331822, 29331824, 66714117, 29331827, 35696052, 264508, 264905, 264908, 264907, 264908, 52644045, 264909, 56182435, 265008, 264910, 33657402, 55812038, 264758, 265010, 265011, 265017, 265018, 264760, 264762, 18108351, 264764, 284288, 264766, 264886, 264768, 21906768, 55811957, 285020, 264691, 264692, 264693, 284628, 55811576, 264630, 264634, 264635, 284636, 284637, 264558, 284558, 56182323, 83373044, 60432113, 22279002
2482	87393165 (4963, 4964)	Novel Protein sim. GBank gj321249 [pir S28407] - guanine nucleotide-exchange activator CDC25 homolog - mouse		UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 284508, 264905, 264508, 264906, 264907, 284908, 284511, 284591, 284768, 284693, 284831, 284632, 284636, 284638, 284639, 284563
2483	87731583 (4965, 4966)			UNCLASSIFIED	264488, 22278995, 264093, 264095, 60432048, 60433356, 60433438, 264448, 284288, 263967, 18108370, 18108385, 18108388, 264482
2484	94187774 (4967, 4968)	Novel Protein sim. GBank gj728631 [sp P39188] ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		kinase	284563
2485	87786556 (4969, 4970)	Novel Protein sim. GBank gj1185397 (U25281) - SH3 domain binding protein [Rattus norvegicus]		UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 284259, 60432049, 29331824, 60432289, 29331827, 285007, 284910, 264593, 264600, 284603, 264604, 265019, 264448, 264288, 284685, 264686, 284769, 284689, 35695917, 285022, 264692, 264693, 56182323

2486	87748978 (4971, 4972)	Novel Protein sim. GBank gi 2662167 dbj BAA23715 - (AB007803) KIAA0443 [Homo sapiens]			265017, 264555
2487	95343105 (4973, 4974)	Novel Protein sim. GBank gi 464559 sp P35287 RB14_RAT RAS-RELATED PROTEIN RAB-14	Contains protein domain (PF00071) - Ras family	glycoprotein	22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264259, 29331822, 35696052, 264106, 264905, 264907, 29331830, 264909, 265006, 264511, 265008, 265009, 60433438, 21906754, 33109954, 87168559, 265018, 264681, 264288, 264687, 21908785, 21908786, 21908787, 21908788, 21908789, 35695917, 265021, 265022, 264534, 33857023, 264692, 33657109, 263972, 18108377, 35698423, 35695855, 60170394, 18108385, 56526486, 22278000, 22279002, 264563, 264482, 264565, 20281169, 18108391
2488	87652451 (4975, 4976)			UNCLASSIFIED	284910, 264448, 284288, 264684, 264691, 264634
2489	82990585 (4977, 4978)	Novel Protein sim. GBank gi 4886439 emb CAB43355.1 - (AL050253) hypothetical protein [Homo sapiens]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	complementrecept	264688, 264693, 55811576, 22279002
2490	88068608 (4979, 4980)	Novel Protein sim. GBank gi 2588624 (AC003083) - Rap2 interacting protein-like; similar to U73941 (PID:g1916018) [Homo sapiens]		UNCLASSIFIED	264907, 255008, 22279002
2491	91242116 (4981, 4982)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII		tm7	264258, 29331826, 265008, 264762, 18108370, 18108376, 18108379
2492	95308202 (4983, 4984)	Novel Protein sim. GBank gi 3355303 (AF001549) - Unknown gene product [Homo sapiens]		transcriptfactor	264488, 22278998, 22278999, 29331828, 264591, 33109954, 265017, 55811150, 21908784, 21908788, 264692, 60431528, 87168518, 60432113, 22279000

2493	95422415 (4985, 4986)	Novel Protein sim. GBank gi 4240307 dbj BAA74932.1 - (AB020716) KIAA0909 protein [Homo sapiens]	Contains protein domain (PF01424) - struct R3H domain	18108394, 284887, 65274572, 56182575, 22278985, 58994075, 80432049, 29331822, 29331824, 29331825, 29331826, 29331827, 29148498, 284508, 284905, 284509, 284906, 284907, 29331830, 284909, 284510, 285008, 284511, 285007, 284512, 285008, 285009, 284910, 21908754, 285011, 284600, 285017, 285018, 284604, 284605, 285019, 55811150, 284782, 18108351, 284681, 284448, 284683, 284369, 284288, 18108355, 18108357, 284687, 21906765, 21906766, 21906767, 21906768, 21906769, 285020, 284691, 284692, 33857023, 33857349, 18108370, 18108374, 18108376, 55810764, 18108379, 65274791, 284630, 284632, 284634, 284635, 284636, 284555, 284637, 284557, 284558, 284639, 284559, 83373044, 18108385, 87168518, 60432113, 22279000, 22279002, 284482, 284586, 284486
2494	30793118 (4987, 4988)		UNCLASSIFIED	284907, 284601
2495	94234551 (4989, 4990)	Novel Protein sim. GBank gi 5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]	collagen	263994, 22278997, 35898052, 284509, 284905, 284906, 284907, 284908, 284909, 285006, 285009, 284595, 284604, 284448, 284682, 284764, 284288, 284685, 284766, 284769, 284689, 285020, 284692, 65274620, 284629, 55810764, 35898423, 55811576, 284636, 284637, 18108385, 22278000, 284584, 284587, 284486
2496	80018765 (4991, 4992)	Novel Protein sim. GBank gi 4808220 emb CAB42832.1 - (AL022315) dJ1177i5.1 (PUTATIVE novel protein) [Homo sapiens]	struct	29147620, 284905, 285006, 285007, 18108348, 18108362, 18108370, 18108374, 284555, 284556, 18108381, 18108383, 18108388
2497	81723554 (4993, 4994)		UNCLASSIFIED	52844507, 22278986, 22278999, 29331824, 29331828, 33857402, 21908754, 87168474, 285019, 284369, 284689, 21906765, 21906766, 21906767, 21908768, 285020, 33857023, 18108376, 18108387
2498	87724633 (4995, 4996)	Novel Protein sim. GBank gi 1200503 (U47924) - B [Homo sapiens]	UNCLASSIFIED	29331827, 284512, 284910, 284288, 18108374, 35895855
2499	94685125 (4997, 4998)	Novel Protein sim. GBank gi 3510234 (AC005581) - R31237_1, partial CDS [Homo sapiens]	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	284909, 55812036, 284631, 284637, 284558

2500	94849324 (4999, 5000)	Novel Protein sim. GBank gi 3881275 emb CAA21725 - (AL032655) predicted using GeneFinder; similar to Inositol monophosphatase family; cDNA EST yk255e11.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00459) - Inositol monophosphatase family	transport	52644507, 52645158, 22278995, 56994075, 35698286, 22278998, 264259, 52645080, 29331824, 29331825, 66714117, 60432289, 29331828, 29331827, 35696052, 29331828, 264508, 264509, 264510, 264512, 33657402, 60433438, 21906754, 52644296, 87188474, 87188559, 264603, 264681, 264448, 264683, 264288, 264389, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 33657023, 264693, 33657182, 35695763, 35698423, 35695855, 52644332, 83373044, 18108387, 87168518, 22279002
2501	94303898 (5001, 5002)	Novel Protein sim. GBank gi 4929615 gb AAD34088.1 AF15183 - (AF151831) CGI-73 protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	dna_ma_bind	65274572, 56182575, 35696286, 22278998, 56994075, 22278997, 60432049, 264259, 29331822, 29331824, 29331826, 29331827, 35698052, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 265007, 264910, 264591, 60432229, 33657402, 60433356, 264595, 55812038, 264758, 264598, 87168474, 87168559, 264600, 264601, 264602, 265017, 264604, 265018, 264605, 265019, 18108351, 264448, 264369, 264288, 264766, 18108357, 21906765, 21906766, 21906767, 21906769, 29148629, 35695917, 264692, 33657023, 264629, 35698423, 55811576, 35695855, 264630, 264634, 264635, 264555, 264636, 264638, 264558, 60170394, 83373044, 18108385, 18108387, 87168518, 60432113, 22279002, 264566
2502	90993716 (5003, 5004)	Novel Protein sim. GBank gi 3041847 (AC004542) - OXYSTEROL-BINDING PROTEIN-like; similar to P22059 (PID:g129308) [Homo sapiens]	Contains protein domain (PF01237) - Oxysterol-binding protein	UNCLASSIFIED	65274572, 264907, 56182435, 265007, 264592, 264760, 18108351, 264448, 264369, 264288, 264684, 264686, 55811957, 265021, 264692, 33657109, 263973, 55811576, 264635, 264555, 264556, 264557, 264558, 56182323, 264559, 87168518, 264563, 264482
2503	87878345 (5005, 5006)	Novel Protein sim. GBank gi 2198874 emb CAA72638 - (Y11896) BRX protein [Mus musculus]			264905, 264907, 264512, 265008, 265011, 18108351, 264448, 264288, 29148627, 264693, 18108370, 18108374, 18108385

2504	87868706 (5007, 5008)	Novel Protein sim. GBank gij550420[embjCAA48220] - (X68101) trg [Rattus norvegicus]			264488, 52644507, 52645156, 52646842, 22278994, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 264908, 264908, 52644045, 265009, 60433356, 33657402, 60433438, 264585, 33109854, 87188474, 265017, 265019, 264448, 264288, 264766, 52644229, 21906765, 21906766, 21906767, 21906768, 52644150, 264692, 27486261, 27486262, 27486264, 27486265, 35695763, 35698423, 35695855, 52644332, 58182323, 18108387, 87188518, 60432113, 22279002, 264564
2505	8760559 (5009, 5010)			UNCLASSIFIED	264605
2506	91232326 (5011, 5012)	Novel Protein sim. GBank gij2137562[pirj]49635 - mouse Dhml protein - mouse		nuclease	264488, 52644507, 52645156, 52646365, 65274572, 22278995, 56994075, 22278998, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 29331826, 29331828, 264509, 56182435, 264112, 264593, 60433356, 55812038, 21906754, 285011, 265017, 265018, 265019, 284605, 264762, 18108351, 284448, 264288, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 60170615, 33657023, 27486284, 18108379, 35695855, 264637, 83373044, 18108385, 87188518, 60432113, 22279000, 264563, 264482, 264585
2507	95316233 (5013, 5014)	Novel Protein sim. GBank gij5174489[refjNP_006035.1]pKIAA - histone deacetylase 6	Contains protein domain (PF00850) - Histone deacetylase family	histone	264488, 263994, 264592, 264585, 264359, 264886, 264768, 35695917, 35696423, 264563
2508	95315505 (5015, 5016)	Novel Protein sim. GBank gij4826433[embjCAB42889.1] - (AL031447) dJ126A5.2.1 (novel protein) (isoform 1) [Homo sapiens]		UNCLASSIFIED	22278995, 22278999, 60432049, 264259, 29331828, 265006, 265007, 60433438, 33657084, 265010, 265017, 265018, 265019, 18108351, 264448, 18108354, 284369, 18108359, 21906765, 21906769, 55811957, 265020, 265022, 27486281, 33657349, 18108377, 35695855, 60432113, 22279002, 264563, 264565
2509	87813741 (5017, 5018)	Novel Protein sim. GBank gij1263289 (U47856) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	285007, 285008, 18108357, 264556, 264567

2510	85421379 (5019, 5020)	Novel Protein sim. GBank gi 3293537 gb AAC25762.1 - (AF071059) zinc finger RNA binding protein [Mus musculus]		dna_ma_bind	65274572, 22278894, 22278996, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 33856970, 264908, 66712502, 265007, 264810, 60170831, 60432228, 60433356, 60433438, 21906754, 87168474, 265017, 265018, 284448, 284288, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265022, 264691, 33657023, 264693, 65274620, 33657109, 33657182, 27488262, 33657349, 18108370, 35695855, 264555, 56182323, 83373044, 60432113, 22279002, 265017, 21906764, 265020, 264692
2511	87384281 (5021, 5022)	Novel Protein sim. GBank gi 4323152 gb AAD16228.1 - (AF098863) Ets-protein Spl-C [Mus musculus]			
2512	88084771 (5023, 5024)	Novel Protein sim. GBank gi 4502075 ref NP_001135.1 pAMFR - autocrine motility factor receptor	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	transport	22278999, 264259, 29331825, 29331826, 29146498, 264907, 264908, 265006, 265008, 264591, 60432229, 21906754, 264763, 264863, 264766, 18108357, 264689, 21906769, 264693, 18108370, 263972, 18108374, 264558, 22279000
2513	95357843 (5025, 5026)	Novel Protein sim. GBank gi 3004657 (AF017777) - bobby sox [Drosophila melanogaster]		UNCLASSIFIED	60424179, 52845156, 18108394, 22278994, 35896286, 56994075, 22278996, 29331822, 29331824, 60424269, 29331825, 29331827, 33856970, 60431735, 33657084, 87168559, 265017, 264448, 264369, 56181562, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 33657023, 18108366, 33657109, 27486261, 27486262, 33657349, 18108374, 55810784, 35698423, 56182323, 264558, 18108385
2514	88094578 (5027, 5028)	Novel Protein sim. GBank gi 2258437 (AF008197) - syncoilin [Rattus norvegicus]		UNCLASSIFIED	264510
2515	87994509 (5029, 5030)	Novel Protein sim. GBank gi 3757727 emb CAA18783 - (AL022727) dJ80119.7 (olfactory receptor-like protein (hs6M1-3)) [Homo sapiens]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	- tm7	
2516	87786808 (5031, 5032)			UNCLASSIFIED	264259, 29146498, 264905, 264288, 29146829, 35695917, 27486281, 264634
2517	87784966 (5033, 5034)	Novel Protein sim. GBank gi 4220527 emb CAA23000 - (AL035358) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	264091, 29331824, 29331825, 29331826, 29331828, 35696052, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264511, 264910, 33657402, 264757, 33109954, 265017, 265018, 264605, 264760, 264762, 264763, 264766, 264768, 264769, 33657108, 33657182, 264628, 55811576, 35698423, 264631, 264634, 264637, 264638, 264639, 87168518, 22279002, 264564

2516	94147410 (5035, 5036)	Novel Protein sim. GBank gi 4928591 gb AAD34056.1 AF15181 - (AF151818) CGI-61 protein [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	UNCLASSIFIED	35696286, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 264907, 264909, 264511, 265007, 60432229, 60433356, 60433438, 55812038, 265010, 265017, 264448, 264288, 264689, 21906768, 21906769, 265022, 52844150, 264693, 18108370, 263972, 264555, 56182323, 83373044, 18108385, 60432113, 264088
2519	94326180 (5037, 5038)	Novel Protein sim. GBank gi 4263748 gb AAD15420 - (AC004883) similar to KIAA0766; similar to PID:g3882253 [Homo sapiens]		kinase	264259, 6671417, 29331826, 29331827, 29331828, 264907, 66712502, 265006, 265008, 264594, 265010, 265011, 265018, 264288, 21906769, 265020, 60431528, 55811576, 65274791, 264632, 264555, 264636, 22279002, 264564
2520	87413235 (5039, 5040)	Novel Protein sim. GBank gi 4826722 ref NP_005085.1 pFATP - fatty acid transport protein 4		transport	264259, 264908, 264910, 264682, 21906769, 265020, 264563
2521	95316244 (5041, 5042)	Novel Protein sim. GBank gi 5174489 ref NP_006035.1 pKIAA - histone deacetylase 6	Contains protein domain (PF00850) - Histone deacetylase family	histone	264488, 264489, 263984, 65274572, 22278995, 22278998, 264259, 29331822, 29331826, 264508, 264905, 264509, 264906, 264907, 66712502, 264511, 265008, 265007, 264591, 264592, 264593, 264594, 264595, 264596, 264681, 264448, 264763, 264682, 264764, 264684, 264369, 264288, 264685, 264686, 21906768, 55811957, 264692, 264693, 27486261, 18108370, 264628, 264629, 18108374, 55811576, 35696423, 35695855, 264632, 264558, 18108385, 65274727, 60432113, 264563, 264564, 264565, 264566, 264567
2522	87754052 (5043, 5044)	Novel Protein sim. GBank gi 4580011 gb AAD24201.1 U81002_ - (U81002) TRAF4 associated factor 1 [Homo sapiens]		transport	264489, 22278997, 20281171, 21908754, 35695917, 263987, 263976, 263981, 20281169
2523	95340467 (5045, 5046)				263969
2524	95340469 (5047, 5048)	Novel Protein sim. GBank gi 1809327 (U76374) - skm- BOP2 [Mus musculus]	Contains protein domain (PF01753) - MYND finger		56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 29331830, 56182435, 264512, 265008, 60170831, 33657402, 265010, 87168559, 265019, 264288, 21906765, 21908769, 35695917, 265020, 265021, 265022, 52644150, 264691, 33657023, 33657109, 27486281, 35696423, 65274791, 264559, 83373044, 56526486, 87168518, 264567

2525	94126928 (5049, 5050)	Novel Protein sim. GBank gi 2073564 (U80223) - eukaryotic initiation factor eIF-2 alpha kinase; DGCN2 [Drosophila melanogaster]		kinase	264488, 22278997, 22278999, 60432049, 60432289, 29331828, 264905, 265008, 55812038, 21906754, 265019, 264369, 21908765, 21906766, 21906767, 21906769, 35695917, 265020, 265021, 33857109, 60431528, 83373044, 60432113, 22279000, 22279002, 264585
2526	95289404 (5051, 5052)	Novel Protein sim. GBank gi 4589628 dbj BAA76836.1 - (AB023209) KIAA0992 protein [Homo sapiens]	Contains protein domain (PF00238) - Ribosomal protein L14	ribosomalprot	60424179, 264768, 264687, 264769, 264689, 65274572, 21908767, 56182575, 21906768, 21908769, 55811957, 22278994, 22278995, 35696286, 35695917, 22278998, 22278997, 265020, 22278998, 265021, 22278999, 265022, 264680, 264691, 60432049, 264259, 264097, 33857023, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 27486282, 264508, 264509, 264905, 264907, 18108370, 66712502, 60431528, 264828, 264909, 18108372, 18108374, 56182435, 18108376, 55810764, 55811576, 35696423, 35695855, 265006, 265007, 264512, 265008, 265009, 264634, 264635, 60431850, 264636, 264555, 264592, 60431735, 264638, 33857402, 56182323, 60433356, 60433438, 264595, 55812038, 264596, 264758, 83373044, 52648317, 18108385, 33857084, 18108387, 55811386, 65274727, 56526486, 87188518, 60432113, 265017, 22279000, 265018, 265019, 264564, 18108351, 264448, 264566, 264286, 264488, 264587, 264766
2527	88094580 (5053, 5054)	Novel Protein sim. GBank gi 2258437 (AF008197) - syncollin [Rattus norvegicus]		UNCLASSIFIED	264510, 284512, 284630, 284591, 264592, 264259, 284594, 284595, 284603, 284605, 18108351, 264565, 264369, 18108354
2528	88078380 (5055, 5056)	Novel Protein sim. GBank gi 2085766 (AC002086) - similar to zinc finger 5 protein from Gallus gallus, U51640 (PID:gi1399185) [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	dna_ma_bind	55812038, 265017, 264689, 35695917, 35695763, 60431528, 60432113, 22279002
2529	86670926 (5057, 5058)	Novel Protein sim. GBank gi 3786433 (AF098505) - similar to Arabidopsis thaliana male sterility protein 2 (SW:Q08891) [Caenorhabditis elegans]		synthase	264908, 264769, 265020, 265021, 18108383
2530	80259978 (5059, 5060)				264369, 264556
2531	87768931 (5061, 5062)			UNCLASSIFIED	26331822, 29331824, 60432289, 264508, 264509, 264908, 265011, 264769, 21906768, 33857023, 67168518, 22279000
2532	87419778 (5063, 5064)	Novel Protein sim. GBank gi 2864625 emb CAA16972 - (AL021811) putative protein [Arabidopsis thaliana]			264593
2533	87000255 (5065, 5066)	Novel Protein sim. GBank gi 437181 (U02289) - GTPase-activating protein [Caenorhabditis elegans]		UNCLASSIFIED	264535

2534	87332322 (5087, 5088)	Novel Protein sim. GBank gij3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]		UNCLASSIFIED	264259, 35696052, 264905, 265017, 21906769, 265020, 265022, 33657109, 22279000
2535	91225056 (5068, 5070)	Novel Protein sim. GBank gij4468311[emb]CAB37992] - (AL031432) dJ485N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]			65274572, 35696286, 60432289, 29331828, 66712502, 265006, 60432229, 265017, 265018, 265019, 264288, 264369, 264689, 21906768, 265020, 265021, 264636, 60170394, 22279002
2536	94218540 (5071, 5072)	Novel Protein sim. GBank gij728836[sp]P39193[ALU8_HUMAN - III] ALU SUBFAMILY SP WARNING ENTRY IIII	kinase		18108398, 56182575, 35696286, 22278997, 22278998, 60432049, 284259, 29331824, 29331826, 29331827, 29331828, 264905, 264511, 265009, 284910, 264596, 52646317, 18108351, 264681, 264683, 18108354, 264288, 264687, 264769, 264689, 21906765, 21906766, 21906767, 265021, 52645129, 33657109, 18108374, 18108380, 56182323, 18108381, 18108388, 87168518, 60432113, 22279000, 22279002, 264567, 18108391
2537	95422283 (5073, 5074)	Novel Protein sim. GBank gij4557026[ref]NP_003913.1[pHERC - guanine nucleotide exchange factor p532	ubiquitin		65274572, 35696286, 29331822, 29331825, 29331827, 29331828, 35696052, 264906, 66712502, 284909, 265008, 285011, 284760, 284288, 264685, 35695917, 60170615, 284691, 33657023, 65274620, 33657109, 18108374, 35696423, 35695855, 264636, 264558, 60170394, 56182323, 83373044
2538	36853454 (5075, 5076)			UNCLASSIFIED	
2539	94144916 (5077, 5078)			UNCLASSIFIED	22278996, 22278999, 29331822, 29331825, 29331828, 29146499, 264908, 264112, 60170831, 87168558, 264604, 265019, 264685, 264766, 87168518, 22279000, 264565, 264586
2540	94218545 (5079, 5080)	Novel Protein sim. GBank gij1362647[pir]S53876 - sex-regulated protein janus A - fruit fly (Drosophila pseudoobscura)		UNCLASSIFIED	22278997, 29331828, 265008, 265009, 264758, 265010, 18108351, 264683, 264288, 21906765, 35695917, 265020, 18108374, 264567
2541	95308238 (5081, 5082)	Novel Protein sim. GBank gij1711658[sp]P54797[T10_MOUSE - SER/THR-RICH PROTEIN T10 IN DGCR REGION		UNCLASSIFIED	264488, 264768, 264689, 264511, 20281171, 264634, 264635, 264691, 264639, 29331824, 264603, 264604, 264905, 264907, 264908, 264768

2542	95298162 (5083, 5084)	Novel Protein sim. GBank gil5225320 gb AAD40850.1 AF08310 - (AF083107) sirtuin type 2 [Homo sapiens]	Contains protein domain (PF00220) - Neurohypophysial hormones, N- terminal Domain	UNCLASSIFIED	264488, 18108384, 52846385, 52846842, 65274572, 22278994, 35898288, 22278996, 264259, 52845080, 29331822, 29331824, 29331827, 35898052, 33858970, 264907, 264909, 52844045, 284510, 265008, 284512, 265007, 265008, 265009, 264910, 60431735, 52846317, 52844288, 285010, 285011, 265018, 265019, 18108351, 284883, 284288, 284885, 284887, 52844229, 284789, 21908768, 21908767, 21908769, 52844150, 33857023, 33857109, 52845129, 33857182, 27488261, 27486264, 33857349, 35695763, 18108374, 35896423, 35895855, 284831, 264634, 264635, 284558, 83373044, 18108385, 18108387, 87168518, 264563, 284584
2543	94139088 (5085, 5086)	Novel Protein sim. GBank gil5419857 emb CAB46374.1 - (AL086723) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)		65274572, 56182575, 22278999, 264259, 29331828, 284907, 284510, 284511, 284592, 284595, 284784, 284389, 264288, 264884, 284786, 284889, 21908765, 21908767, 21908769, 60170815, 284692, 284693, 55811576, 65274791, 284636, 284556, 18108381, 60170394, 284639, 18108385, 60432113, 22279000
2544	94218549 (5087, 5088)	Novel Protein sim. GBank gil2498110 sp Q83191 AEGP_RAT - APICAL ENDOSOMAL GLYCOPROTEIN PRECURSOR	Contains protein domain (PF00529) - MAM domain.	glycoprotein	18108397, 52846385, 22278997, 264259, 60432049, 29331822, 29331825, 29331826, 29331827, 29331828, 284905, 284908, 265006, 265007, 265008, 87168559, 285017, 285018, 265019, 18108351, 284448, 284888, 284887, 284889, 21908765, 265020, 265021, 18108370, 18108374, 18108376, 18108381, 18108385, 18108387, 58526488, 22279000, 284482, 264563, 264567
2545	87742845 (5089, 5090)	Novel Protein sim. GBank gil3327046 dbj BAA31591 - (AB014516) KIAA0816 protein [Homo sapiens]			29331825, 264906, 265009, 60170831, 285017, 264389, 21908767, 60170815, 284892, 33857109
2546	88093861 (5091, 5092)	Novel Protein sim. GBank gil2996032 (AF054586) - brain finger protein [Rattus norvegicus]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	29331824, 285007, 22279002

2547	84143869 (5093, 5094)	Novel Protein sim. GBank gil4929607 gb AAD34084.1 AF15182 - (AF151827) CGI-69 protein [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	- transport	264488, 18108394, 52646842, 18108397, 56182575, 22278995, 56994075, 22278998, 22278997, 22278999, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 35698052, 29331828, 264104, 264508, 264905, 264906, 264908, 66712502, 264909, 56182435, 265006, 265007, 264512, 265008, 265009, 80170831, 60432228, 60431735, 264594, 60433438, 21906754, 52646317, 265010, 265011, 264600, 264601, 265018, 265019, 264760, 18108351, 264682, 264448, 264288, 264369, 264684, 264886, 264687, 56181562, 264688, 264689, 21906765, 21906766, 21906767, 21906768, 29148627, 21906769, 55811957, 265020, 265021, 265022, 264690, 264691, 18108362, 264692, 264693, 27488261, 18108370, 18108374, 55810764, 55811576, 35698423, 35695855, 264635, 264636, 264555, 264637, 263981, 264557, 18108380, 264638, 56182323, 264558, 264559, 83373044, 18108385, 87188518, 22279002, 264564, 264566, 264486
2548	88179079 (5085, 5096)			UNCLASSIFIED	264488, 18108394, 52646365, 22278994, 35698286, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 56182435, 264511, 265007, 264512, 60433356, 87188559, 264684, 264369, 52644229, 265021, 33657023, 264692, 18108374, 52644332, 264557, 18108380, 18108381, 18108382, 18108384, 18108385, 60432113, 22279000, 22279002, 264563, 264567
2549	94196893 (5097, 5098)	Novel Protein sim. GBank gil728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	Contains protein domain (PF00412) - LIM domain containing proteins	- struct	56182575, 22278998, 22278997, 22278998, 22278999, 264259, 264508, 264908, 29331830, 265009, 265010, 265018, 264688, 21906764, 21906765, 21906766, 21906767, 21906769, 265020, 265021, 52644150, 264691, 18108368, 60431602, 18108376, 35698423, 56182323, 18108387, 264567
2550	87778584 (5089, 5100)	Novel Protein sim. GBank gil2143886 pir 52523 - nucleoporin p62 homolog - rat (fragment)		UNCLASSIFIED	56182575, 29331822, 264105, 264512, 18108351, 35695917, 264637, 264638

2551	95308400 (5101, 5102)	Novel Protein sim. GBank gi 4337103 gb AAD18079 - (AF129756) NG28 [Homo sapiens]	Contains protein domain (PF00561) - alpha/beta hydrolase fold	UNCLASSIFIED	18108396, 65274572, 22278995, 22278998, 22278999, 284259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 284905, 58182435, 265007, 60433438, 55812038, 21906754, 65274444, 265017, 265018, 264605, 265019, 264288, 21906766, 21906768, 21906769, 265020, 60170615, 264693, 33657109, 35698423, 264638, 58182323, 83373044, 22279000
2552	95332620 (5103, 5104)			UNCLASSIFIED	58182575, 35696286, 29331824, 29331826, 35696052, 29331828, 284508, 264907, 58182435, 265006, 264591, 33109954, 264760, 55811857, 35695917, 33657023, 33657109, 18108374, 55811576, 35698423, 35695855, 58182323, 264558
2553	95308243 (5105, 5106)	Novel Protein sim. GBank gi 1711658 sp P54797 T10_MOUSE - SER/THR-RICH PROTEIN T10 IN DGCR REGION		UNCLASSIFIED	264686, 264488, 263976, 264768, 29331826, 35698052, 35698423, 284601, 284511, 284602, 284910, 284634, 264780, 284555, 264762, 264906, 264592, 264691, 264566, 264908, 264684, 264567, 264909, 264768
2554	87761520 (5107, 5108)	Novel Protein sim. GBank gi 728835 sp P39182 ALU5_HUMAN - IIII ALU SUBFAMILY SC WARNING ENTRY IIII		cadherin	22278997, 29331822, 284508, 21906769, 33657023, 33657109, 58182323
2555	87627551 (5109, 5110)	Novel Protein sim. GBank gi 4884319 emb CAB43260.1 - (AL050084) hypothetical protein [Homo sapiens]		nuclease	29331824, 263972
2556	87645533 (5111, 5112)	Novel Protein sim. GBank gi 4106984 (AC003038) - R30923_1 [Homo sapiens]	Contains protein domain (PF00514) - Armadillo/beta-catenin-like repeats	UNCLASSIFIED	22278998, 264509, 33657402, 264683, 264684, 264766, 264689, 33657023, 33657109, 35695855, 284558, 284567
2557	78437803 (5113, 5114)				284595
2558	87617591 (5115, 5116)	Novel Protein sim. GBank gi 119110 sp P0321 EBN1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	22278997, 29331824, 66714117, 29331825, 284906, 264511, 265018, 264448
2559	86096382 (5117, 5118)	Novel Protein sim. GBank gi 4539998 emb CAB39819.1 - (AL049481) AIG1-like protein [Arabidopsis thaliana]		UNCLASSIFIED	22278997, 29331822, 29331828, 60433356, 265011, 284288, 264765, 264766, 264769, 21908765, 21908766, 60432113, 264482
2560	87994530 (5119, 5120)	Novel Protein sim. GBank gi 5051399 emb CAB44995.1 - (AL078630) 573K1.3 (mm17M1-4 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor LIKE) protein)) [Mus musculus]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)		
2561	88176575 (5121, 5122)	Novel Protein sim. GBank gi 5326825 gb AAD42056.1 AF04495 - (AF044953) NADH:ubiquinone oxidoreductase PGIV subunit [Homo sapiens]		UNCLASSIFIED	22278995, 35698286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 265007, 60432229, 87188559, 265017, 265018, 265019, 264689, 21906768, 21906769, 35695917, 265020, 33657023, 33657109, 18108374, 264634, 284559, 18108385, 87188518, 22279002

2562	87645539 (5123, 5124)	Novel Protein sim. GBank gi 4106984 (AC003038) - R30923_1 [Homo sapiens]		UNCLASSIFIED	56994075, 22278996, 22278997, 22278999, 264259, 29331822, 60432289, 33657402, 60433356, 21906765, 55811957, 60170615, 33657023, 264693, 35695855, 87168518, 264488, 35696286, 22278999, 264259, 29331822, 29331824, 35696052, 264508, 264907, 264908, 264909, 52844045, 264510, 264511, 265009, 264910, 264591, 264593, 33657402, 265017, 265018, 265019, 18108351, 264686, 21906767, 21906768, 55811957, 35695917, 265020, 264691, 264693, 27486262, 264628, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264636, 264638, 18108384, 87168518, 22279000, 22279002, 264482, 264563, 264565, 264566, 264486, 29331822, 265007, 265010, 265019, 264769, 55811576, 56182323
2563	88095497 (5125, 5126)	Novel Protein sim. GBank gi 4886447[emb][CAB43371.1] - (AL050270) hypothetical protein [Homo sapiens]		UNCLASSIFIED	
2564	80502783 (5127, 5128)	Novel Protein sim. GBank gi 1352944[sp P47179 YJ9P_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DALS INTERGENIC REGION PRECURSOR		sulfotransferase	
2565	85530908 (5129, 5130)			UNCLASSIFIED	66714117, 264909, 263978, 264632
2566	80224956 (5131, 5132)	Novel Protein sim. GBank gi 628012[pir A53933 - myosin I myr 4 - rat	Contains protein domain (PF00063) - struct		18108370, 35695855, 264556, 264558, 18108383
2567	86143590 (5133, 5134)				265020, 60170615
2568	91233099 (5135, 5136)	Novel Protein sim. GBank gi 466009[sp P34548 YNUJ4_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN R10E11.4 IN CHROMOSOME III		synthase	60424179, 18108394, 56181686, 56994075, 22278998, 264490, 264259, 29331822, 56182181, 29331824, 60424269, 29331825, 29331826, 29331828, 264509, 29331830, 265007, 265008, 265009, 33657402, 265010, 265011, 265019, 264448, 264683, 264286, 18108354, 264769, 21906766, 21906767, 35695917, 265021, 33657023, 18108362, 33657109, 33657182, 35695763, 60431528, 55810764, 18108379, 83373044, 18108385, 60432113, 264482

2568	95313764 (5137, 5138)	Novel Protein sim. GBank gi 2598560 gb AAB84166.1 - (AF028674) basic leucine zipper protein LZIP [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	transcriptfactor	18108394, 56182575, 56181886, 22278995, 22278998, 56984075, 35696286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 56182181, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264905, 284908, 56182435, 265008, 265009, 264910, 60432229, 264592, 60433356, 60433438, 21908754, 87168559, 265017, 265018, 265019, 264682, 264448, 264288, 21908765, 21908768, 21908767, 21908768, 29148627, 21908769, 35695917, 265021, 265022, 52844150, 264690, 264691, 264692, 264693, 65274620, 263967, 35695763, 20281089, 263974, 18108374, 55810764, 35698423, 35695855, 264558, 18108381, 56182323, 18108382, 83373044, 18108385, 56526486, 87168518, 22278000, 22279002, 264566
2570	84136754 (5139, 5140)	Novel Protein sim. GBank gi 4758954 ref NP_004567.1 pPPP2 - protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	Contains protein domain (PF01240) - Protein phosphatase 2A regulatory subunit PR55	phosphatase	22278996, 29331822, 29331824, 66714117, 29331825, 60432289, 29331827, 35696052, 264907, 264510, 265007, 265009, 264758, 33109954, 265019, 264688, 264689, 265020, 265021, 264691, 264692, 264693, 18108374, 35695855, 264634, 56182323, 264639, 60170394, 83373044, 22279002, 264482
2571	87733750 (5141, 5142)	Novel Protein sim. GBank gi 732218 sp P34609 YO60_CAEEL - HYPOTHETICAL 128.6 KD PROTEIN ZK1098.10 IN CHROMOSOME III		struct	264508, 264905, 284907, 264828, 18108351, 264555, 264556, 264557, 264558, 264559
2572	87627560 (5143, 5144)	Novel Protein sim. GBank gi 4884319 emb CAB43260.1 - (AL050084) hypothetical protein [Homo sapiens]		UNCLASSIFIED	35696286, 29331827, 35696052, 264100, 264104, 264110, 264592, 21908754, 29148627, 29148629, 263972, 263974, 18108374, 263976, 35695855, 60170394, 264559, 18108385

2573	95313929 (5145, 5146)	Novel Protein sim. GBank gi 399138 sp P02745 C1QA_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, A CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain		26488, 60424179, 65274572, 56182575, 56181886, 22278995, 56994075, 22278997, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 264104, 264107, 264508, 264906, 29331830, 264909, 264510, 265006, 264512, 265008, 265009, 264910, 264591, 264592, 60432228, 264583, 60433356, 264584, 60433438, 264585, 55812038, 264759, 21906754, 87188474, 265010, 265011, 87188559, 265017, 265018, 265019, 264781, 264782, 264763, 264764, 264369, 264288, 264685, 264766, 264686, 264687, 264688, 264769, 56181562, 264689, 21906765, 21906768, 21906767, 29148627, 21906768, 21906769, 265020, 265021, 265022, 60170815, 264690, 52644150, 264691, 264692, 33657023, 65274620, 18108365, 18108368, 27488265, 60431602, 264629, 60431528, 263976, 65274791, 35695855, 20281071, 60431850, 264637, 264638, 264558, 264639, 58182323, 60170394, 83373044, 18108384, 87188518, 60432113, 264482, 264364, 264565, 264566, 264567, 22278995, 264259, 60432289, 29331827, 29331828, 33658970, 264908, 265008, 264910, 264591, 33657402, 265018, 265019, 264448, 264764, 264369, 264288, 18108357, 21906765, 21908768, 21908768, 55811857, 60170815, 264691, 33657023, 264693, 33657109, 33657182, 27488281, 27488264, 33657349, 264636, 264555, 83373044, 18108385, 264482
2574	94746814 (5147, 5148)	Novel Protein sim. GBank gi 3334982 (AC005306) - R27216_1 [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	UNCLASSIFIED	
2575	87754408 (5149, 5150)	Novel Protein sim. GBank gi 4929729 gb AAD34125.1 AF15188 - (AF151888) CGI-130 protein [Homo sapiens]		UNCLASSIFIED	
2576	95357881 (5151, 5152)	Novel Protein sim. GBank gi 4680681 gb AAD27730.1 AF13295 - (AF132955) CGI-21 protein [Homo sapiens]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	264259, 35696052, 264806, 60433438, 264681, 18108351, 264288, 52644150, 264628, 35898423
2577	86996621 (5153, 5154)	Novel Protein sim. GBank gi 4337103 gb AAD18079 - (AF129758) NG28 [Homo sapiens]		UNCLASSIFIED	29331825, 265018, 265019, 264685
2578	87786941 (5155, 5156)			UNCLASSIFIED	264488, 264906, 264908, 264910, 264596, 264603, 264604, 264605, 264766, 21906769, 264628, 264630, 264634, 264638, 264563
2579	87292879 (5157, 5158)			UNCLASSIFIED	29331822, 29331824, 264767

2580	88166788 (5159, 5160)	Novel Protein sim. GBank gi 2588628 (AC003080) - Similar to KIAA0299; 60% similarity to AB002297 (PID:g2224539) [Homo sapiens]			265007, 265018, 264762
2581	87899048 (5161, 5162)	Novel Protein sim. GBank gi 4406642[gb AAD20049] - (AF131809) Unknown [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	collagen	56994075, 29331824, 29331826, 29331828, 264905, 60433356, 80433438, 264758, 87188559, 21908769, 265022, 35695855, 263981
2582	87786789 (5163, 5164)	Novel Protein sim. GBank gi 2739367 (AC002505) - putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]		eph	264488, 264907, 264908, 264910, 264764, 264684, 264766, 264636, 264555, 264565
2583	91220850 (5165, 5166)	Novel Protein sim. GBank gi 4378112[emb CAA16521.1] - (AL021578) dJ453C12.2 (similar to transcription factor RBP-L) [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	transcript factor	56181686, 264259, 264510, 264512, 264591, 264592, 264593, 264594, 264595, 264596, 264603, 264629, 55810764, 264630, 264637, 264565
2584	80430941 (5167, 5168)			UNCLASSIFIED	264908, 264910, 264768, 264693, 18108374, 55811576, 56182323
2585	80436126 (5169, 5170)	Novel Protein sim. GBank gi 2736151 (AF021935) - myotonic dystrophy kinase-related Cdc42-binding kinase [Rattus norvegicus]		kinase	264768
2586	91226136 (5171, 5172)				22278998, 264259, 29331822, 29331824, 29331827, 29331828, 264908, 265007, 265009, 264591, 60433356, 33657402, 265018, 264762, 264288, 21908766, 21908767, 21908769, 265022, 264691, 83373044, 58528486, 22279002
2587	80430943 (5173, 5174)				264908, 265018, 264768, 264693, 55811576, 56182323
2588	80074385 (5175, 5176)			UNCLASSIFIED	264584
2589	85515607 (5177, 5178)	Novel Protein sim. GBank gi 3021598[emb CAA71415] - (Y10389) nuclear protein [Xenopus laevis]		UNCLASSIFIED	35696052, 264905, 264906, 264907, 264908, 264909, 265009, 265018, 264769, 35698423, 264636
2590	87054526 (5179, 5180)	Novel Protein sim. GBank gi 2104688 (U92793) - alpha glucosidase II, alpha subunit [Mus musculus]	Contains protein domain (PF01055) - Glycosyl hydrolases family 31	glucoamylase	22278995, 29331830, 265008, 265010, 265017, 264639
2591	94192167 (5181, 5182)	Novel Protein sim. GBank gi 5702202[gb AAD47199.1]AF12916 - (AF129166) long-chain acyl-CoA synthetase 5 [Homo sapiens]		eph	264259, 29331822, 264106, 264906, 56182435, 265007, 265008, 33109954, 264448, 55811957, 265020, 18108370, 55811576, 22279002

2592	95332648 (5183, 5184)	Novel Protein sim. GBank gil3024988 sp O60936 YAB1_MOUSE - HYPOTHETICAL HEART PROTEIN		transport	18108397, 56182575, 35696286, 56994075, 264259, 29331822, 29331824, 29331828, 60432288, 29331827, 29331828, 264906, 264908, 265007, 265008, 264910, 60432228, 264594, 60433356, 60433438, 55812038, 18108348, 21906754, 265011, 87168559, 265017, 265019, 264764, 264369, 264288, 264766, 265021, 60170615, 33657023, 33657109, 264629, 35696423, 35695855, 264557, 264638, 60170394, 58182323, 83373044, 56526488, 87168518, 264563, 264482, 264585
2593	87754416 (5185, 5186)	Novel Protein sim. GBank gil4929729 gb AAD34125.1 AF15188 - (AF151888) CGI-130 protein [Homo sapiens]	tm7		22278999, 29331825, 264758, 21906754, 52646317, 265010, 18108351, 264288, 264369, 21906768, 264693, 18108370, 264637, 264638, 264482
2594	95305758 (5187, 5188)	Novel Protein sim. GBank gil4929587 gb AAD34054.1 AF15181 - (AF151817) CGI-59 protein [Homo sapiens]	UNCLASSIFIED		264488, 18108398, 58182575, 35696286, 22278997, 264093, 264259, 29331822, 29331825, 66714117, 29331826, 264905, 264909, 52644045, 58182435, 264510, 264512, 265007, 264757, 21906754, 87168474, 265017, 264760, 264448, 264764, 264288, 264766, 264689, 21906768, 33657109, 263975, 263977, 264634, 264556, 60170394, 58182323, 56526488, 264482, 264563, 264564, 264586, 264567
2595	79561676 (5189, 5190)		UNCLASSIFIED		264692
2596	87538537 (5191, 5192)	Novel Protein sim. GBank gil4309681 gb AAD15478 - (AC006930) R33423.1 [Homo sapiens]	UNCLASSIFIED		22278999, 264259, 265018, 264448, 265021, 60431528
2597	94784089 (5193, 5194)		UNCLASSIFIED		264905, 264509, 264908, 264762, 264768, 35695917, 35695855, 264635, 264636, 83373044, 264486
2598	88084948 (5195, 5196)	Novel Protein sim. GBank gil1001351 db BAA10838 - (D64008) hypothetical protein [Synechocystis sp.]	UNCLASSIFIED		22278998, 264259, 29331824, 87168474, 264683, 21906766, 35695917, 264691, 33657023, 33657109, 18108370, 18108374, 264564, 264585
2599	87842889 (5197, 5198)	Novel Protein sim. GBank gil3941737 (AF109719) - BAT2 [Mus musculus]	MHC		264766, 264769, 21906768, 33657182, 35695763, 18108370, 18108374, 264635, 264636, 56526488, 22279000, 264568
2600	87787846 (5199, 5200)	Novel Protein sim. GBank gil4263521 gb AAD15347 - (AC004044) putative WD-repeat protein [Arabidopsis thaliana]	kinasereceptor	Contains protein domain (PF00400) - WD domain, G-beta repeat	35696286, 264093, 264288, 21906769, 35696423, 35695855

2601	91243070 (5201, 5202)	Novel Protein sim. GBank gi 728837 sp P39184 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	56182575, 22278999, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 264906, 265007, 265008, 264591, 60433356, 33657402, 60433438, 21906754, 265011, 265018, 265019, 18108351, 264448, 264369, 21906769, 265020, 60170815, 284693, 33857109, 18108370, 18108376, 58182323, 18108381, 18108385, 22279002, 264563 60433438, 21906754, 87168559, 264601, 264369, 264288, 21906767
2602	88180022 (5203, 5204)	Novel Protein sim. GBank gi 4406632 gb AAD20047 - (AF131801) Unknown [Homo sapiens]			
2603	94325821 (5205, 5206)	Novel Protein sim. GBank gi 3122387 sp Q61211 LIGA_MOUSE - LIGATIN		UNCLASSIFIED	284488, 65274572, 22278995, 22278996, 58994075, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35696052, 58182435, 264113, 265008, 265009, 60433356, 264757, 60433438, 264759, 33857084, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264683, 18108354, 264288, 264767, 264689, 21906765, 21906768, 21906767, 21906768, 21906769, 55811857, 265020, 265021, 265022, 60170615, 264691, 33657023, 264693, 33857109, 27486262, 18108374, 35698423, 85274791, 35695855, 264555, 264636, 264637, 58182323, 83373044, 58526486, 87168518, 60432113, 22279000
2604	94676601 (5207, 5208)	Novel Protein sim. GBank gi 5454030 ref NP_008468.1 pRRP2 - RAS-related on chromosome 22		oncogene	264259, 35696052, 264508, 264906, 264907, 264908, 264909, 264510, 264512, 265008, 264910, 33657402, 264604, 264605, 264762, 264763, 264682, 264764, 264683, 264768, 264769, 264689, 33657023, 264693, 18108365, 264628, 35698423, 264631, 264632, 264634, 264635, 264637, 18108381, 264639, 83373044, 264565
2605	94316756 (5209, 5210)	Novel Protein sim. GBank gi 3628745 db BAA33366 - (AB013721) mitsugumin 23 [Oryctolagus cuniculus]		UNCLASSIFIED	22278998, 264490, 60432049, 264259, 60432289, 264909, 265008, 60433356, 60433438, 264758, 21906754, 265010, 265011, 265018, 264681, 18108351, 264288, 264766, 264685, 21906765, 21906766, 21906768, 21906769, 264691, 264692, 264693, 85274791, 264634, 264555, 264636, 22278996, 264510, 264512, 265009, 264768, 22279002, 264566
2606	87748406 (5211, 5212)				

2607	87627742 (5213, 5214)	Novel Protein sim. GBank gi 4826826 gb AAD30202.1 - (AF135022) mediator [Homo sapiens]			29331822, 29331825, 29331826, 29331827, 29331828, 264906, 264907, 264908, 66712502, 264828, 56182435, 55812038, 265010, 265017, 265018, 265019, 264788, 264889, 21908785, 55811957, 265020, 265022, 264892, 33857023, 264693, 33857109, 18108370, 264839, 56182323, 264509, 264907, 264908, 264592, 264758, 264631
2608	81734786 (5215, 5216)	Novel Protein sim. GBank gi 2226005 (U49973) - ORF2: function unknown [Homo sapiens]			264488, 65274572, 35696286, 22278997, 22278999, 60432049, 264259, 56182181, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264905, 264907, 60433356, 60433438, 55812038, 265011, 87168559, 265017, 265018, 264448, 264765, 264288, 264766, 264689, 21908785, 21908767, 21906769, 265020, 265021, 264691, 264892, 33857109, 27488261, 18108370, 65274791, 264636, 264556, 56182323, 18108385, 56526486
2609	94843791 (5217, 5218)	Novel Protein sim. GBank gi 3024889 sp P56524 Y288_HUMAN - HYPOTHETICAL PROTEIN KIAA0288 (HA6116)	Contains protein domain (PF00850) - Histone deacetylase family	histone	18108394, 22278994, 56994075, 60432049, 264259, 29331822, 29331825, 60432289, 29331827, 264107, 264109, 264905, 56182435, 264112, 265008, 265007, 265008, 265009, 60433356, 60433438, 265011, 87168559, 265017, 264448, 264882, 264764, 264288, 265021, 33857023, 263987, 33657182, 27486261, 18108374, 263976, 55811576, 264638, 87168518, 60432113, 22278999, 265017, 264684, 21908768, 22278000
2610	88177654 (5219, 5220)	Novel Protein sim. GBank gi 4338855 gb AAD17989 - (AF106473) leucine-rich-domain inter-acting protein 1; LeR inter-acting protein 1; LEAP1 [Mus musculus]		transcription factor	265009, 264910, 264759, 265017, 21908767, 18108385, 18108388, 60432113
2611	87428890 (5221, 5222)	Novel Protein sim. GBank gi 3876761 emb CAA92994 - (Z68760) predicted using GeneFinder. Similarly to Mouse FK506-binding protein (SW:FKB3_MOUSE) [Caenorhabditis elegans]	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	isomerase	264685
2612	87771198 (5223, 5224)	Novel Protein sim. GBank gi 5679138 gb AAD46874.1 AF16093 - (AF160834) BcDNA.LD14189 [Drosophila melanogaster]		transport	265009, 264910, 264759, 265017, 21908767, 18108385, 18108388, 60432113
2613	79481496 (5225, 5226)	Novel Protein sim. GBank gi 5533081 gb AAD45009.1 AF16118 - (AF161181) P55T protein [Mus musculus]	Contains protein domain (PF00625) - Guanylate kinase	UNCLASSIFIED	264685
2614	87643948 (5227, 5228)				22278998, 22278999, 29331825, 264508, 264906, 21908754, 264602, 264788, 264789, 52844229, 21908785, 33857109, 27488264, 18108370, 263972, 264555, 60432113
2615	87381988 (5229, 5230)			UNCLASSIFIED	264768, 18108394, 264692, 264693, 264508, 264509, 264907, 264628, 264908, 264909, 18108377, 264511, 264512, 264810, 264635, 264585, 265010, 264404, 264563, 264784, 264685, 264768

2816	87428895 (5231, 5232)	Novel Protein sim. GBank gi 3876761 emb CAA92994 - (Z68760) predicted using GeneFinder; Similarity to Mouse FKBP-type peptidyl-prolyl cis-trans isomerases	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	isomerase	22278995, 22278997, 22278998, 60432048, 60432289, 264828, 60433356, 264594, 60433438, 33109954, 87188474, 265011, 265017, 265019, 264288, 264766, 21906765, 21908787, 265020, 265021, 18108378, 18108377, 18108387, 87168518, 264482, 264567
2817	88976888 (5233, 5234)	Novel Protein sim. GBank gi 728831 sp P39189 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		kinase	265010, 265019, 264369, 264693, 55811576, 22279002
2818	91231662 (5235, 5236)	Novel Protein sim. GBank gi 3318282 (AF049103) - Huntingtin interacting protein [Homo sapiens]	Contains protein domain (PF00397) - WW domain	UNCLASSIFIED	284489, 22278996, 264490, 264259, 29331822, 264102, 264509, 264908, 264907, 66712502, 29331830, 265008, 264910, 265009, 60433356, 60433438, 264758, 21906754, 265011, 87168559, 265017, 265018, 264369, 264288, 264766, 264768, 264689, 21906765, 21906766, 21906787, 35695917, 265020, 265022, 33657023, 264692, 33657108, 264628, 18108374, 35695855, 18108381, 83373044, 18108385, 18108388, 56526486, 264563
2819	87694000 (5237, 5238)	Novel Protein sim. GBank gi 2431772 (U86411) - putative type III alcohol dehydrogenase [Drosophila melanogaster]	Contains protein domain (PF00465) - Iron-containing alcohol dehydrogenases	dehydrogenase	264259, 60432289, 60433438, 21906754, 264369, 80432113, 264568
2820	95314841 (5239, 5240)	Novel Protein sim. GBank gi 4322567 gb AAD16097 - (AF090438) dachshund variant 1 [Mus musculus]	Contains protein domain (PF00628) - PHD-finger	UNCLASSIFIED	52644507, 52645156, 52646842, 65274572, 22278995, 56994075, 35698286, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331828, 35698052, 264907, 66712502, 265008, 60433356, 33657402, 52646317, 21906754, 87168474, 265010, 265017, 265018, 264448, 264369, 264288, 264687, 264768, 52644228, 264688, 264689, 21906765, 21906768, 35695917, 52644150, 264692, 33657109, 35695783, 35698423, 264556, 52644332, 18108382, 83373044, 18108385, 18108387, 65274727, 87168518, 60432113, 22279002
2821	80253495 (5241, 5242)				264594, 264638
2822	61780390 (5243, 5244)	Novel Protein sim. GBank gi 4557341 ref NP_001174.1 pATP6 - ATPase, H ⁺ transporting, lysosomal subunit 1; vacuolar proton pump; H-ATPase subunit			284488, 264908, 264907, 264908, 264512, 265007, 264758, 35695917, 264634, 264636, 264563, 264462
2823	91639306 (5245, 5246)	Novel Protein sim. GBank gi 3880355 emb CAB05299 - (Z62285) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	29331824, 35696052, 265007, 265010, 264288, 29148629

2624	81639308 (5247, 5248)	Novel Protein sim. GBank gi 3880355 emb CAB05299 - (Z82285) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	56181688, 22278996, 22278997, 22278998, 22278999, 284259, 29331822, 29331824, 56182181, 29331825, 60432289, 29331828, 35698052, 29146499, 66712502, 52644045, 285007, 265008, 60433356, 33109954, 21908754, 265010, 265011, 265019, 264448, 284288, 21908785, 21908766, 21906767, 29148629, 35695917, 265021, 265022, 27486265, 18108370, 60431528, 55811576, 35695855, 56182323, 18108385, 87168518, 22279002, 18108391
2625	86452068 (5249, 5250)	Novel Protein sim. GBank gi 2887429 dbj BAA24857 - (AB007887) KIAA0427 [Homo sapiens]		UNCLASSIFIED	264091, 284511, 263981
2626	16533797 (5251, 5252)	Novel Protein sim. GBank gi 487416 (L20302) - actin filament protein [Gallus gallus]		struct	265008
2627	87636823 (5253, 5254)	Novel Protein sim. GBank gi 88462 pir J27307 - proline-rich phosphoprotein (gene PRH1, Db allele) - human		UNCLASSIFIED	22278996, 265007, 265009, 264448, 21908767, 265021, 264558, 87168518
2628	94848254 (5255, 5256)	Novel Protein sim. GBank gi 3123552 emb CAA18609 - (AL022578) dJ393P12.2 (hypothetical Proline-rich protein KIAA0269 LIKE) [Homo sapiens]		UNCLASSIFIED	22278997, 22278999, 284259, 60432048, 29331822, 29331824, 29331825, 29331827, 35698052, 29331828, 284907, 284909, 265008, 264591, 60433356, 60433438, 265010, 265017, 265018, 264369, 264288, 18108357, 21908765, 21908768, 265022, 65274791, 264638, 18108387, 87168518, 22279002
2629	87376490 (5257, 5258)	Novel Protein sim. GBank gi 4929595 gb AAD34058.1 AF15182 - (AF151821) CGI-83 protein [Homo sapiens]		synthase	29331825, 29331826, 264102, 265006, 264766, 35695917, 264691, 33657023, 263972, 18108374, 22279000
2630	79188384 (5259, 5260)			UNCLASSIFIED	264636, 18108385
2631	94845909 (5261, 5262)	Novel Protein sim. GBank gi 321605 pir JQ1161 - Gag protein - Visna virus (strain EV1)	Contains protein domain (PF00098) - Zinc finger, CCHC class	UNCLASSIFIED - dna_rna_bind	52644507, 52645156, 52646365, 52646842, 22278994, 22278995, 35696286, 56994075, 22278997, 22278999, 284259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 284905, 284509, 284907, 264908, 264511, 284512, 265007, 265008, 264910, 52646317, 33657084, 52644296, 265010, 87168559, 265017, 265018, 265019, 264760, 264762, 264448, 284288, 284369, 284768, 264768, 52644229, 21906764, 21906765, 21906766, 21908767, 21908769, 35695917, 265020, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 35695763, 35696423, 65274791, 35695855, 264634, 264637, 52644332, 56182323, 60432113, 264566, 264486
2632	36730414 (5263, 5264)				284685

2633	95011617 (5265, 5266)	Novel Protein sim. GBank gi 139548 dbj BAA10889 - (D84006) seizure-related gene product 6 type 2 precursor [Mus musculus]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)		22278995, 22278997, 22278998, 264259, 29331822, 29331824, 29331825, 29331827, 264508, 284908, 265008, 265007, 265008, 265009, 55812038, 33657084, 55811388, 265010, 265011, 87168559, 265018, 265019, 284883, 284288, 284886, 29148829, 33657023, 284693, 33657182, 35895763, 55811578, 284639, 56182323, 83373044, 18108385, 58528486, 87168518, 22279000, 22279002, 284585
2634	87330821 (5267, 5268)	Novel Protein sim. GBank gi 544161 emb CAB46854.1 - (AJ388555) hypothetical protein [Canis familiaris]	UNCLASSIFIED		29331826, 263972, 264089
2635	86623144 (5269, 5270)	Novel Protein sim. GBank gi 4680663 gb AAD2721.1 AF13284 - (AF132946) CGI-12 protein [Homo sapiens]			22278997, 284259, 29331824, 66714117, 29331827, 29331828, 284907, 33657084, 265017, 265018, 284448, 284288, 21906766, 21906767, 21906768, 29148829, 18108376, 55811576, 35895855, 87168518, 22279000, 264589, 29331822, 29331828, 265008, 60170831, 284681, 284765, 264685, 29148627, 21906769, 29148784, 265022, 60170815, 284635, 18108385, 56528486, 22279002, 284567
2636	87260534 (5271, 5272)	Novel Protein sim. GBank gi 3879146 emb CAB07846 - (Z93386) Similarly to Yeast hypothetical 52.9 KD protein (SW:P43816); cDNA EST EMBL:M89432 comes from this gene; cDNA EST EMBL:D71008 comes from this gene; cDNA EST EMBL:D73578 comes from this gene; cDNA EST EMBL:D69025 comes ...	Contains protein domain (PF01546) - Peptidase family M20/M25/M40		264488, 264489, 52644507, 264887, 52646365, 52646842, 22278994, 22278998, 22278999, 20281171, 264259, 29331822, 52645080, 66714117, 29331825, 29331826, 29331827, 35896052, 29331828, 29146498, 284508, 284905, 284908, 284907, 284908, 284909, 284511, 284512, 284910, 284591, 264592, 60432229, 264593, 264594, 33657402, 60433356, 264757, 60433438, 264596, 264758, 52846317, 21906754, 52844296, 285010, 284600, 284602, 284603, 284605, 284761, 284762, 284681, 284448, 264784, 284765, 284288, 284786, 284688, 284788, 284687, 284789, 21906765, 21906766, 21906767, 21906768, 21906769, 35895917, 285021, 60170815, 284691, 33657023, 264692, 264693, 65274620, 27486264, 18108370, 284628, 284629, 18108374, 35896423, 35895855, 264632, 264634, 264635, 284637, 264638, 52844332, 264639, 284558, 83373044, 60432113, 264584, 264585, 264586, 284486, 264567
2637	95011299 (5273, 5274)	Novel Protein sim. GBank gi 4758208 ref NP_004081.1 pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase catalytic domain	phosphatase	

2638	94326733 (5275, 5276)	Novel Protein sim. GBank gi 4929889 gb AAD34105.1 AF15186 - (AF151868) CGI-110 protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	60424179, 52644507, 52648842, 18108398, 58182575, 22278995, 22278998, 35898288, 22278997, 22278999, 284259, 60432049, 29331822, 60424269, 29331828, 35898052, 29146498, 284905, 52644045, 58182435, 60433358, 33857402, 55812038, 55811388, 265019, 284288, 284769, 52644228, 58181562, 29148827, 29148829, 55811957, 29148784, 35895917, 265021, 52644150, 33857023, 65274620, 33857109, 35895763, 18108374, 55810784, 35898423, 55811578, 35895855, 60431850, 58182323, 60432113, 264404
2639	95361348 (5277, 5278)	Novel Protein sim. GBank gi 2190007 dbj BAA20355 - (AB004109) phosphatidylserine synthase II [Cricetus griseus]		synthase	284488, 29331825, 35898052, 264508, 264509, 284909, 284512, 33857402, 60433438, 284758, 85858542, 284600, 285020, 265021, 33857109, 284628, 35898423, 284555, 284639, 284563, 284584, 264565, 284568, 264488
2640	87781330 (5279, 5280)	Novel Protein sim. GBank gi 3158516 (AF067617) - contains similarity to chromo (chromatin organization modifier) domains (Pfam: chromo.hmm. score: 17.78 and 27.94) and to helicases conserved C-terminal domain (Pfam: helicase_C.hmm. score: 67.00) [Caenorhabditis elegans]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	29331822, 29331826, 284906, 33109954, 265017, 265019, 21906788, 35895763, 284636, 284637, 18108387
2641	11689834 (5281, 5282)			UNCLASSIFIED	264828
2642	87412575 (5283, 5284)	Novel Protein sim. GBank gi 2584955 (AF030001) - unknown [Mus musculus]		UNCLASSIFIED	284259, 29331822, 33857402, 265019, 284369, 284691, 284634, 56526488, 22279002
2643	87643961 (5285, 5286)	Novel Protein sim. GBank gi 4490304 emb CAC38795.1 - (AL035678) putative protein [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	22278997, 264259, 29148499, 58182435, 264910, 265010, 18108351, 284682, 284683, 284369, 284684, 264685, 264686, 29148827, 284690, 33857109, 18108370, 263973, 18108374, 264634, 264557, 284558, 18108385, 264482
2644	88177671 (5287, 5288)	Novel Protein sim. GBank gi 3789797 gb AAC67502.1 - (AF059569) actin binding protein MAYVEN [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	nuc_recpt	284107, 264687
2645	17277228 (5289, 5290)			UNCLASSIFIED	265007
2646	94148542 (5291, 5292)	Novel Protein sim. GBank gi 1706722 sp P49749 EVX2_MOUSE - HOMEBOX EVEN SKIPPED HOMOLOG PROTEIN 2 (EVX-2)		UNCLASSIFIED	264908, 264687, 284632, 83373044

2847	91212878 (5283, 5284)				UNCLASSIFIED	56182575, 22278998, 35896286, 22278998, 264259, 29331822, 56182181, 29331825, 60424269, 60432289, 35896052, 66712502, 264908, 265007, 55812038, 33109954, 21908754, 33657084, 265019, 264448, 264288, 56181562, 21908765, 21908768, 21908768, 21908768, 35895917, 265020, 265021, 52644150, 264693, 33657109, 33657349, 60431528, 18108374, 55810764, 35896423, 56182323, 60432113, 22279002, 264584
2848	87600587 (5295, 5296)					29148498, 58182435, 33109854, 265011, 264682, 55811957, 35895917, 264690, 263978, 18108377, 35896423, 60432113
2849	94128783 (5287, 5288)	Novel Protein sim. GBank gij3041852 (AC004539) - unknown function; similar to Y09105 (PID:g1666171) [Homo sapiens]			UNCLASSIFIED	56182575, 35896286, 22278998, 29331824, 29331828, 60432289, 66712502, 56182435, 60170831, 60432229, 33657402, 33109954, 21908754, 265017, 264688, 264688, 21908765, 21908768, 60170815, 264693, 263987, 18108370, 263976, 60170394, 60432113, 22279002, 264583
2850	87297533 (5289, 5300)	Novel Protein sim. GBank gij360271 [dbj BAA81908.1] - (AB029335) HRPET-3 [Halocynthia roretzi]				264685
2851	88088745 (5301, 5302)	Novel Protein sim. GBank gij4240225 [dbj BAA74891.1] - (AB020675) KIAA0868 protein [Homo sapiens]	Contains protein domain (PF00054) - Laminin G domain		synthase	29331824, 29331826, 29331827, 265007, 55812038, 21908754, 18108366, 18108384, 22279002, 264587
2852	10343125 (5303, 5304)	Novel Protein sim. GBank gij4493956 [embj CAB11123.2] - (Z88551) predicted using hexExon; MAL3P6.28			UNCLASSIFIED	264692
2853	87798735 (5305, 5308)	(PFC0845c), Hypothetical protein, len: 167 aa; Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S.cerevisiae & S.pombe). C.elegans protein ZK287.5 (TR....			UNCLASSIFIED	265016, 18108370, 18108387, 264586
2854	95103240 (5307, 5308)					60424179, 65274572, 56182575, 264259, 56182181, 264908, 56182435, 55811957, 35895917, 265021, 263976, 55810764, 65274791, 56182323, 83373044, 65274727
2855	91228018 (5309, 5310)	Novel Protein sim. GBank gij3875272 [embj CAB02861] - (Z81051) predicted using GeneFinder; similar to Zinc finger, C3HC4 type (RING finger); cDNA EST yk443h5.3 comes from this gene; cDNA EST yk443h5.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)		transcriptfactor	56182575, 56181866, 264092, 264259, 56182181, 60432289, 264907, 33657402, 55812038, 21908754, 87168559, 265017, 264448, 264369, 264288, 21908765, 21908768, 21908767, 21908768, 33657109, 18108370, 264628, 55811576, 264558, 264639, 83373044, 56526486, 264404, 60432113
2856	84562601 (5311, 5312)	Novel Protein sim. GBank gij3043718 [dbj BAA25523] - (AB011189) KIAA0597 protein [Homo sapiens]				264693

2657	52561728 (5313, 5314)	Novel Protein sim. GBank gi 5689509 dbj BAA83038.1 - (AB029009) KIAA1086 protein [Homo sapiens]			dna_rna_bind	264693
2658	88062454 (5315, 5316)	Novel Protein sim. GBank gi 3688089 (AC005757) - R32611_1 [Homo sapiens]		Contains protein domain (PF00580) - Leucine Rich Repeat	nucleaseinhib	35696286, 264259, 29331822, 29331824, 29331828, 29331828, 265018, 264683, 21906768, 35695917, 264683, 35695855, 264637, 87168518, 264486, 264567
2659	87600755 (5317, 5318)	Novel Protein sim. GBank gi 5420387 emb CAB46878.1 - (AJ243459) proteophosphoglycan [Leishmania major]		Contains protein domain (PF01426) - BAH domain	UNCLASSIFIED	284909, 264910, 265018, 264369, 264769, 21906769, 264693, 263972, 18108388
2660	91718472 (5319, 5320)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		Contains protein domain (PF00036) - EF hand	kinase	264488, 65274572, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331828, 35696052, 264908, 56182435, 265008, 265009, 60433356, 264594, 265010, 265018, 55811150, 18108351, 264682, 264684, 264369, 264288, 264687, 21906765, 29148784, 35695917, 60170615, 52644150, 33657023, 33657109, 35696423, 35695855, 264556, 60170394, 18108385, 22279000, 22278002
2661	95342817 (5321, 5322)	Novel Protein sim. GBank gi 4758048 ref NP_004739.1 pCPR8 - cell cycle progression 8 protein			glycoprotein	60432049, 264259, 29331824, 29331825, 29331828, 29331827, 29331828, 264908, 264909, 264593, 33109854, 265010, 265017, 265018, 265019, 264760, 264448, 264369, 264288, 21906765, 21906768, 265022, 264691, 33657023, 27486282, 60431528, 18108374, 35695855, 18108388, 264482
2662	80228739 (5323, 5324)	Novel Protein sim. GBank gi 3874714 emb CAA91263 - (Z68484) similar to choline dehydrogenase; cDNA EST yk346d5.5 comes from this gene; cDNA EST yk346d5.3 comes from this gene [Caenorhabditis elegans]				264555, 264556, 264558, 264486
2663	87780623 (5325, 5326)	Novel Protein sim. GBank gi 1389670 (U58977) - Notch homolog Scalloped wings [Lucilia cuprina]			dehydrogenase	264906, 264909, 264757, 264758, 264767, 264691, 33657023, 264638
2664	85518329 (5327, 5328)	Novel Protein sim. GBank gi 1389670 (U58977) - Notch homolog Scalloped wings [Lucilia cuprina]		Contains protein domain (PF00008) - EGF-like domain	oncogene	35696286, 264509, 264595, 264288, 264685, 264686
2665	87770662 (5329, 5330)	Novel Protein sim. GBank gi 4884406 emb CAB43311.1 - (AL050190) hypothetical protein [Homo sapiens]			UNCLASSIFIED	35696286, 22278999, 29331822, 35696052, 264906, 264907, 264909, 264510, 264511, 264512, 264593, 60433438, 265019, 264681, 21906765, 21906768, 21908767, 21906768, 265020, 265022, 35696423, 35695855, 22279002, 264482, 264488
2666	87826472 (5331, 5332)	Novel Protein sim. GBank gi 5106956 gb AAD39906.1 AF11361 - (AF113615) FH1/FH2 domain-containing protein FHOS [Homo sapiens]			UNCLASSIFIED	29331825, 265007, 264910, 60432229, 265019, 264288, 21906767, 264558, 22279002
2667	87422720 (5333, 5334)	Novel Protein sim. GBank gi 2500570 sp Q17533 RNPH_CAEEL - RIBONUCLEASE PH-LIKE PROTEIN B0564.1		Contains protein domain (PF01138) - 3' exoribonuclease family	nuclease	264907, 29331830, 264681, 264683, 264288, 35695855, 264632, 264556, 264557, 264558, 264559, 264563, 264565, 264567

2668	91216716 (5335, 5336)	Novel Protein sim. GBank gi 5454188 ref NP_006327.1 pZYG - ZYG homolog		UNCLASSIFIED	56181686, 35696286, 22278998, 22278999, 56182181, 29331824, 60424289, 29331825, 35696052, 29331828, 66712502, 56182435, 60433356, 284758, 21908754, 55811386, 265011, 87168559, 265017, 265019, 55811150, 284448, 284369, 284288, 21906765, 21908768, 21908768, 55811957, 35695917, 265020, 265021, 33657023, 284692, 33657109, 35695763, 60431528, 18108374, 35698423, 55811576, 284634, 60431850, 83373044, 18108385, 87168518, 22279000, 264583, 264584
2669	95415721 (5337, 5338)	Novel Protein sim. GBank gi 2147012 pir JC4898 - proline rich protein - rat			264488, 264688, 21906767, 65274572, 56182575, 21906768, 29148627, 21906769, 29148628, 35696286, 35695917, 22278998, 22278998, 265021, 265022, 60170615, 52844150, 60432049, 284259, 284691, 33657023, 284692, 29331822, 29331824, 29331825, 60432288, 33657109, 29331826, 29331827, 35696052, 29331828, 29148488, 29148499, 264905, 264908, 52844045, 284909, 56182435, 35698423, 65274791, 35695855, 265008, 284910, 284635, 60432229, 284592, 284638, 56182323, 60433356, 60170394, 60433438, 284559, 264595, 55812038, 33109954, 87168559, 60432113, 265018, 264448, 264369, 264684, 264288
2670	87613234 (5339, 5340)	Novel Protein sim. GBank gi 1723523 sp Q10382 YDBB_SCHPO - HYPOTHETICAL 94.9 KD PROTEIN C22E12.11C IN CHROMOSOME I	Contains protein domain (PF00628) - PHD-finger		18108370, 263974
2671	91214836 (5341, 5342)	Novel Protein sim. GBank gi 4768277 gb AAD28444.1 AF06425 - (AF06425) very long-chain acyl-CoA synthetase homolog 2: VLCS-H2 [Homo sapiens]		transport	52846842, 56994075, 264259, 29331822, 29331824, 29331825, 29331827, 33658970, 284509, 265008, 33109954, 21906754, 264682, 264288, 265021, 33657023, 33657109, 33657182, 27486261, 27486282, 27486285, 18108376, 18108385
2672	87399123 (5343, 5344)	Novel Protein sim. GBank gi 4966346 gb AAD34677.1 AC00834 - (AC00834.1) Contains two PF01344 Kelch motif domains. [Arabidopsis thaliana]	Contains protein domain (PF01344) - Kelch motif	UNCLASSIFIED	264767

2673	87430749 (5345, 5346)	Novel Protein sim. GBank gi 5457337 emb CAB41505.2 - (AJ236876) poly(ADP-ribose) polymerase-2 (Homo sapiens)	Contains protein domain (PF00644) - Poly(ADP-ribose) polymerase catalytic region.	22278995, 22278996, 22278997, 22278999, 29331822, 29331824, 29331828, 35896052, 60433438, 87168474, 87188559, 285017, 265018, 265019, 264448, 21908768, 21908769, 265020, 265021, 33657109, 27486262, 35895763, 60431850, 60170394, 87168518, 284563
2674	94847721 (5347, 5348)	Novel Protein sim. GBank gi 4758824 ref NP_004280.1 pNRF3 - nuclear factor (erythroid-derived 2)-like 3	Contains protein domain (PF00170) - bZIP transcription factor	264488, 22278996, 35896286, 264091, 264259, 29331824, 29331828, 35896052, 264511, 55812038, 85858542, 264766, 21908765, 35895917, 264629, 35896423, 18108383, 87168518
2675	79563835 (5349, 5350)		UNCLASSIFIED	264691
2676	79828393 (5351, 5352)		UNCLASSIFIED	264806, 265008
2677	94329800 (5353, 5354)	Novel Protein sim. GBank gi 1079042 pir S52154 - acetyl-CoA synthetase - fruit fly (Drosophila melanogaster)	Contains protein domain (PF00501) - AMP-binding enzyme	18108384, 85274572, 56182575, 22278994, 22278995, 56994075, 22278996, 35896288, 22278997, 22278999, 264490, 264259, 52845080, 29331824, 29331825, 60432289, 29331827, 29331828, 35896052, 29146499, 29331830, 284908, 52844045, 265006, 265007, 265008, 265009, 60432229, 60433356, 60433438, 55812038, 265010, 265011, 87168559, 265017, 265019, 18108351, 264682, 264448, 264683, 264288, 21908765, 21908766, 21908767, 21908768, 21908769, 55811957, 265020, 265021, 60170615, 52644150, 264691, 33657023, 263967, 33857109, 27486264, 27486265, 33657349, 35895763, 18108370, 18108374, 18108377, 55811576, 35896423, 35895855, 83373044, 18108387, 22279000, 22279002, 264584

2678	95001694 (5355, 5356)	Novel Protein sim. GBank gi 86760 pir A40465 - alanine transaminase (EC 2.6.1.2). cytosolic - human		UNCLASSIFIED	264488, 263984, 264489, 18108394, 52646842, 35698286, 22278999, 264259, 29331825, 35698052, 264508, 264905, 284509, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265008, 264593, 264594, 264596, 264758, 33109954, 52646317, 21908754, 265010, 265011, 87188559, 264600, 264601, 264602, 264603, 265017, 265019, 264605, 264760, 264762, 18108351, 264763, 264682, 264683, 264764, 264288, 264766, 264687, 264768, 264769, 264689, 21908765, 21908767, 35695917, 265020, 265021, 52644150, 264691, 33657023, 264693, 18108384, 18108385, 33657109, 33657349, 264628, 18108374, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 18108385, 264563, 264584, 264585, 264586, 264488, 264587
2679	95361544 (5357, 5358)	Novel Protein sim. GBank gi 1709233 sp P07514 NC5R_BOVIN - NADH-CYTOCHROME B5 REDUCTASE	Contains protein domain (PF00970) - FAD/NAD-binding Cytochrome reductase	reductase	264488, 22278996, 35696286, 264259, 29331828, 29331827, 29331828, 264909, 56182435, 264113, 264511, 265008, 60433438, 264758, 85658542, 87168474, 265011, 265017, 265019, 264288, 21908766, 21908767, 21908768, 21908769, 55811957, 265021, 264690, 33657023, 55810764, 35696423, 55811576, 264631, 18108381, 60170394, 83373044, 87188518, 264588
2680	87800356 (5359, 5360)	Novel Protein sim. GBank gi 4589604 db BAA76824.1 - (AB023197) KIAA0980 protein [Homo sapiens]	Contains protein domain (PF00036) - EF hand	struct	264259, 264102, 264905, 264908, 265007, 265008, 33109954, 265011, 18108351, 264768, 33657023, 20281149, 263972, 264630, 264635, 264638
2681	90933844 (5361, 5362)	Novel Protein sim. GBank gi 728637 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	264489, 22278995, 264508, 264905, 264806, 284907, 264908, 264909, 264510, 265008, 284512, 264910, 264594, 60433438, 264758, 264803, 264604, 265019, 264605, 264760, 264764, 264887, 264768, 264769, 21908769, 35695917, 265020, 33657023, 264631, 264635, 264637, 264638, 264639, 264488
2682	94138934 (5363, 5364)	Novel Protein sim. GBank gi 423468 pir JQ1974 - HTF9-C protein - mouse	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	35696288, 264908, 55811386, 265017, 55811150, 55811957, 35695917, 60431528, 55810764, 55811576, 35696423, 65274791, 56528486
2683	87774405 (5365, 5366)	Novel Protein sim. GBank gi 5114351 gb AAD40286.1 - (AF156271) RING finger protein terf [Homo sapiens]	Contains protein domain (PF00622) - SPRY domain	interleukinrecept	264909, 264759, 264635, 264638

2684	85787151 (5367, 5368)	Novel Protein sim. GBank gi 4886469 emb CAB43385.1 - (AL050284) hypothetical protein [Homo sapiens]			264593
2685	88054289 (5369, 5370)	Novel Protein sim. GBank gi 3342728 (AC005331) - R31341_2 [Homo sapiens]		UNCLASSIFIED	
2686	87628680 (5371, 5372)	Novel Protein sim. GBank gi 4650844 db BAA77027.1 - (AB026190) Kelch motif containing protein [Homo sapiens]	Contains protein domain (PF01344) - Kelch motif	struct	264259, 29331822, 60432289, 29331827, 29331830, 264909, 264512, 264598, 264769, 264534, 264555, 264556, 264557, 264558, 60170394, 264559, 264486
2687	87698183 (5373, 5374)	Novel Protein sim. GBank gi 5281314 gb AAD41475.1 AF13312 - (AF133123) transcription factor IIC102 [Homo sapiens]	Contains protein domain (PF00515) - TPR Domain	transcriptfactor	18108384, 18108396, 22278998, 35696286, 22278997, 29331826, 29331828, 66712502, 21908754, 265011, 264760, 264761, 264763, 264689, 21908765, 35698423, 264559, 18108385, 264563
2688	79959584 (5375, 5376)				264908, 264760
2689	94122440 (5377, 5378)	Novel Protein sim. GBank gi 3880023 emb CAA87339 - (Z73098) Similarity to yeast hypothetical protein (Swiss Prot accession number Q09095); cDNA EST EMBL:D72982 comes from this gene; cDNA EST EMBL:D75947 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00560) - Leucine Rich Repeat		22278997, 22278998, 22278999, 29331824, 35696052, 264908, 264908, 56182435, 264512, 264910, 265009, 60433438, 21908754, 18108351, 264682, 264683, 264767, 21908765, 21908766, 21908768, 33657023, 33857182, 27486282, 27486284, 33657349, 18108370, 18108372, 18108374, 35696423, 35695855, 18108385, 22279002
2690	88003055 (5379, 5380)	Novel Protein sim. GBank gi 2477513 (AC002398) - F25965_3 [Homo sapiens]	Contains protein domain (PF00620) - RhoGAP domain	struct	
2691	91219241 (5381, 5382)	Novel Protein sim. GBank gi 4107276 emb CAA67130 - (X98506) acetyl-CoA synthetase [Solanum tuberosum]		synthase	65274572, 56182575, 264259, 29331822, 29331824, 29331826, 29331828, 264112, 265009, 55812038, 264598, 33109954, 265017, 264448, 264288, 264389, 264684, 21908769, 60170615, 60431528, 55810764, 264634, 264636, 264556, 264637, 22279002, 264564, 264568
2692	94111914 (5383, 5384)	Novel Protein sim. GBank gi 3513303 (AC005594) - R26984_1 [Homo sapiens]	Contains protein domain (PF00326) - Prolyl oligopeptidase family	peptidase	
2693	20438807 (5385, 5386)			UNCLASSIFIED	264592
2694	94111918 (5387, 5388)	Novel Protein sim. GBank gi 3122400 sp O35682 MUG_MOUSE - MYELOID UPREGULATED PROTEIN			264559
2695	95345513 (5389, 5390)	Novel Protein sim. GBank gi 4972740 gb AAD34765.1 - (AF132177) unknown [Drosophila melanogaster]		collagen	35696286, 56994075, 22278999, 264259, 35696052, 29331830, 265011, 264288, 56181562, 264680, 264682, 33857023, 27486282, 263976, 18108376, 35698423, 35695855, 60170394, 83373044, 56526486, 22279000, 22279002, 264568
2696	87674040 (5391, 5392)	Novel Protein sim. GBank gi 728631 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		synthase	264594, 21908768, 18108370, 18108372

2697	91638472 (5383, 5394)	Novel Protein sim. GBank gi 5689473 dbj BAA83020.1 - (AB028991) KIAA1088 protein [Homo sapiens]		UNCLASSIFIED	35686286, 284259, 29331824, 29331825, 29331826, 29331827, 29331828, 35686052, 265008, 265007, 264512, 265009, 60170831, 60433356, 264595, 264758, 57168474, 265010, 265011, 87168558, 264601, 265017, 265018, 265019, 264781, 18108351, 284448, 264288, 264768, 264688, 264689, 21908765, 21908768, 265020, 265021, 60170815, 33857109, 18108376, 35698423, 35695855, 264555, 264556, 60170394, 264559, 18108387, 56526486, 87188518, 22279002, 264563, 264482
2698	94325891 (5395, 5396)	Novel Protein sim. GBank gi 841318 (U22818) - mutant sterol regulatory element binding protein-2 [Cricetulus griseus]	Contains protein domain (PF00412) - LIM domain containing proteins	transcriptfactor	22278995, 35686288, 22278996, 22278997, 22278998, 22278999, 264258, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 33856870, 264806, 28331830, 284908, 52844045, 284910, 60433356, 33857402, 33109954, 265017, 265018, 265019, 264288, 21908765, 21908766, 21908767, 21908769, 29148629, 35695917, 265021, 265022, 52844150, 33857023, 33857182, 27488261, 35698423, 65274791, 264638, 60432113, 22279000
2699	87780850 (5397, 5398)			UNCLASSIFIED	264768, 18108357, 264690, 264691
2700	94139838 (5399, 5400)	Novel Protein sim. GBank gi 5174395 ref NP_006006.1 pB120 - Brain protein 120		UNCLASSIFIED	60424268, 56182435, 60432229, 60433438, 55811386, 265017, 55811150, 264448, 56181582, 55811957, 264693, 33857109, 60431528, 264629, 55810784, 55811576, 65274791, 60431850, 60432113
2701	94148584 (5401, 5402)	Novel Protein sim. GBank gi 1572801 (U70854) - F38A5.1 gene product [Caenorhabditis elegans]			18108394, 52045158, 35698288, 284259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 29148499, 265008, 60433356, 33857402, 60433438, 264595, 33857084, 18108351, 264288, 264769, 18108359, 21908768, 35695917, 33857023, 27486261, 18108374, 18108379, 35698423, 18108382, 83373044, 18108384, 18108388, 60432113, 22279000
2702	57295368 (5403, 5404)	Novel Protein sim. GBank gi 2605967 (AF030027) - 24 [Equine herpesvirus 4]		UNCLASSIFIED	29331828, 264512, 264555, 264556, 264557, 264558, 264559
2703	87649514 (5405, 5406)	Novel Protein sim. GBank gi 5689399 dbj BAA82983.1 - (AB028954) KIAA1031 protein [Homo sapiens]	Contains protein domain (PF00642) - Zinc finger C-x8-C-x5-C-x3-H type (and similar).		60432288, 265007, 21906765, 21906768, 265021, 264563

2704	87849515 (5407, 5408)	Novel Protein sim. GBank gi 4335894 gb AAB63284 - (AF008554) Implantation-associated protein [Rattus norvegicus]			264488, 22278995, 22278996, 29331828, 29146499, 264905, 264806, 264807, 52644045, 264511, 33657402, 264800, 264802, 265017, 264805, 264761, 18108351, 264764, 264887, 264769, 265021, 264691, 264892, 18108382, 264693, 18108370, 18108374, 264634, 264635
2705	87771745 (5408, 5410)				264489, 264509, 264511, 264512, 264910, 264593, 87168474, 264604, 264288, 264687, 264769, 264638, 264586, 264486
2706	94326789 (5411, 5412)	Novel Protein sim. GBank gi 3255952 emb CAA16821.1 - (AL021728) /prediction=(method:: /match=(desc: [Drosophila melanogaster])	UNCLASSIFIED		264488, 52646842, 65274572, 22278994, 58994075, 22278997, 264259, 29331824, 29331825, 29331826, 29331828, 33856970, 264907, 264908, 264909, 52644045, 56162435, 265006, 265007, 60433438, 55812038, 21908754, 52644298, 265010, 264601, 265017, 265018, 264681, 264448, 264682, 264288, 264686, 264687, 264688, 21906766, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 264690, 264691, 33657023, 264692, 264693, 65274620, 27486284, 263972, 18108374, 18108377, 264635, 264636, 264556, 60170394, 83373044, 65274727, 87168518, 22279000, 22278996, 22278998, 56182435, 21906754, 87168559, 265017, 264448, 52645129
2707	88099839 (5413, 5414)	Novel Protein sim. GBank gi 3417294 (AC004381) - Unknown gene product [Homo sapiens]			65274572, 264259, 29331822, 29331825, 60432289, 29331826, 29331827, 29331828, 264909, 264510, 265007, 264910, 60433356, 60433438, 33109854, 265010, 265011, 284369, 264288, 264765, 264693, 264585
2708	91011351 (5415, 5416)	Novel Protein sim. GBank gi 545790 bbs 147178 - DARPP-32=dopamine and cAMP-regulated phosphoprotein [human, brain, Peptide, 204 aa]	UNCLASSIFIED		29331822, 18108370, 18108374, 83373044
2709	94853988 (5417, 5418)	Novel Protein sim. GBank gi 3169705 (AC004780) - F17127_1 [Homo sapiens]	UNCLASSIFIED		29331824, 264759, 264693, 18108382, 18108386
2710	87627979 (5419, 5420)	Novel Protein sim. GBank gi 4468311 emb CAB37992 - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]			

2711	94111920 (5421, 5422)	Novel Protein sim. GBank gi 3122400 sp O35882 MUG_MOUSE - MYELOID UPREGULATED PROTEIN		UNCLASSIFIED	284488, 264687, 52645156, 264769, 21908784, 21908785, 21908767, 21908768, 21908789, 55811957, 56994075, 22278997, 22278998, 265020, 265021, 284690, 284258, 264691, 264692, 33657023, 29331822, 29331824, 60424269, 29331826, 33657182, 29331827, 27486262, 33657349, 264508, 264905, 264907, 60431528, 284908, 284909, 55810764, 35898423, 65274791, 35695855, 265007, 284910, 60431850, 60432228, 264557, 264558, 55812038, 33108954, 18108385, 21908754, 33657084, 87188518, 87188474, 87188559, 60432113, 265017, 22279000, 265018, 265019, 22279002, 264760, 55811150, 264681, 18108351, 264585, 264764, 264588, 264288, 264768 264488, 35898288, 22278998, 264259, 29331824, 60432289, 35898052, 264508, 264908, 66712502, 52644045, 265006, 60432229, 33657402, 60433356, 265010, 265019, 18108351, 264681, 264288, 264685, 21908785, 21908768, 21908768, 21908769, 55811957, 35895917, 265020, 265021, 60170815, 284691, 284692, 33657023, 33657109, 33657182, 33657349, 18108370, 18108374, 35898423, 35895855, 264555, 52644332, 58182323, 87188518, 60432113 66714117, 264908, 284563
2712	94312071 (5423, 5424)	Novel Protein sim. GBank gi 5081315 gb AAD39343.1 AF07660 - (AF076607) prediabetic NOD sera-reactive autoantigen [Mus musculus]	Contains protein domain (PF00515) - TPR Domain	transferase	
2713	88003064 (5425, 5426)	Novel Protein sim. GBank gi 2477513 (AC002398) - F25985_3 [Homo sapiens]		UNCLASSIFIED	
2714	13528218 (5427, 5428)			UNCLASSIFIED	264636
2715	94122454 (5429, 5430)	Novel Protein sim. GBank gi 4321868 gb AAD1597 - (AF067430) Smarca1-related protein [Mus musculus]		UNCLASSIFIED	264508, 264905, 264907, 264908, 264909, 264910, 264758, 265011, 264760, 264784, 284288, 264786, 284786, 264636
2716	88003068 (5431, 5432)	Novel Protein sim. GBank gi 2477513 (AC002398) - F25985_3 [Homo sapiens]		glycoprotein	264081, 264259, 29331822, 66714117, 264908, 264369, 284693, 284556, 264563
2717	80077461 (5433, 5434)	Novel Protein sim. GBank gi 3327046 dbj BAA31591 - (AB014516) KIAA0816 protein [Homo sapiens]			264593, 264556
2718	78604062 (5435, 5436)				264693
2719	88180423 (5437, 5438)	Novel Protein sim. GBank gi 746495 (U23515) - weakly similar to gastrula zinc finger protein [Caenorhabditis elegans]		UNCLASSIFIED	29331822, 87188559, 265019, 265021, 52644150, 264891

2720	95086242 (5439, 5440)	Novel Protein sim. GBank gi 1335873 (U46690) - ATP-dependent RNA helicase [Mus musculus]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	18108374, 60424179, 264489, 56182435, 21906765, 21906766, 35696423, 22278997, 265020, 265022, 265006, 265008, 264082, 264636, 60432229, 264691, 264692, 33657023, 264693, 33657402, 83373044, 29331824, 18108366, 60424268, 29331826, 18108385, 52645129, 21906754, 35696052, 29331828, 87168474, 264100, 265010, 265011, 265019, 22278002, 264905, 264482, 264563, 264906, 18108351, 264681, 18108370, 28331830, 264908, 66712502, 52644045, 264909, 264828, 18108354, 22278995, 35696286, 264259, 29331822, 29331824, 66714117, 29331826, 264906, 60433438, 265017, 18108351, 264448, 264288, 264769, 21906768, 265021, 33657109, 263969, 60431528, 264629, 55811576, 65274791, 35695855, 264631, 264637, 60170394, 56182323, 22279000, 35696286, 22278999, 21906754, 265017, 264762, 264288, 21906765, 21906767, 21906768, 35695917, 18108362, 27486262, 35695855, 264558, 264559
2721	95345523 (5441, 5442)	Novel Protein sim. GBank gi 4929663 gb AAD34092.1 AF15185 - (AF151855) CGI-97 protein [Homo sapiens]	Contains protein domain (PF01172) - Uncharacterized protein family UPF0023		
2722	91638807 (5443, 5444)	Novel Protein sim. GBank gi 3212997 gb AAC23434.1 - (AC004997) match to ESTs AA667999 (NID:g2526700), AA165465 (NID:g1741481), Z45871 (NID:g575105), and T84026 (NID:g712314); similar to various tre-like proteins including: AF040654 (PID:g2746883), D13644 (PID:g2104571), AL02114...	Contains protein domain (PF00566) - TBC domain	oncogene	
2723	87387732 (5445, 5446)			UNCLASSIFIED	264508, 264509, 264906, 264908, 264910, 55812038, 264766, 264687, 264629, 264636, 264488
2724	87638563 (5447, 5448)	Novel Protein sim. GBank gi 4680881 gb AAD27730.1 AF13295 - (AF132855) CGI-21 protein [Homo sapiens]		ubiquitin	18108396, 22278999, 20281099, 29331824, 29331826, 60432289, 28331828, 60170831, 60432228, 60433438, 18108351, 264682, 21906766, 21906767, 21906769, 35695917, 33657023, 33657109, 18108372, 18108374, 35695855, 22279000, 22279002
2725	94853891 (5449, 5450)	Novel Protein sim. GBank gi 3169705 (AC004780) - F17127_1 [Homo sapiens]		UNCLASSIFIED	264488, 52644507, 264259, 29331827, 21906754, 265011, 18108351, 264448, 264288, 264685, 264689, 35695917, 265020, 33657182, 27486261, 18108370, 18108374, 35696423, 18108385, 22279000
2726	88880599 (5451, 5452)	Novel Protein sim. GBank gi 3342738 (AC005328) - R26660_1, partial CDS [Homo sapiens]		MHC	264488, 264628, 264685

2727	91010470 (5453, 5454)	Novel Protein sim. GBank gi 731267 sp P39219 RLUA_ECOLI - RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE A (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE)	Contains protein domain (PF00848) - synthase RNA pseudouridyate synthase	65274572, 56182575, 22278994, 56994075, 22278998, 22278997, 22278999, 60432049, 29331822, 29331824, 66714117, 29331826, 29331827, 35696052, 29331828, 33656970, 284509, 66712502, 284910, 33657402, 60433438, 264758, 55812038, 21906754, 33657084, 55811386, 265018, 265019, 284767, 21906765, 21906767, 21906769, 55811957, 35695917, 52644150, 33657023, 33657108, 33657182, 27486261, 27486282, 27486285, 33657349, 55811576, 35696423, 35695855, 284630, 60431850, 284636, 58182323, 87168518, 60432113, 22278000, 284564, 284565
2728	94126022 (5455, 5456)	Novel Protein sim. GBank gi 3880433 emb CAA91399 - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	18108394, 56182435, 21906767, 55811957, 35695855, 285021, 284690, 284558, 284259, 284557, 29331822, 284559, 284448, 284288
2729	94126024 (5457, 5458)	Novel Protein sim. GBank gi 2408095 emb CAB16300 - (Z69168) putative RNA splicing protein [Schizosaccharomyces pombe]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	65274572, 284259, 60432288, 66712502, 56182435, 284448, 284288, 284389, 55811957, 285021, 284557, 60432113
2730	94126026 (5459, 5460)	Novel Protein sim. GBank gi 3880433 emb CAA91399 - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - transport Mitochondrial carrier proteins	284887, 29331824, 29331826, 35698052, 284107, 56182435, 285008, 265009, 284592, 60431735, 285011, 284601, 265017, 18108351, 284288, 28148627, 55811957, 265021, 284690, 18108368, 18108374, 284557, 284558, 284559, 18108387, 56528486, 284566, 284486
2731	87723022 (5461, 5462)	Novel Protein sim. GBank gi 1723239 sp Q10166 YAUB_SCHPO - HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I	Contains protein domain (PF00795) - Carbon-nitrogen hydrolase	284259, 35696052, 285008, 284758, 284762, 284448, 284288, 29148627, 21906769, 87168518, 22279002
2732	94126028 (5463, 5464)	Novel Protein sim. GBank gi 3880433 emb CAA91399 - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	284887, 284489, 18108358, 56182435, 284689, 35696423, 55811957, 265021, 265006, 265008, 264910, 265009, 284680, 284555, 284259, 284556, 284557, 284558, 284559, 18108383, 33657109, 87168518, 265010, 284601, 60432113, 265017, 264805, 284448, 263972, 284368, 284567
2733	87363060 (5465, 5466)		UNCLASSIFIED	29331825, 284509, 284809
2734	94140286 (5467, 5468)	Novel Protein sim. GBank gi 451962 dbj BAA75670.1 - (AB017614) OASIS protein [Mus musculus]	Contains protein domain (PF00170) - bZIP transcription factor	60424179, 52644507, 56182575, 284259, 29331828, 284907, 264510, 264910, 60433356, 265019, 55811150, 284881, 284763, 284887, 33657182, 18108370, 60431528, 60431850, 56182323, 83373044

2735	87712338 (5469, 5470)	Novel Protein sim. GBank gi 3850569 (AC005278) - ESTs gb T21276, gb T45403, and gb AA586113 come from this gene. [Arabidopsis thaliana]		glycoprotein	22278998, 60432289, 29331827, 29146498, 264108, 264909, 284112, 33657402, 87168474, 265017, 264782, 264448, 264784, 264684, 21908765, 264693, 33657109, 263976, 264636, 264638, 264557, 22279000, 22279002, 264567
2736	80247655 (5471, 5472)			UNCLASSIFIED	264905, 264628, 264629, 263978, 264632, 264564
2737	87604526 (5473, 5474)				264690
2738	85731808 (5475, 5476)	Novel Protein sim. GBank gi 2558501 dbj BAA22898 - (D63850) hepatoma-derived growth factor [Mus musculus]			264486, 265009, 264768, 264691
2739	94319834 (5477, 5478)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264684, 83373044, 264566
2740	94148762 (5479, 5480)	Novel Protein sim. GBank gi 3417386 emb CAA75495 - (Y15197) mikrotubule-associated protein, MAP-115 [Mus musculus]		UNCLASSIFIED	264488, 56162575, 22278995, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 29146498, 29331830, 265006, 265007, 265008, 80432229, 33857402, 55812038, 87168474, 265010, 265011, 265017, 265018, 265019, 264605, 264681, 264288, 264369, 52644229, 21908765, 21908768, 21908767, 21908768, 21908769, 265020, 265022, 264691, 264692, 33857109, 18108370, 18108374, 55810784, 35695855, 264634, 60431850, 264639, 56182323, 18108382, 18108385, 65274727, 22279002, 264584
2741	88047518 (5481, 5482)	Novel Protein sim. GBank gi 3242764 (AC005154) - similar to protein U28928 (PID:9861308) [Homo sapiens]		UNCLASSIFIED	22278998, 52644045, 52644229, 21906768, 21908769, 265020, 60170615, 264691
2742	87648644 (5483, 5484)	Novel Protein sim. GBank gi 4758412 ref NP_004472.1 pGALN - UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 2 (GALNAC-T2)	Contains protein domain (PF00852) - Similarity to lectin domain of ricin beta-chain, 3 copies.	transferase	264259, 264905, 264758, 55812038, 264389, 29148627
2743	87627991 (5485, 5486)	Novel Protein sim. GBank gi 4468311 emb CAB37992 - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]		UNCLASSIFIED	35696286, 264259, 264908, 264908, 265006, 60433438, 265017, 18108351, 264448, 264784, 264288, 21906765, 21906767, 264690, 264691, 264693, 263989, 263971, 35695855, 264637, 264558, 18108382, 60432113
2744	94126030 (5487, 5488)	Novel Protein sim. GBank gi 3880433 emb CAA91389 - (Z68521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	kinase	18108374, 264488, 56182435, 21906765, 35696423, 35695917, 35695855, 265020, 265021, 264511, 265009, 264490, 264558, 264259, 264557, 56182323, 264558, 264559, 18108383, 29331824, 18108385, 33657109, 29331828, 21908754, 29331827, 29331828, 33657349, 87168518, 265018, 264905, 264482, 264448, 264486, 264389, 264288

2745	87740125 (5489, 5490)	Novel Protein sim. GBank gij4405785jgb AAD19826j - (AF038963) RNA helicase [Homo sapiens]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	35696288, 284509, 284905, 284907, 284908, 284909, 264510, 264512, 265008, 284758, 264801, 265017, 264804, 264783, 264288, 264886, 264769, 264693, 35696423, 35695855, 264634, 264636, 264563, 264564, 264565
2746	95418601 (5491, 5492)	Novel Protein sim. GBank gij4758738jref NP_004680.1 pMTA1 - metastasis associated 1	Contains protein domain (PF00320) - GATA zinc finger	UNCLASSIFIED	22278998, 22278998, 22278999, 29331822, 29331826, 29331827, 35696052, 29331828, 264905, 264906, 264907, 264908, 264909, 52844045, 285008, 60170831, 264598, 55812038, 285018, 264883, 264288, 21908765, 21908767, 21908768, 21908769, 265020, 264690, 33657023, 264693, 33657109, 18108368, 18108374, 264558, 18108385, 22279000, 264563
2747	94112677 (5493, 5494)	Novel Protein sim. GBank gij4557803jref NP_000262.1 pNPC1 - Niemann-Pick disease, type C1		glycoprotein	284569, 52844507, 18108394, 22278995, 35696288, 22278997, 22278999, 52845080, 29331824, 58182181, 29331828, 29331827, 35696052, 264907, 264908, 264909, 265009, 33109954, 55811386, 87188474, 265010, 87188559, 264603, 265019, 264760, 264688, 264768, 21908769, 35695917, 60170815, 264692, 33657023, 52645128, 27486264, 60431528, 18108374, 35698423, 35695855, 284558, 58182323, 18108385, 264482
2748	91214983 (5495, 5496)	Novel Protein sim. GBank gij4191272jemb CAA09984j - (AJ012295) apaG protein [Rhizobium etli]	Contains protein domain (PF00646) - F-box domain.		65274572, 29331828, 284112, 264511, 265019, 264760, 284767, 284768, 284769, 21908768, 21908769, 265020, 27486262, 56526486, 87188518, 22279000
2749	87346307 (5497, 5498)				264258, 264908, 264510, 265008, 265009, 264760, 264389, 264768, 264563
2750	87336344 (5499, 5500)	Novel Protein sim. GBank gij1872498 (U74297) - PiUS [Oryctolagus cuniculus]		UNCLASSIFIED	264488, 52844507, 18108386, 56994075, 264259, 29331825, 29331826, 29331827, 29331828, 264508, 265009, 264910, 264591, 264595, 33657084, 265011, 265019, 18108351, 264288, 264686, 264769, 264689, 55811957, 264693, 27486264, 18108370, 18108374, 264558, 18108385, 264482, 264563
2751	87057465 (5501, 5502)			UNCLASSIFIED	29331822, 29331824, 265017, 33657023
2752	88062675 (5503, 5504)	Novel Protein sim. GBank gij3041859 (AC004534) - OG-2 homeodomain protein-like, similar to U85067 (PID:g1575526) [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	homeobox	

2753	94138972 (5505, 5506)	Novel Protein sim. GBank gjl3851648 (AF098301) - neural F-box protein NFB42 [Rattus norvegicus]	Contains protein domain (PF00646) - F-box domain.	UNCLASSIFIED	56182575, 56894075, 22278988, 29331822, 29331824, 29331825, 29331826, 265007, 264593, 55812038, 33109954, 18108351, 264288, 56181562, 21908767, 21908768, 265021, 264683, 18108374, 65274791, 264632, 56182323, 22278002, 264563, 264567
2754	94115513 (5507, 5508)	Novel Protein sim. GBank gjl535428 (U13736) - calmodulin-like protein [Pisum sativum]	Contains protein domain (PF00038) - EF hand	struct	22278989, 66714117, 29331827, 35696052, 29331828, 264808, 264808, 264809, 265011, 265017, 265018, 265019, 264288, 21908765, 21908767, 265022, 33657023, 264683, 56182323, 18108382, 22278000
2755	88001472 (5508, 5510)	Novel Protein sim. GBank gjl2896653 (AC004510) - R30385_2 [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	transcriptfactor	
2756	11465908 (5511, 5512)	Novel Protein sim. GBank gjl173539 (U30473) - putative src-like adapter protein; non-catalytic src-like adapter protein containing SH3 and SH2 domains; homolog of mouse SLAP; Method: conceptual translation supplied by author [Homo sapiens]	Contains protein domain (PF00017) - Src homology domain 2	UNCLASSIFIED	264594
2757	95381590 (5513, 5514)	Novel Protein sim. GBank gjl3608372 (AF053768) - brain specific cortadin-binding protein CBP90 [Rattus norvegicus]		eph	85658542, 264693
2758	78637846 (5515, 5516)	Novel Protein sim. GBank gjl2072200 (U94863) - p40 [Borna disease virus]		struct	264693
2759	91005312 (5517, 5518)	Novel Protein sim. GBank gjl2072200 (U94863) - p40 [Borna disease virus]			65274572, 35696286, 66714117, 29331828, 264508, 56182435, 21906754, 55811957, 264629, 264636, 56182323, 22279002
2760	78824788 (5518, 5520)	Novel Protein sim. GBank gjl4914573[emb]CAB43885.1] - (AL050380) hypothetical protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	264808
2761	87639597 (5521, 5522)	Novel Protein sim. GBank gjl3136150 (AF050182) - PERIOD 3 [Mus musculus]	Contains protein domain (PF00989) - PAS domain	nuclease	22278998, 29331822, 29331830, 265010, 265019, 264288, 21906765, 21906768, 21906769, 265020, 56182323, 22278002, 264563
2762	87592689 (5523, 5524)	Novel Protein sim. GBank gjl3136150 (AF050182) - PERIOD 3 [Mus musculus]	Contains protein domain (PF00989) - PAS domain	struct	18108394, 22278998, 264806, 264909, 265006, 265007, 264757, 265010, 265011, 265017, 265019, 18108351, 264448, 264683, 264688, 264768, 265020, 265021, 265022, 264691, 18108362, 264693, 18108365, 33657109, 18108368, 18108370, 18108381, 18108382, 18108384, 18108388, 87168518, 264389, 35698423
2763	87539988 (5525, 5526)	Novel Protein sim. GBank gjl3511122 (AF080503) - zinc finger protein [Homo sapiens]	Contains protein domain (PF01352) - KRAB box	transcriptfactor	
2764	94305140 (5527, 5528)	Novel Protein sim. GBank gjl2905643 (AF045244) - ribitol kinase [Klebsiella pneumoniae]	Contains protein domain (PF00370) - FGGY family of carbohydrate kinases		52646842, 264259, 29331822, 29331825, 29331826, 29331828, 33656970, 264905, 264907, 29331830, 265006, 265009, 21906754, 265019, 264448, 21906769, 27486262, 56182323, 56526486, 87168518, 264487

2765	84315105 (5529, 5530)	Novel Protein sim. GBank gi 4688672 emb CAA17688.2 - (AL022018) /prediction=(method:: /prediction=(method:: /match=(desc: [Drosophila melanogaster]			264488, 65274572, 22278995, 35686286, 22278998, 22278999, 264259, 29331822, 29331824, 35686052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264512, 264910, 265009, 264592, 264595, 264758, 55812038, 33109954, 265010, 87188559, 264600, 265018, 264760, 264761, 264762, 264763, 264448, 264764, 264288, 264766, 264767, 264768, 56181562, 21908764, 21908765, 21908768, 35695917, 265021, 264691, 264692, 33657023, 33657109, 264628, 18108370, 264629, 18108374, 55811576, 35696423, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 264558, 264639, 83373044, 87188518, 22279000, 22279002, 264563, 264482
2766	94315109 (5531, 5532)	Novel Protein sim. GBank gi 5441611 emb CAB46854.1 - (AJ388555) hypothetical protein [Cantis familiaris]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	284488, 65274572, 60432289, 264907, 284908, 284511, 264512, 60433356, 264288, 284885, 264689, 35695917, 265022, 264693, 264628, 65274791, 264635, 264555, 264556, 264557, 264638, 264558, 264559, 83373044, 60432113
2767	80204297 (5533, 5534)	Novel Protein sim. GBank gi 1079451 pir A55463 - tropomodulin, skeletal muscle - chicken		struct	264112, 263974, 264558
2768	94322238 (5535, 5536)	Novel Protein sim. GBank gi 5441322 emb CAB46721.1 - (AL031427) dJ167A19.1 (novel protein) [Homo sapiens]		UNCLASSIFIED	264488, 263994, 264489, 35686286, 22278998, 22278999, 264259, 29331822, 60432289, 29331826, 35688052, 264508, 264508, 264905, 264906, 264907, 29331830, 264908, 264909, 264510, 264511, 264512, 265008, 264910, 265009, 264591, 264592, 264593, 33657402, 264594, 264595, 264757, 264596, 265011, 264604, 265019, 264760, 264681, 18108351, 264764, 264288, 264766, 264688, 264768, 18108357, 264769, 264689, 21908766, 21908768, 21908769, 35695917, 265021, 265022, 33657023, 33657109, 264628, 264629, 18108374, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264555, 264638, 264639, 83373044, 264563, 264564, 264565, 264566, 264486, 264567

2769	95311088 (5537, 5538)	Novel Protein sim. GBank gi 5419859 emb CAB46375.1 - (AL098725) hypothetical protein [Homo sapiens]		tubulin	264488, 56182575, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331828, 264908, 29331830, 56182435, 264592, 33657402, 264448, 264369, 264288, 60170615, 264691, 33657023, 264892, 33657109, 18108374, 55811576, 264634, 264636, 56182323, 83373044, 60432113
2770	87730182 (5539, 5540)	Novel Protein sim. GBank gi 5701965 emb CAB52157.1 - (AL109736) WD repeat protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	18108398, 22278995, 22278996, 22278999, 264105, 265006, 265019, 18108351, 264687, 21908765, 18108364, 264629, 18108374, 264631, 18108385, 18108388
2771	88084071 (5541, 5542)	Novel Protein sim. GBank gi 3093433 (AC004125) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	264259, 29331822, 29331824, 29331825, 284369
2772	95357309 (5543, 5544)	Novel Protein sim. GBank gi 4885631 ref NP_005465.1 pNY C - histone deacetylase 5	Contains protein domain (PF00850) - Histone deacetylase family	histone	284259, 29331822, 29331824, 66714117, 60432289, 29331827, 284905, 265009, 284592, 55812038, 65274444, 264766, 21908769, 33657109, 263978, 264555, 264638, 284557, 83373044, 264563, 264564, 264486
2773	94138994 (5545, 5546)	Novel Protein sim. GBank gi 3288898 (AC005253) - R26445_1 [Homo sapiens]		UNCLASSIFIED	18108374, 264686, 264687, 263978, 56182435, 264689, 55810764, 21908768, 35896423, 55811576, 65274791, 56181686, 55811957, 35895855, 264110, 265021, 264112, 265022, 265008, 265008, 264092, 264094, 60431850, 264637, 264691, 264259, 264692, 263981, 284594, 60433356, 56182323, 264693, 264757, 56182181, 55812038, 29331825, 60424289, 18108385, 29331826, 29331827, 27486261, 29331828, 35898052, 55811388, 264107, 60432113, 265017, 55811150, 18108351, 264681, 264906, 18108370, 264484, 264682, 20281089, 284448, 68712502, 264683, 264764, 264288, 264684, 264768, 263974
2774	87819908 (5547, 5548)	Novel Protein sim. GBank gi 465652 sp P34388 YLS3_CAEEL - HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III	Contains protein domain (PF00380) - Ribosomal protein S9/S16	ribosomal prot	22278995, 35898286, 22278996, 22278999, 264259, 29331826, 60432289, 35898052, 264112, 33657402, 21908754, 87168559, 265017, 265018, 264288, 21908766, 21908767, 21908769, 35895917, 265020, 265021, 33657023, 33657109, 18108370, 263976, 35898423, 35895855, 87168518, 22279000, 264482

2775	95307987 (5549, 5550)	Novel Protein sim. GBank gi 4689132 gb AAD27775.1 AF07704 - (AF077042) 30S ribosomal protein S7 homolog [Homo sapiens]	Contains protein domain (PF00177) - Ribosomal protein S7p/S5e	- ribosomal prot	264488, 22278995, 56994075, 22278998, 35698288, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331827, 29331828, 35698052, 265007, 21906754, 265017, 265019, 284448, 264682, 264369, 264288, 18108354, 52644229, 264689, 21806765, 21806766, 21906767, 21906768, 21906768, 35695917, 265021, 265022, 60170615, 264891, 18108370, 35698423, 65274791, 35695855, 264634, 60431850, 60170384, 58182323, 264558, 18108388, 22279000, 264563, 264565, 264488, 264567
2776	87791557 (5551, 5552)				56182575, 22278998, 22278999, 264259, 29331822, 29331824, 264908, 29331830, 264510, 33657402, 21908754, 55811388, 265017, 265019, 264448, 264288, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 60170615, 55810764, 55811576, 264555, 56526486, 22279000
2777	79818729 (5553, 5554)			UNCLASSIFIED	264907, 264786
2778	82112411 (5555, 5556)			UNCLASSIFIED	264907, 264593, 264780, 264628
2779	87849729 (5557, 5558)	Novel Protein sim. GBank gi 4680711 gb AAD27745.1 AF13297 - (AF132970) CGI-36 protein [Homo sapiens]		UNCLASSIFIED	22278997, 264259, 29331824, 66714117, 35698052, 265006, 264512, 264448, 264288, 29148627, 18108364, 20281149, 18108370, 264629
2780	94678397 (5559, 5560)	Novel Protein sim. GBank gi 4758524 ref NP_004825.1 p HGK - HPK/GCK-like kinase	Contains protein domain (PF00780) - CNH domain	kinase	29148499, 65274791, 264634, 264639
2781	91220057 (5561, 5562)	Novel Protein sim. GBank gi 4469352 gb AAD21222 - (AF069502) ubiquitin specific protease UBP43 [Mus musculus]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	60424179, 29331824, 60424269, 66714117, 29331828, 56182435, 87168474, 265017, 264764, 56181562, 21906765, 21906766, 21906768, 35695917, 265020, 33657023, 35695855, 58182323, 67188518
2782	94233146 (5563, 5564)	Novel Protein sim. GBank gi 4505013 ref NP_002310.1 p LRN - leucine-rich neuronal protein	Contains protein domain (PF00560) - Leucine Rich Repeat	struct	65274572, 22278998, 22278998, 60432049, 264259, 29331822, 29331824, 29331828, 60432289, 29331828, 264905, 264907, 264908, 264909, 52644045, 265009, 265017, 265018, 264804, 265019, 264760, 264683, 264288, 264766, 264685, 264688, 264788, 52644229, 264689, 21906768, 265020, 265021, 264691, 18108382, 264692, 33657023, 264693, 33657109, 33657349, 18108370, 264628, 263978, 35695855, 264557, 56182323, 83373044, 18108385

2783	80016829 (5565, 5568)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII			tm7	264809, 264628, 263978, 263981
2784	87614360 (5587, 5588)					264259, 29331822, 29331824, 29331825, 264482
2785	88071930 (5569, 5570)	Novel Protein sim. GBank gi 2134933 pr S58890 - collapsin response mediator protein - human			UNCLASSIFIED	22278999, 264908, 264758, 265018, 264769, 21908765, 21908768, 21908769, 265020, 264584
2786	87408542 (5571, 5572)	Novel Protein sim. GBank gi 2073564 (U80223) - eukaryotic initiation factor eIF-2 alpha kinase; DGCN2 [Drosophila melanogaster]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain		kinase	284905, 265017
2787	87901268 (5573, 5574)	Novel Protein sim. GBank gi 5174507 ref NP_006020.1 pMA1 - paraneoplastic neuronal antigen			UNCLASSIFIED	264768, 21908765, 21908768, 55811957, 22278999, 264093, 60170815, 264259, 29331822, 18108385, 29331824, 33657109, 29331827, 35698052, 264100, 264105, 264808, 263977, 55811576, 264635, 264637, 60433438, 60432113, 265017, 265019, 22279002, 55811150, 264369, 264288
2788	88080644 (5575, 5576)	Novel Protein sim. GBank gi 3252826 (AC004382) - Unknown gene product [Homo sapiens]			UNCLASSIFIED	
2789	85491275 (5577, 5578)	Novel Protein sim. GBank gi 2485729 sp Q92558 Y281_HUMAN - HYPOTHETICAL PROTEIN KIAA0281 (HA6725)			UNCLASSIFIED	264103, 21908769, 264693
2790	87602784 (5579, 5580)	Novel Protein sim. GBank gi 5101772 emb CAB45135.1 - (AJ242978) p621 [Homo sapiens]			struct	264488, 264769, 264910, 264631, 264636, 264690, 264691, 264259, 264638, 29331824, 264508, 264509, 264905, 264583, 264906, 264628, 18108370, 264907, 264764, 264908, 264288, 264908
2791	88083195 (5581, 5582)	Novel Protein sim. GBank gi 2911266 (AC002550) - Unknown gene product [Homo sapiens]				21908764, 18108368
2792	95083783 (5583, 5584)	Novel Protein sim. GBank gi 2854183 gb AAC02581.1 - (AF045842) No definition line found [Caenorhabditis elegans]				22278998, 22278997, 264259, 29331822, 29331824, 29331825, 68714117, 29331826, 60432289, 29331827, 35698052, 264908, 68712502, 29331830, 264909, 60432229, 60433356, 60433438, 33109954, 265010, 265011, 265017, 265018, 265019, 264682, 264448, 264288, 264369, 264768, 52644229, 21908765, 21908768, 265020, 265021, 33657023, 263974, 18108374, 65274791, 35695855, 264636, 264556, 264558, 56182323, 63373044, 18108385, 56526486, 60432113, 22279000, 264587
2793	87425476 (5585, 5586)				UNCLASSIFIED	264259, 60432289, 66712502, 265009, 264636
2794	85794830 (5587, 5588)				UNCLASSIFIED	264689, 265022, 264691, 18108388, 264567

2785	85334888 (5589, 5590)	Novel Protein sim. GBank gi 5454146 ref NP_006348.1 pUBE2 - ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBCA15)	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	65274572, 56182575, 35696286, 22278988, 22278988, 60432049, 284259, 29331822, 29331825, 66714117, 60432289, 29331826, 29331827, 35696052, 29331828, 284907, 66712502, 56182435, 284511, 265007, 284512, 284910, 60432229, 60433356, 60433438, 33109954, 85658542, 265018, 265019, 284288, 284686, 21906764, 21906765, 21906768, 21906768, 21906769, 55811957, 265020, 265021, 265022, 52844150, 33857023, 264693, 65274620, 33657109, 35696423, 55811576, 65274791, 56182323, 56528486, 60432113, 22279002, 264482, 264563, 284484, 264567
2786	84848857 (5591, 5592)	Novel Protein sim. GBank gi 4680851 gb AAD27715.1 AF13294 - (AF13294) CGI-08 protein [Homo sapiens]		UNCLASSIFIED	18108394, 65274572, 56182575, 56994075, 22278989, 264480, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 264509, 264808, 284907, 284908, 66712502, 56182435, 264510, 265006, 284512, 265007, 265008, 284910, 265009, 284591, 264592, 60433356, 284594, 284595, 55812038, 284596, 21906754, 60174639, 87168474, 265010, 265011, 265017, 265018, 265019, 55811150, 264762, 18108351, 284448, 264682, 264369, 264288, 264685, 264766, 264687, 56181562, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170815, 52644150, 264692, 33657023, 18108362, 264693, 65274620, 33657109, 33657182, 27486265, 33857349, 18108374, 35696423, 65274781, 35695855, 264556, 284557, 56182323, 284558, 60170394, 63373044, 65274727, 87168518, 22279000, 264563, 264564, 264565, 264566, 264567
2787	85110780 (5593, 5594)	Novel Protein sim. GBank gi 4838557 gb AAD31040.1 - (AF143859) potassium channel modulatory factor DEBT-91 [Mus musculus]	Contains protein domain (PF00569) - Zinc finger present in dystrophin, CBP/p300	UNCLASSIFIED	56182575, 22278985, 22278986, 22278997, 29331827, 29146499, 264509, 264806, 56182435, 264757, 21906754, 265010, 265017, 265018, 284681, 264682, 264683, 264686, 21906765, 21906767, 21906768, 21906769, 29146829, 265020, 52844150, 264690, 33657182, 264629, 18108376, 56182323, 22279002, 264563
2788	86198005 (5595, 5596)	Novel Protein sim. GBank gi 2852645 (AF007160) - unknown [Homo sapiens]		UNCLASSIFIED	264488, 284480, 284259, 284448, 20281149, 20281152, 284556, 284557, 284558, 284559, 264483, 264486, 264567

2799	88090651 (5597, 5598)	Novel Protein sim. GBank gi 3252825 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	22278986, 22278997, 22278998, 22278999, 60432049, 264259, 29331826, 35896052, 29331828, 264909, 60433356, 33857402, 33108954, 87168474, 264448, 52844229, 21908768, 21908767, 21908768, 35895917, 265020, 265021, 265022, 52844150, 35895853, 264634, 60432113, 22279000
2800	88316481 (5599, 5600)	Novel Protein sim. GBank gi 4240301 dbj BAA74929.1) - (AB020713) KIAA0908 protein [Homo sapiens]		glycoprotein	284488, 56994075, 264259, 20281099, 29331825, 29331827, 264905, 56182435, 265008, 265011, 87168559, 265017, 265019, 264448, 264288, 264766, 264688, 60170815, 264691, 264692, 27486265, 264628, 264629, 264636, 264557, 264558, 264559, 87168518, 264564, 264566, 264567
2801	86068814 (5601, 5602)		Contains protein domain (PF00627) - UBA domain		265007, 264687
2802	88082477 (5603, 5604)	Novel Protein sim. GBank gi 2337865 (AC002464) - organic cation transporter; 50% similarity to JC4884 (PID:g2143892) [Homo sapiens]	Contains protein domain (PF00083) - Sugar (and other) transporter	transport	264448, 35695855
2803	79577446 (5605, 5606)			UNCLASSIFIED	264639
2804	57111131 (5607, 5608)	Novel Protein sim. GBank gi 4559368 gb AAD23029.1 AC006585) hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF01585) - G-patch domain	peptidase	264566
2805	87398486 (5609, 5610)				264092, 264259, 29331822, 29331824, 29331827, 29331828, 264506, 265007, 265009, 21908754, 264369, 264288, 264632, 80170394, 264563, 264482
2806	87898951 (5611, 5612)	Novel Protein sim. GBank gi 1168973 sp P44403 CLPB_HAEIN - CLPB PROTEIN		UNCLASSIFIED	22278995, 22278996, 22278998, 264259, 29331822, 29331824, 29331826, 29331827, 29146488, 265008, 265009, 60433438, 265017, 265018, 265019, 264448, 264288, 21908765, 21908767, 21908769, 29146629, 265022, 52844150, 56182323

2807	91720702 (5613, 5614)	Novel Protein sim. GBank gi 4468310 emb CAB37891 - (AL031432) dJ465N24.1 (PUTATIVE novel protein similar to predicted yeast and worm proteins) [Homo sapiens]		UNCLASSIFIED	52644507, 52845156, 52846842, 18108398, 56182575, 22278994, 22278995, 22278996, 56994075, 35698286, 22278997, 22278998, 22278999, 264259, 52845080, 29331822, 29331824, 29331825, 29331826, 35698052, 29331828, 33656970, 284100, 284105, 284907, 52844045, 60433358, 264594, 60433438, 52846317, 21908754, 33109954, 33657084, 52844296, 87188474, 265011, 87188559, 265017, 265018, 265019, 18108351, 264448, 264783, 264687, 52844229, 21908765, 21908766, 21908767, 21908768, 21908769, 35695917, 265021, 265022, 52844150, 33657023, 52845129, 33657109, 33657182, 27486261, 27486262, 27486284, 27486285, 35695763, 18108370, 18108372, 18108374, 18108376, 263977, 18108377, 35698423, 35695855, 52644332, 83373044, 18108385, 18108387, 87188518, 60432113
2808	95359111 (5615, 5616)	Novel Protein sim. GBank gi 5541863 emb CAB51071.1 - (AL096857) hypothetical protein [Homo sapiens]	MHC		80432289, 264510, 265010, 265017, 265018, 264881, 264886, 265021, 264690, 22278000, 264586
2809	88083530 (5617, 5618)	Novel Protein sim. GBank gi 27272561 (AC004002) - similar to ciliary dynein beta heavy chain; 78% Similarity to P23098 (PID:gi18965) [Homo sapiens]	ATPase_associated		18108351
2810	87259032 (5619, 5620)			UNCLASSIFIED	284569, 22278996, 264091, 264259, 29331828, 29146499, 29146629, 29146784, 264693
2811	91235845 (5621, 5622)			UNCLASSIFIED	22278999, 264259, 66712502, 264693
2812	88093334 (5623, 5624)	Novel Protein sim. GBank gi 3264583 (AC005189) - match to ESTs H97758 (NID:gi118843) and AA085546 (NID:gi1628773) [Homo sapiens]		UNCLASSIFIED	264108
2813	91218755 (5625, 5626)	Novel Protein sim. GBank gi 4240273 db BAA74915.1 - (AB020699) KIAA0892 protein [Homo sapiens]		UNCLASSIFIED	56182575, 29331828, 264906, 66712502, 55811386, 265017, 265018, 265019, 264683, 265020, 87188518, 60432113
2814	90980906 (5627, 5628)	Novel Protein sim. GBank gi 3548791 (AC005620) - R33590_1 [Homo sapiens]	transcription factor		65274572
2815	78774521 (5629, 5630)			UNCLASSIFIED	264907, 264909
2816	95358228 (5631, 5632)	Novel Protein sim. GBank gi 5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	284488, 35698286, 29331825, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 265011, 264760, 264681, 264766, 264769, 264689, 21908765, 264693, 264628, 18108370, 264629, 264631, 264634, 264563, 264564, 264566, 264486

2817	87749542 (5633, 5634)	Novel Protein sim. GBank gi 1293846 (U56966) - coded for by <i>C. elegans</i> cDNA yk30b3.5; coded for by <i>C. elegans</i> cDNA yk30b3.3 [<i>Caenorhabditis elegans</i>]			264259, 28331822, 28331827, 264508, 264509, 264905, 264907, 264908, 264909, 58182435, 264510, 265006, 264511, 264512, 264593, 264758, 265010, 264780, 264781, 264784, 264288, 264687, 264789, 55811957, 35695917, 33657109, 263878, 264634, 264636, 264639, 264584, 264585, 264586, 264486, 264587
2818	88073579 (5635, 5636)	Novel Protein sim. GBank gi 549986 (U13149) - possible apospory-associated protein [<i>Pennisetum ciliare</i>]	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	56712502
2819	87793527 (5637, 5638)			UNCLASSIFIED	264808, 264511
2820	87765744 (5639, 5640)	Novel Protein sim. GBank gi 4929773 gb AAD34147.1 AF15209 - (AF152097) CGI-05 protein [<i>Homo sapiens</i>]	Contains protein domain (PF00919) - Uncharacterized protein family UPF0004	UNCLASSIFIED	18108394, 52646365, 52644045, 264112, 265009, 21906754, 265017, 18108351, 264683, 264369, 264686, 264769, 21906769, 33657023, 33657109, 18108370, 18108374, 18108377, 18108385
2821	95320511 (5641, 5642)	Novel Protein sim. GBank gi 399144 sp P02747 C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264636
2822	94260221 (5643, 5644)	Novel Protein sim. GBank gi 2224671 db BAA20820 - (AB002363) KIAA0365 [<i>Homo sapiens</i>]		UNCLASSIFIED	264259, 29331822, 60432289, 284905, 60433356, 33657402, 285011, 264780, 21908785, 60170815, 264638
2823	95320513 (5645, 5646)	Novel Protein sim. GBank gi 399144 sp P02747 C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264766
2824	95320515 (5647, 5648)	Novel Protein sim. GBank gi 399144 sp P02747 C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR		UNCLASSIFIED	264907
2825	19742170 (5649, 5650)				264780
2826	94311905 (5651, 5652)	Novel Protein sim. GBank gi 385683 emb CAA22020 - (AL033503) conserved hypothetical protein [<i>Candida albicans</i>]			52645156, 22278994, 35696286, 22278997, 22278998, 52645080, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 33656970, 52644045, 52646317, 33657084, 52644298, 265017, 265018, 265019, 264288, 21908784, 21908785, 21908786, 21908787, 21908769, 35695917, 52644150, 33657109, 33657182, 27486261, 27486262, 33657349, 27486285, 35695783, 35698423, 35695855, 52644332, 18108385, 87168518, 264484

2827	95320518 (5653, 5654)	Novel Protein sim. GBank gi 389144 sp P02747 C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - complement C1q domain	264488, 263984, 264489, 65274572, 29331822, 66714117, 29331827, 29331828, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 265007, 264512, 265008, 264910, 264591, 60432228, 264592, 264593, 264595, 264596, 21906754, 265011, 264600, 264601, 264602, 265017, 264604, 264605, 264288, 264766, 264767, 264689, 55811957, 264534, 264690, 264691, 264692, 264693, 263972, 264629, 35695855, 264631, 264634, 264635, 264555, 264636, 264637, 264558, 264638, 264558, 83373044, 18108385, 80432113, 22279002, 264563, 264564, 264585, 264586, 264587, 264486, 18108391
2828	91228615 (5655, 5656)	Novel Protein sim. GBank gi 3598974 (AF077000) - protein tyrosine phosphatase TD14 [Rattus norvegicus]	Contains protein domain (PF00102) - Protein-tyrosine phosphatase	29331822, 35698052, 264104, 264908, 265007, 264591, 265010, 265011, 265019, 264768, 264688, 55811957, 18108370, 18108374, 55810764, 35698423, 55811576, 56182323, 83373044, 87168518
2829	87651244 (5657, 5658)	Novel Protein sim. GBank gi 4880689 gb AAD27734.1 AF13295 - (AF132959) CGI-25 protein [Homo sapiens]		22278996, 22278997, 264091, 264093, 60432049, 264259, 29331822, 29331825, 29331827, 29331828, 264905, 264509, 68712502, 264510, 264511, 264593, 60433438, 21908754, 285011, 264603, 18108351, 264288, 21908765, 21908768, 21908769, 29148629, 52644150, 264693, 33657109, 18108374, 264634, 18108385, 60432113, 22279000, 264585, 264486 265008, 265019, 264639, 22279002
2830	88087109 (5659, 5660)	Novel Protein sim. GBank gi 2498667 sp Q61200 NPH1_MOUSE - NEUREXOPHILIN 1		
2831	87614717 (5661, 5662)		UNCLASSIFIED	265017
2832	87631809 (5663, 5664)		UNCLASSIFIED	22278997, 22278999, 52846317, 264288, 264688, 21906767, 60431528, 264638, 22279000
2833	87612938 (5665, 5666)	Novel Protein sim. GBank gi 5262615 emb CAB45747.1 - (AL080158) hypothetical protein [Homo sapiens]	UNCLASSIFIED	284555, 264556, 264558
2834	86974703 (5667, 5668)	Novel Protein sim. GBank gi 2224567 dbj BAA20772 - (AB002311) KIAA0313 [Homo sapiens]		263972
2835	87775712 (5669, 5670)	Novel Protein sim. GBank gi 4589532 dbj BAA76788.1 - (AB023161) KIAA0944 protein [Homo sapiens]	ATPase_associated	60432289, 29331828, 265008, 265010, 265017, 264448, 55811957, 265020, 18108370
2836	85724748 (5671, 5672)	Novel Protein sim. GBank gi 2351568 (U76618) - N-RAP [Mus musculus]	Contains protein domain (PF00412) - LIM domain containing proteins	284259, 284112, 265010, 264762, 264764, 263974, 264555, 264558, 264559

2837	87785482 (5673, 5674)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	18108394, 22278997, 22278998, 29331822, 264907, 264909, 265006, 265007, 265018, 265019, 264682, 264288, 21906766, 21906767, 55811957, 35695917, 18108374, 56182323, 22279000, 22279002
2838	87775392 (5675, 5676)	Novel Protein sim. GBank gi 973378 (U31263) - core protein [Hepatitis C virus]		UNCLASSIFIED	18108394, 18108397, 264259, 29331826, 265007, 265019, 264448, 18108388, 20281149, 264565, 264567
2839	85789317 (5677, 5678)			UNCLASSIFIED	264555
2840	87774665 (5679, 5680)	Novel Protein sim. GBank gi 1575515 (U64899) - thrombospondin-related anonymous protein [Plasmodium gallinaceum]			264509, 264511, 265011, 264288, 264769, 265020, 264634, 264636, 264556
2841	86982568 (5681, 5682)	Novel Protein sim. GBank gi 2224605 dbj BAA20790 - (AB002330) KIAA0332 [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)		56182575, 35698052, 264907, 264908, 264909, 264910, 264593, 264595, 264768, 265022, 264691, 33657182, 35695763, 18108370, 35695855, 264631, 264559, 264563, 264567
2842	80080086 (5683, 5684)				264600
2843	91012494 (5685, 5686)	Novel Protein sim. GBank gi 5578957 emb CAB51350.1 - (AL050306) dJ47587.1 (novel KIAA0615 and KIAA0323 LIKE protein) [Homo sapiens]		UNCLASSIFIED	264906, 264907, 264908, 264909, 264910, 264764, 35695855, 83373044, 18108385
2844	56731154 (5687, 5688)	Novel Protein sim. GBank gi 585123 sp Q08878 FBL_C_MOUSE - FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90)	Contains protein domain (PF00008) - EGF-like domain		264685
2845	94321719 (5689, 5690)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]	homeobox		29146498, 87168474, 264688, 35698423, 83373044, 264564
2846	88318613 (5691, 5692)	Novel Protein sim. GBank gi 5306263 gb AAD41995.1 AC00623 - (AC006233) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	29331830, 264909, 265008, 265011, 87168559, 264629, 264556
2847	81811757 (5693, 5694)	Novel Protein sim. GBank gi 3398676 (AC005390) - R31180_1 [Homo sapiens]		UNCLASSIFIED	264908, 264766, 264769, 264629, 264637, 264566
2848	87612943 (5695, 5696)	Novel Protein sim. GBank gi 5262615 emb CAB45747.1 - (AL080156) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264490, 264259, 264508, 264905, 264907, 264510, 265007, 265008, 264591, 264592, 264593, 264594, 264595, 55812038, 265010, 265011, 264604, 264763, 264764, 264765, 264768, 264886, 264628, 264629, 264555, 264636, 264556, 264557, 264638, 264558, 264559, 264563, 264566, 264567
2849	88084263 (5697, 5698)	Novel Protein sim. GBank gi 3342218 (AC004131) - Unknown gene product [Homo sapiens]			29331822, 35696052, 264509, 264906, 265007, 264594, 265018, 264288, 263972, 35698423, 18108384, 56526486, 18108390
2850	87623636 (5699, 5700)			UNCLASSIFIED	35696288, 265008, 265009, 265018, 264288, 35695917, 264693, 18108374, 35695855, 22279000

2851	87820548 (5701, 5702)	Novel Protein sim. GBank gjl4321619[gb]AAD15788.1] - (AF051088) seven transmembrane domain orphan receptor [Mus musculus]		UNCLASSIFIED	264906, 264907, 58182435, 264758, 55811386, 265010, 18108351, 264448, 264389, 21908765, 264691, 264692, 264693, 35695855, 264556, 18108385, 264567, 264591
2852	86987023 (5703, 5704)	Novel Protein sim. GBank gjl1825728 (U88308) - similar to drosophila membrane protein PATCHED SP:P18502 (PID:g129645) [Caenorhabditis elegans]		UNCLASSIFIED	
2853	87784630 (5705, 5706)	Novel Protein sim. GBank gjl2702347 (AF027503) - putative membrane-associated guanylate kinase 1 [Mus musculus]	Contains protein domain (PF00397) - kinase WW domain		56182575, 55811150, 264690, 27486262, 27486265, 264632, 58182323, 56528486, 22279002
2854	88083557 (5707, 5708)	Novel Protein sim. GBank gjl2785825 (AC004021) - kelch protein; ring canal component involved in cytoplasmic bridges; 77% Similarity to A45773 (PID:g1079086) [Homo sapiens]	Contains protein domain (PF01344) - dna_ma_bind Kelch motif		35698286, 29331824, 29331826, 29331828, 264908, 264766, 264768, 264693, 22279002, 264482
2855	94723856 (5709, 5710)	Novel Protein sim. GBank gjl1504040[dbj]BAA13219] - (D86983) similar to D.melanogaster peroxidasin(U11052) [Homo sapiens]	Contains protein domain (PF00560) - glycoprotein Leucine Rich Repeat		22278994, 29331822, 29331824, 29331825, 264908, 264908, 265009, 33109954, 265018, 265019, 264448, 21908765, 265020, 264690, 27486265, 83373044, 22279000, 22279002, 264482
2856	88093359 (5711, 5712)	Novel Protein sim. GBank gjl3264583 (AC005189) - match to ESTs H97758 (NID:g1118843) and AA085546 (NID:g1628773) [Homo sapiens]			21908766, 22278997, 265022, 29331822, 29331826, 27486262, 265007, 265009, 265017, 264482, 284563, 18108351
2857	95348286 (5713, 5714)	Novel Protein sim. GBank gjl3041855 (AC004537) - similar to tumor suppressor p33ING1; similar to AF044076 (PID:g2829208) [Homo sapiens]	Contains protein domain (PF00628) - struct PHD-finger		22278995, 35698286, 29331824, 29331825, 35698052, 264103, 264108, 58182435, 21908765, 21908769, 265020, 18108368, 35695763, 22279002, 264563
2858	87434748 (5715, 5716)	Novel Protein sim. GBank gjl482585[sp]P35227[ME18_HUMAN - DNA-BINDING PROTEIN MEL-18 (ZINC FINGER PROTEIN 144)]	Contains protein domain (PF00097) - dna_ma_bind Zinc finger, C2HC4 type (RING finger)		264569, 264887, 22278995, 22278998, 22278997, 22278999, 264259, 29331826, 29331827, 29331828, 264509, 264905, 264908, 29331830, 264808, 52844045, 284909, 284511, 264512, 265007, 265008, 264910, 265009, 284593, 80433356, 264585, 284758, 21908754, 265010, 265011, 264604, 265018, 264760, 18108351, 264763, 264682, 284764, 284765, 284288, 264368, 264685, 284768, 284768, 18108357, 264769, 21908766, 21908767, 265021, 284534, 60170615, 264691, 264692, 18108370, 284629, 18108374, 264631, 264636, 263981, 18108381, 264558, 18108385, 22279002, 264584, 264586, 264486, 264587, 60424179, 65274572, 29331828, 264905, 284511, 264758, 265011, 21806767, 21908769, 55811957, 265021, 58182323
2859	90937675 (5717, 5718)	Novel Protein sim. GBank gjl4325320[gb]AAD17331.1] - (AF124427) claudin-15 [Mus musculus]		UNCLASSIFIED	

2860	87532589 (5719, 5720)	Novel Protein sim. GBank gi 4469186 emb CAB38414.1 - (AL031588) dJ1163J1.2.1 (novel protein similar to C. elegans B0035.16 and bacterial tRNA (5-Methylaminomethyl-2-thiouridyate)-Methyltransferases) (isoform 1) [Homo sapiens]		UNCLASSIFIED	284259, 28331822, 28331824, 28331825, 28331826, 28331827, 28331828, 284510, 284511, 33109954, 18108351, 284683, 284765, 284369, 284886, 21908785, 284691, 284692, 284693, 18108388, 22279002, 284482
2861	86698507 (5721, 5722)	Novel Protein sim. GBank gi 3941730 (AF108083) - BS4 [Homo sapiens]			284369, 284892
2862	87569585 (5723, 5724)	Novel Protein sim. GBank gi 4505013 ref NP_002310.1 pLRN - leucine-rich neuronal protein		UNCLASSIFIED	284691, 284638
2863	91220421 (5725, 5726)	Novel Protein sim. GBank gi 3249088 (AC004473) - Contains similarity to goliath protein gb M97204 from D. melanogaster. [Arabidopsis thaliana]	Contains protein domain (PF00096) - struct Zinc finger, C2H2 type		56994075, 35686286, 22278998, 28331822, 28331824, 35686052, 29331828, 284106, 284511, 55812038, 33657084, 55811386, 265018, 265019, 21906765, 21906766, 21906769, 35695917, 265020, 265022, 33657023, 33657109, 33657349, 284629, 18108376, 60431850, 56182323, 18108385, 18108387, 87168518, 22279002, 284259, 284910
2864	87420030 (5727, 5728)	Novel Protein sim. GBank gi 1079451 pir JAS5463 - Tropomodulin, skeletal muscle - chicken	struct		
2865	95312181 (5728, 5730)	Novel Protein sim. GBank gi 438840 (L19048) - MSA-2 [Plasmodium falciparum]			22278995, 21906764, 284482
2866	85105480 (5731, 5732)	Novel Protein sim. GBank gi 585703 sp Q07086 PMP2_RAT - 22 KD PEROXISOMAL MEMBRANE PROTEIN	glycoprotein		65274572, 22278986, 22278998, 22278999, 284259, 28331824, 28331827, 29331828, 60433438, 21906754, 265018, 284448, 284764, 52844150, 83373044
2867	86908001 (5733, 5734)	Novel Protein sim. GBank gi 4580997 gb AAD24571.1 AF12108 - (AF121081) cAMP Inducible 2 protein [Mus musculus]	UNCLASSIFIED		284488, 284768, 21908788, 22278998, 285022, 284259, 284508, 284905, 284907, 284511, 284910, 284635, 284638, 284637, 285011, 285017, 285018, 285019, 284583, 284088, 284566, 284784, 284369, 284567, 284486, 284288, 284788

2868	95303283 (5735, 5736)	Novel Protein sim. GBank gi 1292868 emb CAA63923 - (X94232) t-Cell activation protein [Homo sapiens]			18108392, 264488, 22278994, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35896052, 29331828, 264508, 52844045, 264828, 265006, 265007, 265008, 265009, 264591, 60432229, 264593, 60433358, 264595, 21906754, 265017, 265019, 264682, 264389, 21906785, 21906766, 21906767, 21906768, 265021, 265022, 264691, 33657182, 18108368, 27486261, 27486262, 27486264, 27486265, 18108370, 18108374, 35898423, 35895855, 264632, 56182323, 87188518, 264404, 22279000, 22279002, 264482, 264563, 264564, 264567, 264487
2869	88084412 (5737, 5738)			UNCLASSIFIED	264369
2870	84404574 (5739, 5740)			UNCLASSIFIED	264905, 264908, 264764, 21906769, 264634
2871	88318621 (5741, 5742)	Novel Protein sim. GBank gi 5306263 gb AAD41995.1 AC00623 - (AC006233) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	264259, 29331822, 60432289, 29331827, 264907, 265008, 265017, 265018, 264682, 264764, 18108354, 265021, 27486265, 264629, 18108387, 264567
2872	95312197 (5743, 5744)	Novel Protein sim. GBank gi 112205 pir B39066 - proline-rich protein 15 - rat		kinase	263981
2873	88084252 (5745, 5746)			UNCLASSIFIED	264488, 18108374, 264768, 264687, 264688, 264689, 35898423, 35898286, 35895917, 264510, 264511, 265007, 264512, 265008, 264910, 264534, 264634, 264635, 264555, 264592, 264259, 264558, 60433438, 60432289, 35898052, 265011, 264600, 264601, 60432113, 264508, 264563, 264482, 264509, 264905, 264906, 264584, 18108351, 264763, 18108370, 264907, 264566, 264908, 264764, 264288, 264587, 264909, 264486, 264765, 18108391

2874	94313549 (5747, 5748)	Novel Protein sim. GBank gi 3212854 (AC004005) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	52644507, 52645156, 52646365, 56182575, 22278994, 22278995, 56994075, 35696286, 60432048, 264259, 52645080, 29331822, 56182181, 28331824, 60424269, 29331825, 66714117, 28331826, 29331827, 35696052, 29331828, 33656970, 66712502, 52644045, 265007, 265009, 60433358, 264758, 55812038, 18108348, 52646317, 33108954, 33657084, 265017, 264604, 265018, 265019, 264882, 264369, 264288, 264688, 52644229, 21908766, 21908767, 21908768, 55811957, 265020, 265021, 265022, 52644150, 33657023, 52645129, 18108374, 18108376, 35696423, 56182323, 18108387, 87168518, 60432113, 22279000, 22279002, 264563, 264565
2875	88083726 (5749, 5750)	Novel Protein sim. GBank gi 2781386 (AC004010) - similar to Leucine-rich transmembrane proteins; 44% similarity to U42767 (PID:gi1736918) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	22278986, 22278997, 22278999, 29331826, 29331828, 28146489, 66712502, 265008, 265017, 18108351, 264683, 264689, 21906767, 18108376, 18108377, 55811576, 60170394, 22279000, 264487
2876	88090854 (5751, 5752)	Novel Protein sim. GBank gi 2979530 (AC004449) - R33883_2 [Homo sapiens]	Contains protein domain (PF00167) - Igf Fibroblast growth factor	Igf	
2877	84747029 (5753, 5754)	Novel Protein sim. GBank gi 4704208 emb CAB41646.1 - (AL035419) dJ1100H13.1 (putative novel protein) [Homo sapiens]			52646365, 65274572, 56182575, 22278997, 22278998, 22278999, 60432048, 52645080, 60424269, 60432289, 29331827, 35696052, 29331828, 66712502, 52644045, 56182435, 60433356, 33657402, 33657084, 265019, 55811150, 264448, 264369, 21908766, 21906768, 21906769, 265020, 33657023, 33657109, 33657182, 27486262, 264629, 60431528, 55811576, 52644332, 56182323, 264558, 83373044, 18108385, 56526486, 60432113, 22278000, 22279002, 264563
2878	88095309 (5755, 5756)	Novel Protein sim. GBank gi 3876775 emb CAB03057 - (Z81077) predicted using GeneFinder; Similarity to Yeast protein 8248 (TR:G587531) [Caenorhabditis elegans]	Contains protein domain (PF01207) - Uncharacterized protein family UPF0034	UNCLASSIFIED	264488, 264259, 28331822, 29331826, 264905, 264509, 264907, 264908, 264510, 265006, 264511, 264512, 33657402, 264758, 21906754, 18108351, 264681, 264682, 264288, 264684, 264685, 264768, 264689, 21906769, 264690, 33657023, 264693, 18108384, 33657109, 264629, 18108374, 264630, 264632, 264556, 264637, 264639, 264558, 18108385, 18108387, 264563, 264564, 264565, 264568, 264486, 264567

2878	87868122 (5757, 5768)	Novel Protein sim. GBank gi 4895145 gb AAD32752.1 - (AF127374) unknown [Streptomyces lavendulae]	Contains protein domain (PF00315) - UNCLASSIFIED Uracil-DNA glycosylase	18108359, 264259, 264905, 18108370, 264629, 264908, 264909, 18108374, 18108377, 265006, 264910, 264637, 60170394, 264558, 265017, 264564, 264565, 264567, 264684, 264369
2880	94851439 (5759, 5760)	Novel Protein sim. GBank gi 4880703 gb AAD27741.1 AF13296 - (AF132966) CGI-32 protein [Homo sapiens]		264488, 52846365, 52646842, 22278994, 35898288, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331828, 29331827, 35898052, 29331828, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 52644045, 264510, 265006, 264511, 265007, 264512, 265008, 264910, 264594, 21908754, 52846317, 52844288, 87168559, 264600, 264604, 264605, 264760, 264784, 264288, 264768, 264768, 264687, 264769, 21908768, 21908769, 35695917, 285021, 264690, 264692, 33657023, 52845129, 33657109, 33657182, 27486262, 33657349, 264629, 18108374, 35695855, 264634, 264635, 264636, 264637, 264638, 264557, 52844332, 264558, 264559, 83373044, 264404, 22279000, 264563, 264483, 264567, 264486
2881	87650539 (5761, 5762)	Novel Protein sim. GBank gi 733571 (U23452) - No definition line found [Caenorhabditis elegans]	UNCLASSIFIED	22278998, 28331822, 52644045, 21906765, 264639, 60432113
2882	87714367 (5763, 5764)	Novel Protein sim. GBank gi 118112 (U41559) - No definition line found [Caenorhabditis elegans]		264488, 22278998, 22278999, 29331822, 29331826, 264908, 60170831, 60433358, 55812038, 264681, 264682, 264686, 264687, 264688, 21908768, 21908769, 264693, 263987, 18108374, 55811578, 56182323, 22279002, 264568
2883	85362875 (5765, 5766)	Novel Protein sim. GBank gi 488008 gb AAD31087.1 AF10693 - (AF106934) vitamin D receptor-interacting protein [Homo sapiens]	Contains protein domain (PF00400) - UNCLASSIFIED WD domain, G-beta repeat	264112, 264582
2884	87784643 (5767, 5768)	Novel Protein sim. GBank gi 2224697 dbj BAA20832 - (AB002376) KIAA0378 [Homo sapiens]		265018, 264634
2885	83006306 (5769, 5770)	Novel Protein sim. GBank gi 2224697 dbj BAA20832 - (AB002376) KIAA0378 [Homo sapiens]	UNCLASSIFIED	264686, 264683
2886	91237823 (5771, 5772)	Novel Protein sim. GBank gi 1255889 (U53344) - T07H6.5 gene product [Caenorhabditis elegans]	Contains protein domain (PF00084) - complementrecept Sushi domain (SCR repeat)	60432049, 264258, 29331828, 264908, 264511, 264595, 60433438, 264596, 265017, 264805, 263989, 263972, 264555, 83373044, 87168518, 264568
2887	91227860 (5773, 5774)	Novel Protein sim. GBank gi 3882323 dbj BAA34521.1 - (AB018344) KIAA0801 protein [Homo sapiens]	UNCLASSIFIED	18108351, 264686, 264629, 264631, 264639, 83373044, 264482
2888	95105816 (5775, 5776)	Novel Protein sim. GBank gi 4508015 ref NP_003447.1 pZNF2 - zinc finger protein 205 [Homo sapiens]	Contains protein domain (PF00096) - transcriptfactor Zinc finger, C2H2 type	264488, 264259, 29331828, 264508, 264908, 264593, 264758, 264766, 264769, 18108374, 83373044, 264486

2889	87606562 (5777, 5778)				UNCLASSIFIED	56994075, 28331824, 265008, 284760, 18108354, 264288
2890	78703853 (5778, 5780)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]			UNCLASSIFIED	284591, 284786
2891	88094428 (5781, 5782)	Novel Protein sim. GBank gi 3877750 emb CAB01508 - (Z78084) predicted using Genefinder; similar to collagen; cDNA EST EMBL:D65865 comes from this gene; cDNA EST EMBL:D69451 comes from this gene; cDNA EST EMBL:D66028 comes from this gene; cDNA EST EMBL:D69658 comes from this gene...			UNCLASSIFIED	284591, 284595, 284389, 284685, 284693, 284628, 284563, 284568
2892	95419745 (5783, 5784)	Novel Protein sim. GBank gi 4929759 gb AAD34140.1 AF15190 - (AF151903) CGI-145 protein [Homo sapiens]			UNCLASSIFIED	65274572, 35696286, 29331828, 264110, 285009, 60433438, 285018, 265019, 18108351, 264288, 21906765, 21906766, 21906769, 55811957, 264690, 65274620, 263967, 35695855
2893	87798014 (5785, 5786)				UNCLASSIFIED	284259, 265010, 264682, 18108370, 264555, 264556
2894	87755985 (5787, 5788)	Novel Protein sim. GBank gi 5669015 gb AAD46135.1 - (AF080171) zinc finger protein ZNF232 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript factor		284259, 265006, 60433438, 52644286, 265011, 284389, 35695917, 18108381, 18108382, 18108388
2895	86938778 (5789, 5790)	Novel Protein sim. GBank gi 3924708 emb CAA84646 - (Z35597) Weak similarity with sea squirt nk1ogen precursor protein (blastp score 71); cDNA EST EMBL:T02069 comes from this gene; cDNA EST EMBL:D76135 comes from this gene; cDNA EST EMBL:D73147 comes from this gene; cDNA EST EMB...	Contains protein domain (PF01437) - Plexin repeat			29331824, 265007, 264762, 264636, 264563
2896	87752122 (5791, 5792)	Novel Protein sim. GBank gi 4885549 ref NP_005456.1 pPKBG - protein kinase B gamma	Contains protein domain (PF00068) - Eukaryotic protein kinase domain	kinase		18108392, 18108394, 18108398, 22278998, 264259, 29331822, 29331824, 29148499, 284908, 264908, 265007, 265009, 265018, 265019, 264389, 264685, 264689, 21906766, 265021, 264693, 33657182, 264639, 18108384, 18108388, 264567
2897	95413057 (5793, 5794)	Novel Protein sim. GBank gi 4502877 ref NP_001296.1 pCLDN - Clostridium perfringens enterotoxin receptor 1			UNCLASSIFIED	60424179, 56182575, 22278996, 35696286, 22278997, 22278999, 60432049, 284259, 29331824, 29331825, 60424269, 60432289, 29331826, 29331828, 35696052, 284908, 58182435, 265009, 264910, 60170831, 60431735, 60433356, 60433438, 65274444, 55811386, 265018, 18108351, 284448, 284288, 284687, 21906765, 21906766, 21906767, 21906769, 55811957, 35695917, 264534, 33657023, 33657109, 35695763, 264628, 264629, 60431528, 18108374, 55810764, 55811576, 35696423, 35695855, 264555, 56182323, 18108385, 264404, 22279000, 22279002, 264568
2898	87750340 (5795, 5796)				UNCLASSIFIED	22278995, 264604, 18108385, 284566

2899	80357670 (5787, 5788)					284764, 21908764, 284692
2800	84233538 (5789, 5800)					65274572, 56182575, 35696286, 60432049, 284259, 29331824, 66714117, 29331826, 35698052, 29331828, 66712502, 56182435, 285006, 265007, 265008, 265009, 60433356, 284758, 265018, 284764, 284765, 284288, 284768, 21908764, 21908768, 21906769, 265020, 284692, 284693, 32833986, 284631, 83373044, 60432113
2801	87444731 (5801, 5802)					22278995, 22278997, 22278999, 60432049, 29331822, 29331824, 29331825, 29331827, 35696052, 33656970, 284910, 265009, 21906754, 33657084, 87168474, 265010, 265018, 21908764, 21908765, 21906766, 21908767, 21908769, 33657023, 284693, 33657109, 33657349, 35696423, 35695855, 263981, 56182323, 22278002
2802	85745271 (5803, 5804)					284683, 284691
2803	87606733 (5805, 5806)					264887, 22278994, 284259, 29331826, 29331828, 284905, 52644045, 56182435, 264511, 265017, 265018, 18108351, 284446, 264683, 284769, 284689, 35695917, 52644150, 87168518, 60432113, 22279002
2804	86458072 (5807, 5808)					52646365, 22278999, 284259, 35696052, 265011, 265017, 284683, 284769, 35695917, 285020, 263967, 18108374, 35695855, 264637, 284952, 18108385, 18108387
2805	84449926 (5809, 5810)					265009, 284681, 284682
2806	85341051 (5811, 5812)					22278996, 35696286, 22278998, 284259, 60432288, 29331828, 29331830, 66712502, 265009, 60170831, 33108954, 284448, 284683, 284288, 284689, 21908766, 21908767, 21908768, 55811957, 35695917, 265022, 52644150, 284691, 33657023, 284692, 284693, 35695855, 60432113, 264586

2807	91211383 (5813, 5814)	Novel Protein sim. GBank gj1707079 (U80451) - contains strong similarity to a DNA-J-like domain (PS:PS00836) [Caenorhabditis elegans]	Contains protein domain (PF00226) - DnaJ domain	eph	52644507, 58182575, 56181686, 22278995, 58994075, 35698286, 60432049, 58182181, 35696052, 60431735, 264595, 55812038, 21906754, 55811388, 265019, 264682, 264369, 58181562, 21906766, 55811957, 35695917, 265020, 265021, 33657023, 33657109, 60431528, 55811576, 35696423, 35695855, 264638, 22279000
2808	80414246 (5815, 5816)	Novel Protein sim. GBank gj12673917 (AC002581) - putative ATP-dependent RNA helicase [Arabidopsis thaliana]		helicase	265008, 33109954, 18108351, 264766, 265021, 264691, 264692, 18108374, 264556, 264638, 264557, 264558
2809	87420225 (5817, 5818)			eph	264259, 87168474, 265018, 18108365, 264628
2810	86601075 (5819, 5820)	Novel Protein sim. GBank gj14539335[emb]CAB37483.1] - (AL035539) putative protein [Arabidopsis thaliana]			22278995, 264508, 264512, 265007, 33657402, 265017, 264369, 265022, 18108365, 264628
2811	94216615 (5821, 5822)	Novel Protein sim. GBank gj1469187[emb]CAB38415.1] - (AL031588) dJ1163J1.3 (novel protein similar to mouse B99) [Homo sapiens]		glucoamylase	52646365, 18108397, 22278995, 22278997, 22278998, 22278999, 29331824, 29331825, 52644045, 265006, 265018, 264448, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265021, 18108370, 18108372, 18108374, 22278000
2812	87731803 (5823, 5824)	Novel Protein sim. GBank gj14929637[gb]AAD34079.1 AF15184 - (AF151842) CGI-84 protein [Homo sapiens]	Contains protein domain (PF00904) - Involutrin repeat		52645156, 264092, 60432049, 264259, 52645080, 29331824, 29331825, 66712502, 33109954, 264760, 264683, 264288, 264886, 265021, 264693, 18108368, 263976, 264404
2813	87713823 (5825, 5826)	Novel Protein sim. GBank gj1854065[emb]CAA58337] - (X83413) U88 [Human herpesvirus 8]	Contains protein domain (PF00996) - Zinc finger, C2H2 type	UNCLASSIFIED	52644507, 52645156, 52646842, 56182575, 35698286, 22278997, 264259, 52645080, 29331827, 35698052, 29331828, 264828, 52644045, 56182435, 55812038, 52646317, 21906754, 52644296, 87168474, 265017, 265018, 265019, 18108351, 264882, 264686, 264689, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 52644150, 27486261, 27486262, 27486265, 35695763, 55811576, 35695855, 52644332, 22278000, 22279002, 264563
2814	87797300 (5827, 5828)				264557

2915	88081972 (5828, 5830)	Novel Protein sim. GBank gi 5174485 ref NP_008030.1 pKIAA - endocytic receptor (macrophage mannose receptor family)	Contains protein domain (PF00059) - eph Lectin C-type domain	264569, 264488, 264687, 284768, 21906788, 52848842, 21906767, 21906768, 58182575, 29148628, 35695917, 22278996, 22278997, 22278998, 265021, 22278999, 52644150, 284691, 284259, 60432048, 264692, 52645129, 33657109, 33657182, 29331827, 27486281, 35696052, 29331828, 27486282, 27486284, 27486285, 33657349, 29146498, 29146499, 284906, 284907, 18108370, 284908, 18108372, 52644045, 18108374, 56182435, 35695855, 284112, 264510, 265008, 60432229, 284593, 60433358, 56182323, 18108382, 55812038, 18108385, 33109954, 21906754, 33657084, 87168518, 265010, 265011, 60432113, 265017, 265018, 22279000, 265019, 55811150, 264681, 18108351, 264763, 264448, 264683, 264566, 18108354, 264369, 264288, 264768 52645156, 65274572, 22278994, 22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 33656970, 284509, 284908, 29331830, 52644045, 264909, 56182435, 60170831, 264592, 264593, 33657402, 60433358, 52646317, 21906754, 33109954, 33657084, 52644296, 85658542, 265011, 265017, 265018, 265019, 18108351, 264448, 284286, 52644229, 21906765, 21906768, 21906767, 21906768, 21906769, 55811957, 35695917, 265021, 265022, 52644150, 33657023, 33657109, 33657182, 27486281, 27486282, 27486284, 35695763, 18108376, 55811576, 35696423, 65274791, 35695855, 52644332, 264557, 264638, 56182323, 18108387, 87168518, 22279002, 264482
2916	95337790 (5831, 5832)	Novel Protein sim. GBank gi 5104851 dbj BAA80165.1 - (AP000061) 305aa long hypothetical dTDP-4- dehydrohamnose reductase [Aeropyrum pernix]	dehydrogenase	
2917	87454546 (5833, 5834)	Novel Protein sim. GBank gi 3169065 emb CAA19260.1 - (AL023704) putative translocation elongation factor-Tu fa mily [Schizosaccharomyces pombe]	UNCLASSIFIED	60433438, 264602, 284682, 87168518, 60432113
2918	85690529 (5835, 5836)	Novel Protein sim. GBank gi 539218 pir S38038 - hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae)		264638
2919	87641497 (5837, 5838)	Novel Protein sim. GBank gi 2564955 (AF030001) - unknown [Mus musculus]		66714117, 66712502, 263981

2820	87769523 (5838, 5840)				3596286, 2227897, 284259, 52845080, 29331824, 29331826, 29331827, 284828, 284909, 56182435, 284511, 284758, 33109954, 21908754, 52844296, 265010, 285011, 284601, 285017, 285019, 284881, 284887, 21908767, 285021, 52644150, 284890, 284891, 284892, 284693, 33857109, 33857182, 27486282, 27486284, 27486285, 35898423, 35898555, 284632, 284636, 284637, 284638, 56182323, 60170394, 18108385, 87168518, 60432113, 35898286, 22278997, 264091, 284092, 284094, 284259, 29331822, 29331824, 29331826, 29331827, 35898052, 29148498, 284104, 284105, 284107, 284508, 264110, 284112, 284512, 60433356, 21906754, 87168474, 265017, 18108351, 264288, 21908765, 21908768, 21908767, 21908769, 35895917, 265021, 263974, 18108374, 263976, 263977, 18108376, 284555, 263981, 56526486, 87168518, 22279000, 22279002, 284906, 284908, 284511, 265006, 285008, 284593, 33857402, 60174639, 18108351, 284763, 21908765, 28148627, 35895917, 284692, 284629, 263978, 55811576, 35895855, 264555, 284558, 56182323, 60170394, 22279000, 284488
2821	91639882 (5841, 5842)	Novel Protein sim. GBank gi 4580013 gb AAD24202.1 U83194_- (U83194) TRAF4-associated factor 2 (Homo sapiens)	Contains protein domain (PF00787) - PX domain		
2822	87749762 (5843, 5844)	Novel Protein sim. GBank gi 4589514 db BAA76779.1 (AB023152) KIAA0935 protein (Homo sapiens)	Contains protein domain (PF01074) - Glycosyl hydrolases family 38	kinase	
2823	95337799 (5845, 5846)	Novel Protein sim. GBank gi 4835268 emb CAB42898.2 (Z83844) dJ37E18.4 (similar to mouse p116Rip protein) (Homo sapiens)	Contains protein domain (PF00169) - PH domain	struct	
2824	87791967 (5847, 5848)	Novel Protein sim. GBank gi 2133095 pir S72254 - ribosomal protein L36, mitochondrial - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00444) - Ribosomal protein L36	ribosomalprot	
2825	95090120 (5849, 5850)	Novel Protein sim. GBank gi 238986 emb CAB11718 (Z98980) actin associated protein (Schizosaccharomyces pombe)		UNCLASSIFIED	56182575, 35898286, 284259, 60432289, 29331827, 284508, 52844045, 284910, 284591, 60432229, 55812038, 21908754, 284881, 284448, 284683, 284288, 284685, 52844229, 284689, 21908765, 21908766, 21908768, 21908769, 285021, 285022, 60170815, 284692, 33857023, 284693, 33857109, 35898423, 65274791, 56182323

2928	95343003 (5851, 5852)				29331828, 265011, 264768, 264689
2927	80408018 (5853, 5854)	Novel Protein sim. GBank gi 283032 pir S22456 - hydroxyproline-rich glycoprotein - perennial teosinte			264764, 264288, 264630, 264637
2928	20452179 (5855, 5856)			UNCLASSIFIED	264559
2929	91622920 (5857, 5858)	Novel Protein sim. GBank gi 3413320 emb CAA06915 - (AJ008215) CMP-N-acetylneuraminic acid synthetase [Mus musculus]		UNCLASSIFIED	264569, 264489, 22278994, 35686286, 22278996, 22278998, 22278999, 264094, 264259, 52645080, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 33856970, 264108, 29331830, 52644045, 265009, 33108954, 52644286, 87168559, 264760, 264762, 264448, 264764, 264288, 264766, 264768, 21906765, 21906766, 21906768, 21906769, 35695917, 264691, 33857023, 264693, 33657109, 18108374, 263976, 35896423, 35685855, 263981, 22279000, 22279002, 264567, 264486
2930	95302755 (5859, 5860)			UNCLASSIFIED	56182575, 56181686, 35696286, 22278996, 22278998, 22278999, 264259, 29331825, 60432289, 29331828, 264905, 52644045, 56182435, 265009, 60170831, 264592, 60432229, 60433356, 67168474, 265010, 265011, 265017, 265018, 265019, 264762, 264448, 264683, 264286, 264766, 21906765, 21906769, 35695917, 60170815, 33657023, 33857109, 264628, 18108370, 18108372, 35696423, 35695855, 264556, 56182323, 60432113, 264567
2931	94312693 (5861, 5862)	Novel Protein sim. GBank gi 3786433 (AF098505) - similar to Arabidopsis thaliana male sterility protein 2 (SW:Q08891) [Caenorhabditis elegans]	Contains protein domain (PF00471) - Ribosomal protein L33	UNCLASSIFIED	52645156, 22278997, 22278998, 29331822, 52645080, 29331824, 60432289, 33656970, 60433356, 60433438, 33108954, 21906765, 21906768, 21906767, 21906768, 265020, 52644150, 33657023, 33857109, 33657182, 27486265, 35696423, 35695855, 264555, 87168518, 60432113, 264566, 264906, 264907
2932	79632623 (5863, 5864)			helicase	264488, 18108382, 56182575, 22278999, 264091, 264259, 29331825, 60432289, 29331827, 264508, 52644045, 56182435, 265007, 265009, 264592, 60433356, 60433438, 21906754, 265017, 264682, 264288, 52644229, 21906765, 21906766, 21906768, 21906769, 265022, 52644150, 33657023, 33857109, 27486265, 264635, 264636, 60170394, 56182323, 18108385, 60432113, 264565, 264566, 264567
2933	91720776 (5865, 5866)	Novel Protein sim. GBank gi 3378056 (AF017777) - helicase [Drosophila melanogaster]			

2934	86576025 (5867, 5868)				22278997, 22278999, 29331824, 33657402, 284691, 27486262, 264628, 87168518, 22279000
2935	86410579 (5869, 5870)			UNCLASSIFIED	56182575, 22278995, 60433356, 33657402, 264758, 33109954, 21908754, 265018, 265019, 284448, 284769, 21908764, 21908765, 265021, 284692, 33657023, 33657109, 33657349, 55810764, 22279000
2936	87605863 (5871, 5872)	Novel Protein sim. GBank gi 4153862 (AC005065) - determined by GENSCAN prediction and spliced EST; match to EST R84329 (NID:942735) [Homo sapiens]	Contains protein domain (PF00856) - SET domain	nuclease	22278997, 29331827, 29331828, 265009, 265017, 264605, 265020, 55811576, 18108387, 60432113, 264563
2937	84853096 (5873, 5874)	Novel Protein sim. GBank gi 5174409 ref NP_006101.1 pCD2B - CD2 antigen (cytoplasmic tail)-binding protein 2		UNCLASSIFIED	56994075, 22278996, 264259, 60432049, 29331822, 56182181, 29331827, 29331828, 284908, 264908, 264909, 56182435, 265006, 284512, 284910, 60170831, 60433356, 265011, 265018, 18108351, 284448, 264288, 264768, 52844229, 21908765, 29148784, 65274791, 284558, 56182323, 60170394, 284558, 60432113, 264565, 264486, 264567
2938	95419773 (5875, 5876)	Novel Protein sim. GBank gi 3319990 emb CAA76720 - (Y17267) ubiquitin-conjugating enzyme [Mus musculus]	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	284488, 56182575, 22278998, 35696286, 22278997, 22278998, 22278999, 264490, 264259, 29331822, 29331824, 66714117, 29331827, 35696052, 264107, 264905, 66712502, 52844045, 56182435, 264511, 265008, 265009, 60432229, 33657402, 60433438, 55812038, 21908754, 85658542, 285010, 265011, 87168559, 265017, 265018, 285019, 264681, 264288, 264689, 21906765, 21906767, 21908768, 55811957, 35695917, 265020, 60170615, 264690, 284691, 264692, 33657023, 284693, 65274620, 33657109, 18108370, 18108374, 263976, 35696423, 35695855, 264555, 284558, 18108381, 56182323, 60170394, 83373044, 18108385, 56528486, 60432113, 22279002
2939	87786622 (5877, 5878)	Novel Protein sim. GBank gi 3978990 emb CAA99909 - (Z75547) similar to WD domain, G-beta repeat; cDNA EST yk371b7.5 comes from this gene; cDNA EST yk312h1.5 comes from this gene; cDNA EST yk465d5.5 comes from this gene; cDNA EST yk472c4.5 comes from this gene; cDNA EST yk292f8...	Contains protein domain (PF00400) - WD domain, G-beta repeat	ATPase-associated	284907, 265018, 264681, 264685, 264686

2940	95011103 (5879, 5880)				UNCLASSIFIED	22278986, 29331822, 29331824, 66714117, 29331828, 29331828, 264905, 264908, 66712502, 29331830, 265011, 265017, 264764, 264369, 21906766, 21906767, 33857023, 33857109, 32833986, 18108374, 18108377, 264634, 83373044, 18108385, 18108387, 264566
2941	21423370 (5881, 5882)	Novel Protein sim. GBank gi 3413872 dbj BAA32300 - (AB007924) KIAA0455 protein [Homo sapiens]			UNCLASSIFIED	264557
2942	67430203 (5883, 5884)	Novel Protein sim. GBank gi 172845 sp P46629 RB25_RABIT - RAS-RELATED PROTEIN RAB-25			glycoprotein	264910, 265010, 264768
2943	95314504 (5885, 5886)	Novel Protein sim. GBank gi 4929653 gb AAD34087.1 AF15185 - (AF151850) CGI-92 protein [Homo sapiens]			collagen	60432049, 264259, 60432288, 29331827, 29146498, 265008, 264593, 60433356, 60433438, 265010, 265011, 265017, 265018, 264683, 264766, 18108381, 65274727, 60432113, 264567
2944	95081063 (5887, 5888)	Novel Protein sim. GBank gi 4678282 emb CAB41190.1 - (AL049660) 1-acylcerol-3-phosphate acyltransferase-like protein [Arabidopsis thaliana]	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)		ATPase-associated	58984075, 22278998, 60432049, 264259, 29331822, 29331824, 60424269, 60432289, 29331826, 29331828, 264905, 264907, 52644045, 264909, 264511, 265008, 265009, 264594, 21906754, 87168559, 264603, 265017, 265018, 18108351, 264682, 264766, 264687, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 60170615, 52644150, 264690, 264691, 33857023, 264692, 264693, 33857109, 33857182, 33857349, 18108370, 18108374, 18108377, 55811578, 35695855, 264635, 264555, 264556, 56182323, 60170394, 264558, 264559, 83373044, 56528486, 87166518, 60432113, 22279002, 264482, 264563, 264484, 264567
2945	94233560 (5889, 5890)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII	Contains protein domain (PF00096) - Zinc finger, C2H2 type		UNCLASSIFIED	60424179, 22278995, 22278996, 22278998, 22278999, 264259, 56182181, 29331824, 60424269, 60432289, 35696052, 264608, 265008, 60433356, 55812038, 264759, 55811386, 265018, 264681, 18108351, 264448, 264683, 264369, 264288, 264687, 56181582, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264693, 60431528, 55810764, 35696423, 35695855, 264630, 60170394, 83373044, 22279000, 264566, 264567

2946	94317315 (5891, 5892)	Novel Protein sim. GBank gi 5441952 gb AAD43195.1 AF07286 - (AF072864) peroxisomal membrane protein PMP 24 [Homo sapiens]		UNCLASSIFIED	284488, 264259, 264508, 264509, 264906, 264907, 264809, 264510, 264511, 265007, 264512, 264810, 264591, 264593, 18108351, 264764, 264288, 264684, 264769, 265021, 264692, 33857109, 264628, 264629, 18108374, 264631, 264634, 264636, 264637, 18108380, 264638, 264639, 83373044, 264565, 264566, 264488, 264567
2947	87362952 (5893, 5894)	Novel Protein sim. GBank gi 3540281 gb AAC34383.1 - (AF056116) All-1 related protein [Fugu rubripes]		UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 29146498, 264508, 29331830, 265007, 265008, 265009, 60432229, 21908754, 265010, 265017, 265019, 264768, 264685, 21908765, 21908766, 21908767, 21908768, 21908769, 265020, 264628, 18108370, 264629, 264630, 18108387, 60432113
2948	87626527 (5895, 5896)	Novel Protein sim. GBank gi 5566614 gb AAB65654.2 - (AF001533) mitogen-induced [Mus musculus]			52846842, 22278995, 264259, 29331824, 29331825, 29331827, 29331830, 264909, 265007, 265009, 265019, 264763, 264684, 264288, 264685, 264686, 21908767, 264691, 264692, 264693, 18108374, 55811576, 18108385, 22279002, 264563, 264567
2949	88175545 (5897, 5898)	Novel Protein sim. GBank gi 2132823 pir S67133 - probable membrane protein YOR240w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	22278998, 22278997, 60432289, 29331826, 29331827, 29331828, 35696052, 29146499, 264104, 264107, 264805, 66712502, 264908, 60433356, 60433438, 87168559, 264764, 52844229, 56181562, 21908767, 21908768, 21908769, 265022, 60170615, 33857023, 35696423, 263981, 264558, 60432113, 22279002
2950	95086870 (5899, 5900)	Novel Protein sim. GBank gi 466102 sp P34629 Y0J6_CAEEL - PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III	Contains protein domain (PF00863) - Cytosol aminopeptidase family	peptidase	284488, 35696286, 264259, 35696052, 264907, 265007, 264910, 265017, 265018, 264288, 264768, 35695917, 265020, 18108362, 18108370, 18108379, 35696423, 65274791, 35695855, 264558, 56526486, 264486
2951	87392357 (5901, 5902)	Novel Protein sim. GBank gi 4688902 emb CAB41450.1 - (AJ238248) centaurin beta2 [Homo sapiens]			264683

2852	95329852 (5903, 5904)	Novel Protein sim. GBank gij5596893jemb[CAB51405.1] - (AL098881) hypothetical protein [Homo sapiens]	Contains protein domain (PF00650) - CRAL/TRIO domain.		264687, 52845156, 21908766, 21906769, 22278998, 265020, 264690, 60432048, 264259, 264693, 29331822, 18108365, 29331825, 60432289, 33657109, 18108368, 29331827, 35696052, 27486252, 264508, 264905, 20281149, 264906, 264907, 29331830, 264908, 264909, 35695855, 264511, 265008, 265009, 264910, 264635, 264636, 60432229, 264638, 60433358, 264639, 264756, 87168518, 265017, 22279000, 22279002, 264760, 264563, 264482, 18108351, 264448, 264288, 18108398, 58994075, 22278996, 29331822, 29331824, 29331825, 29331827, 35898052, 264508, 264905, 264908, 264907, 264510, 264591, 264594, 33657402, 264595, 264586, 264758, 52846317, 21908754, 33657084, 52644286, 87168559, 264600, 264760, 264681, 18108351, 264764, 264369, 264288, 264687, 21906765, 21908766, 21906767, 21906768, 21906769, 35895917, 33657023, 18108364, 52645128, 33657109, 33657349, 18108374, 263978, 35695855, 264637, 264638, 87168518, 264482, 264563, 264565, 29331822
2853	88093575 (5905, 5906)	Novel Protein sim. GBank gij119522spP10658[SERC_RABIT - PROBABLE PHOSPHOSERINE AMINOTRANSFERASE (PSAT) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EPIP)]	Contains protein domain (PF00266) - Amino transferases class-V	UNCLASSIFIED	
2854	88086288 (5907, 5908)	Novel Protein sim. GBank gij4885261refNP_005251.1pGDF9 - growth differentiation factor 9	Contains protein domain (PF00019) - Transforming growth factor beta like domain	Igf	
2855	87698426 (5908, 5910)	Novel Protein sim. GBank gij3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 29331822, 29331824, 29331825, 29331826, 35898052, 264908, 52644045, 264512, 60432228, 265018, 265019, 55811150, 264769, 21908767, 21908768, 21908769, 265021, 60170615, 55810764, 264567
2856	85769745 (5911, 5912)	Novel Protein sim. GBank gij4889254[gblAAD27830.1AF12185 - (AF121857) sorting nexin 7 [Homo sapiens]	Contains protein domain (PF00787) - PX domain		22278996, 264259, 29331827, 264908, 21908768
2857	90933301 (5913, 5914)	Novel Protein sim. GBank gij4503023refNP_000089.1pCPT2 - carnitine palmitoyltransferase II precursor		cadherin	22278998, 264259, 29331824, 29331827, 265008, 264595, 264758, 265010, 265011, 264448, 264763, 264803, 264288, 264685, 18108357, 29146629, 264690, 18108362, 264693, 18108370, 60431528, 18108374, 264634, 18108381, 56182323, 18108382, 18108385, 18108388, 58528486, 87168518, 264482, 264487
2858	87440014 (5915, 5916)	Novel Protein sim. GBank gij4240257dbj[BAA74907.1] - (AB020691) KIAA0884 protein [Homo sapiens]			264595, 264596, 264681, 264369, 264629, 264631, 264567

2859	95109420 (5917, 5918)	Novel Protein sim. GBank gj988221 (U33005) - Tbc1 [Mus musculus]	Contains protein domain (PF00566) - oncogene TBC domain	263994, 22278997, 264259, 60432049, 29331826, 29331828, 35696052, 29331830, 68712502, 56182435, 265008, 264512, 265008, 265009, 60433358, 60433438, 264596, 265017, 265018, 264683, 264288, 264766, 264769, 21908766, 21908767, 21908769, 265020, 60170615, 264692, 27486285, 18108374, 65274791, 35695855, 83373044, 56526486, 60432113
2860	87420091 (5919, 5920)		UNCLASSIFIED	35696286, 56182435, 87188474, 265010, 60170615, 35696423, 56182323, 18108383, 87188518, 264483
2861	95413416 (5921, 5922)	Novel Protein sim. GBank gj5596646[emb] (CA805177.2) - (Z82286) predicted using GeneFinder; similar to WD domain, G-beta repeats [Caenorhabditis elegans]	Contains protein domain (PF00400) - WD domain, G-beta repeat	22278997, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 264907, 264908, 52844045, 265006, 33657402, 21908754, 87188474, 265011, 87188559, 265017, 21908769, 265020, 60170615, 264692, 33657023, 35695763, 18108370, 18108374, 35696423, 264632, 264636, 18108385, 87168518, 22279002, 264564, 264587
2862	87912700 (5923, 5924)		UNCLASSIFIED	35696286, 22278997, 264092, 264094, 264259, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264508, 264905, 264509, 264907, 264908, 264909, 264510, 264512, 264593, 264594, 60433438, 264758, 52846317, 264802, 264603, 264605, 264760, 264762, 264764, 264288, 264768, 264686, 264768, 264769, 35695917, 265020, 264691, 264634, 264636, 264637, 264638, 264639, 18108385, 264563, 264565, 264566, 264567, 264486
2863	95313464 (5925, 5926)	Novel Protein sim. GBank gj4240223[dbj] (BAA74890.1) - (AB020874) KIAA0867 protein [Homo sapiens]	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	18108392, 56994075, 22278998, 22278999, 29331822, 29331825, 29331826, 29331827, 29331828, 265007, 265008, 264592, 264594, 21908754, 265016, 264760, 264687, 29148627, 29148784, 265020, 33657023, 264693, 65274620, 33657182, 27486281, 264629, 55810784, 35696423, 264555, 264636, 264637, 264557, 264558, 264563
2864	94324617 (5927, 5928)		UNCLASSIFIED	264259, 29331826, 33657402, 265017, 265018, 264692, 18108386, 35696423, 83373044, 18108388

2865	80384762 (5929, 5930)	Novel Protein sim. GBank gi 4885447 ref NP_005452.1 pKRML - Kreisler (mouse) mar- related leucine zipper homolog			transcriptfactor	284259, 29331826, 284508, 284509, 284905, 284907, 284908, 284909, 284511, 285008, 284910, 284591, 284593, 284594, 33657402, 285011, 284760, 284762, 284764, 284288, 284885, 284768, 284892, 33657109, 284628, 284628, 35885855, 284630, 284631, 284632, 284634, 284635, 284636, 284637, 284638, 284639, 284563, 284567, 18108391 60432289, 284682, 284448
2866	91725248 (5931, 5932)	Novel Protein sim. GBank gi 5262751 emb CAB45690.1 - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]				
2867	84658303 (5933, 5934)	Novel Protein sim. GBank gi 624225 (U19181) - Rabin3 [Rattus norvegicus]			UNCLASSIFIED	284488, 284508, 284509, 284908, 284909, 284511, 284910, 284594, 284758, 85858542, 284782, 284764, 285021, 284556, 18108381, 284584, 284488
2868	95302776 (5935, 5936)	Novel Protein sim. GBank gi 4929715 gb AAD34118.1 AF15188 - (AF151881) CGI-123 protein [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)			284687, 52645156, 21906765, 52646365, 21906767, 18108398, 35896423, 22278996, 35896286, 22278997, 285020, 22278999, 285021, 285022, 284093, 284636, 284690, 52644150, 284258, 33657023, 52645080, 284693, 29331822, 56182181, 29331824, 66714117, 29331825, 33109954, 52645129, 29331826, 21906754, 33657182, 29331827, 29331828, 35898052, 27486262, 87168518, 87168474, 265010, 87168559, 265018, 22279000, 265019, 22279002, 284563, 18108351, 284806, 284907, 284448, 66712502, 284566, 284369, 284288
2869	95310957 (5937, 5938)	Novel Protein sim. GBank gi 3024743 sp O24734 THSA_SULS7 - THERMOSOME, ALPHA SUBUNIT (CHAPERONIN ALPHA SUBUNIT)			eph	52646842, 22278996, 22278998, 22278999, 60432049, 284259, 29331824, 29331825, 29331826, 29331828, 284509, 284909, 52644045, 56182435, 285009, 60433438, 55812038, 21908754, 265011, 87168559, 285018, 265019, 284448, 284288, 284369, 52644229, 21908768, 21908769, 21908769, 29148784, 285020, 285021, 52844150, 284691, 33657109, 18108374, 56182323, 60170394, 87168518, 60432113, 22279000
2870	88088071 (5939, 5940)	Novel Protein sim. GBank gi 3165407 (AC004755) - fos37502_1 [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain		homeobox	

2971	94196930 (5941, 5942)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		tm7	254488, 56182575, 35696286, 56994075, 29331824, 29331828, 29146499, 284508, 264905, 264907, 264112, 264910, 21908754, 87168559, 285018, 285019, 18108351, 284689, 21908765, 21906767, 21906768, 265020, 265021, 60170615, 18108364, 264628, 264629, 18108374, 264636, 264556, 264558, 83373044, 18108384, 18108385, 87168518, 264584, 264587
2972	86625943 (5943, 5944)	Novel Protein sim. GBank gi 728838 sp P39193 ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		kinase	265017, 35695917, 265021, 33657109, 22279002, 264563
2973	91215301 (5945, 5946)	Novel Protein sim. GBank gi 2746789 (AF040842) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	29331822, 264692, 33657349, 55811576, 264563
2974	91673002 (5947, 5948)	Novel Protein sim. GBank gi 786117 (L41834) - nuclear protein [Ensis minor]		UNCLASSIFIED	18108392, 52644507, 56182575, 56181688, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331824, 29331825, 66714117, 60424269, 29331826, 29331827, 29331828, 35698052, 66712502, 264908, 52644045, 265007, 284910, 265009, 60433438, 33109954, 21908754, 55811386, 52644296, 87168474, 87168559, 265017, 265018, 265019, 18108351, 264448, 264389, 264288, 52644228, 18108359, 21906765, 21908767, 21908768, 35695917, 265020, 265021, 52644150, 264691, 264692, 33657023, 27486262, 27486264, 35695783, 18108370, 18108376, 55810764, 55811576, 35698423, 35695855, 264630, 264635, 264557, 52644332, 264558, 83373044, 18108387, 87168518, 60432113, 22279000, 264482, 264487
2975	85325213 (5949, 5950)	Novel Protein sim. GBank gi 3880812 emb CAA19508 - (AL023839) similar to HECT-domain (ubiquitin-transferase); cDNA EST yk480d10.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00632) - ubiquitin HECT-domain (ubiquitin-transferase).		29331824, 29331827, 29331828, 264910, 85658542, 265011, 265018, 264448, 264288, 264769, 21908767, 265020, 264691, 264559, 83373044
2976	87771202 (5951, 5952)	Novel Protein sim. GBank gi 5679138 gb AAD46874.1 AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]		transport	22278998, 264806, 265007, 265010, 265011, 265017, 265019, 18108351, 264685, 264689, 18108370, 264639, 18108385
2977	91725254 (5953, 5954)	Novel Protein sim. GBank gi 5262751 emb CAB45690.1 - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]		UNCLASSIFIED	264509, 264288

2878	87332059 (5955, 5956)	Novel Protein sim. GBank gi 748549 (U23522) - No definition line found [Caenorhabditis elegans]	Contains protein domain (PF00480) - ROK family	UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 264259, 60432289, 29331827, 29146499, 56182435, 265006, 265007, 265009, 60433356, 60433438, 21906754, 265010, 265011, 265017, 265018, 265019, 264288, 264685, 264688, 21908765, 21908766, 21908767, 21908768, 21908769, 265020, 265021, 265022, 35696423, 264639, 60432113, 22278000, 22279002
2879	91725256 (5957, 5958)	Novel Protein sim. GBank gi 5262751 emb CAB45690.1 - (AJ243177) Xenopus RPA Interacting protein alpha [Xenopus laevis]		complement	264486, 65274572, 56984075, 22278999, 264093, 29331822, 29331824, 264288, 55811957, 33657023, 33657109, 18108370, 55811576, 56182323, 60432113, 264482
2880	86296600 (5959, 5960)				265009, 21908767, 263981, 22278000
2881	87376330 (5961, 5962)				264629, 264564
2882	95303675 (5963, 5964)	Novel Protein sim. GBank gi 4929767 gb AAD34144.1 AF15190 - (AF151907) CGI-149 protein [Homo sapiens]		UNCLASSIFIED	22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 264092, 29331824, 29331827, 29331828, 264905, 264591, 264592, 264594, 264595, 264596, 33657084, 264448, 21908765, 21908766, 21908767, 21908768, 21908769, 265020, 265022, 18108365, 33657182, 33657349, 35696423, 83373044, 22278000, 22279002
2883	91725258 (5965, 5966)	Novel Protein sim. GBank gi 5262751 emb CAB45680.1 - (AJ243177) Xenopus RPA Interacting protein alpha [Xenopus laevis]			60424178, 52646842, 18108398, 22278997, 264093, 60432049, 264259, 29331822, 60432289, 33656970, 264905, 52844045, 265006, 60431735, 87168474, 265018, 265019, 18108351, 264448, 21908765, 21908768, 35695917, 33657023, 52845129, 18108370, 35698423, 83373044, 58528486, 60432113, 264404, 22279002
2884	94136467 (5967, 5968)	Novel Protein sim. GBank gi 2393734 (AC002542) - similar to C. elegans F11A10.5; 80% similarity to Z88297 (PID:g1130619) [Homo sapiens]		ATPase_associated	
2885	87099072 (5969, 5970)	Novel Protein sim. GBank gi 103160 pir S22126 - finger protein unkempt - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	264910, 55812038, 56181562, 55811957, 264626, 55810764, 264632, 264635, 60432113
2886	86284661 (5971, 5972)				55811957, 264566
2887	86455934 (5973, 5974)			UNCLASSIFIED	264369

2988	95357753 (5975, 5978)	Novel Protein sim. GBank gi 4678028 gb AAD27002.1 - (AF077207) HSPC021 [Homo sapiens]		UNCLASSIFIED	284488, 65274572, 22278995, 22278998, 22278997, 22278999, 284092, 284094, 284259, 60432049, 29331824, 29331828, 60432289, 35698052, 29331828, 284107, 284905, 284907, 284908, 66712502, 284828, 284909, 58182435, 265008, 265007, 265008, 60170831, 60432228, 284593, 60433358, 284757, 60433438, 21908754, 265010, 265011, 87168559, 265017, 265018, 284882, 284448, 284389, 284288, 284885, 52844228, 21908765, 21908767, 21908769, 35695917, 265021, 265022, 52644150, 264690, 33657023, 65274620, 263967, 33657109, 27486262, 18108370, 18108372, 18108374, 55810764, 65274791, 35695855, 264635, 264636, 264637, 263981, 264638, 56182323, 83373044, 60432113, 22279000, 284563, 284584, 284565, 264566, 284567
2889	91225118 (5977, 5978)	Novel Protein sim. GBank gi 13671 sp P23984 ALUF_HUMAN - IIII ALU CLASS F WARNING ENTRY IIII		kinase	22278998, 22278997, 284905, 284511, 80170831, 284583, 265019, 21908765, 21908767, 21908768, 18108374
2890	87330444 (5979, 5980)	Novel Protein sim. GBank gi 2829838 sp P97348 RHOD_MOUSE - RHO-RELATED GTP-BINDING PROTEIN RHOD	Contains protein domain (PF00071) - Ras family	oncogene	265007, 284512, 18108351, 284288, 264689, 265020, 264691, 33657023, 33657109
2891	94325361 (5981, 5982)			UNCLASSIFIED	264563
2892	85425184 (5983, 5984)			UNCLASSIFIED	284259, 265018, 264689, 18108385
2893	94325363 (5985, 5986)			UNCLASSIFIED	284488, 29331822, 265017, 264761, 21908769, 65274791, 263981, 284565
2894	94136634 (5987, 5988)	Novel Protein sim. GBank gi 2498549 sp Q50858 YU02_MYCTU - HYPOTHETICAL 29.7 KD PROTEIN CY339.02		transport	22278994, 22278995, 56894075, 22278997, 22278999, 284259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 265006, 265008, 264910, 33109954, 87168474, 87168559, 265018, 285019, 284448, 284288, 21908766, 21908767, 21908768, 21908769, 265021, 265022, 33657023, 284693, 35695855, 83373044, 18108385, 22279000, 284565, 284568
2895	87591070 (5989, 5990)	Novel Protein sim. GBank gi 2734081 (AF000195) - similar to oxysterol-binding proteins [Caenorhabditis elegans]			284905, 264907, 265019, 18108351, 264683
2896	91013788 (5991, 5992)	Novel Protein sim. GBank gi 2829912 (AC002291) - Similar ATP-dependent RNA Helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	65274572, 35698286, 284259, 29331824, 35698052, 29148498, 284508, 284907, 265007, 265008, 60433438, 18108348, 265017, 284681, 264683, 264288, 284768, 284769, 264689, 35695917, 60170815, 33657023, 284692, 284634, 284555, 18108381, 18108382, 18108388, 264484

2997	87627440 (5993, 5994)	Novel Protein sim. GBank gij4589652[dbj BAA76848.1] - (AB023221) KIAA1004 protein [Homo sapiens]		homeobox	264488, 56182575, 284259, 66714117, 29331826, 35698052, 284508, 284509, 284907, 264808, 265008, 87168474, 265019, 264446, 284682, 264685, 264766, 21908764, 21908766, 21908768, 21908769, 27486281, 18108374, 35698423, 284634, 284635, 284636, 284557, 18108385, 87168518
2998	88095381 (5995, 5996)	Novel Protein sim. GBank gij3947589[emb CAA22252] - (AL034384) cDNA EST yk255b8.3 comes from this gene; cDNA EST yk255b9.5 comes from this gene; cDNA EST EMBL:M75923 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	52646365, 22278997, 284508, 284906, 18108351, 21908765, 21906767, 18108370, 18108374, 35698423, 284636, 284639
2999	94847055 (5997, 5998)	Novel Protein sim. GBank gij115408[sp P18835 CC19_CAEEL - CUTICLE COLLAGEN 19		UNCLASSIFIED	56182575, 22278996, 29147620, 29331825, 29148498, 29148499, 284905, 66712502, 265006, 265009, 21908754, 85658542, 18108351, 29148627, 29148629, 60170615, 33657109, 27486282, 18108370, 18108374, 284556, 284557, 284558, 60170394, 18108385, 284563
3000	95099370 (5999, 6000)	Novel Protein sim. GBank gij1163174 (U32575) - similar to yeast Sec8p. Swiss-Prot Accession Number P32844; similar to mammalian B94, Swiss-Prot Accession Number Q03169; Method: conceptual translation supplied by author [Rattus norvegicus]		UNCLASSIFIED	264887, 22278997, 22278999, 284259, 29331822, 29331824, 35698052, 29148498, 284508, 284905, 284908, 284907, 264908, 284909, 264510, 284511, 265008, 265007, 265008, 265009, 284910, 33657402, 264757, 284595, 284596, 284758, 21906754, 265011, 284800, 265017, 265018, 284605, 265019, 264760, 284761, 284762, 284681, 284682, 284764, 284288, 284685, 284768, 284686, 284768, 284769, 21908765, 21908768, 35695917, 265020, 264691, 264692, 33657023, 284693, 33657109, 33657182, 27486261, 284628, 284629, 18108374, 18108376, 35698423, 35695855, 284630, 284631, 284632, 284634, 284635, 284636, 284637, 284556, 284638, 284639, 60170394, 83373044, 20798451, 22279002, 284563, 284488, 284567
3001	88078454 (6001, 6002)	Novel Protein sim. GBank gij2078470 (AC002073) - Putative gene. Genscan predictions confirmed by EST splicing; coded for by human cDNAs AA122029 (NID:g1678048), D31562 (NID:g844442), AA158721 (NID:g1733515), R59640 (NID:g830335) and F13082 (NID:g709111) [Homo sapiens]		cathepsin	18108394, 52646842, 56182575, 29331824, 29331825, 29331827, 284910, 33109954, 52844298, 265017, 265019, 264288, 265020, 265021, 52844150, 284692, 35695763, 55810764, 35698423, 56182323, 18108387, 284563, 284564
3002	87718167 (6003, 6004)	Novel Protein sim. GBank gij3599478 (AF085185) - Myosin-IA [Acanthamoeba castellanii]		UNCLASSIFIED	284488, 29331824, 29331825, 29331826, 29331827, 29331828, 284906, 284510, 265009, 21906754, 284682, 284688, 33657023, 284565

3003	86848079 (6005, 6006)	Novel Protein sim. GBank gij1754869 (U30292) - collagen type XIII alpha-1 chain [Mus musculus]	Contains protein domain (PF01391) - Collagen triple helix repeat (20 copies)	collagen	284512, 284593, 284584, 284587, 284486
3004	88068876 (6007, 6008)	Novel Protein sim. GBank gij2224629[dj]BAA20802] - (AB002342) KIAA0344 [Homo sapiens]			29331830, 21906769, 284691, 33657109, 283972, 18108385
3005	87794843 (6009, 6010)	Novel Protein sim. GBank gij4680859[gb]AAD27719.1[AF13294 - (AF132944) CGI-10 protein [Homo sapiens]	Contains protein domain (PF01360) - Monooxygenase	oxygenase	29331822, 29331824, 29331827, 60433438, 285011, 285019, 21906766, 21906767, 21906768, 265020, 33657023, 33657349, 80170394, 22279002, 284567
3006	87422224 (6011, 6012)	Novel Protein sim. GBank gij3930525 (AF064447) - sex-determination protein homolog Fem1a [Mus musculus]	Contains protein domain (PF00023) - Ank repeat	MHC	264259, 29331822, 284512, 21906754, 285018, 284687, 21906785, 284691, 284555, 284556, 284558, 18108385
3007	80936005 (6013, 6014)	Novel Protein sim. GBank gij2565052 (U80738) - CAGH1a [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	52644507, 52845156, 65274572, 284909, 284512, 285018, 284760, 284448, 284765, 284689, 80170615, 18108374, 20281152, 264636, 52644332
3008	80416249 (6015, 6016)				264905, 284593, 284766, 284636
3009	91213387 (6017, 6018)	Novel Protein sim. GBank gij3127193 (AF062389) - kidney-specific protein [Rattus norvegicus]	Contains protein domain (PF00501) - AMP-binding enzyme	synthase	52646842, 58182575, 22278995, 22278996, 284259, 29331825, 29331826, 29331827, 29331828, 35696052, 284508, 284509, 284907, 56182435, 284511, 285007, 284512, 285008, 284757, 284758, 55812038, 284759, 33109954, 21906754, 285010, 285011, 284600, 285017, 285018, 285019, 284760, 18108351, 284288, 284389, 21906784, 21906785, 21906767, 55811957, 285020, 265021, 284691, 18108368, 27486282, 20281149, 18108370, 55811578, 284637, 284556, 284557, 18108381, 284558, 58182323, 284559, 18108385, 18108388, 22279002, 284486
3010	95317217 (6019, 6020)	Novel Protein sim. GBank gij4927370[gb]AAD33084.1[AF06787 - (AF067972) DNA cytosine methyltransferase 3 alpha [Homo sapiens]	Contains protein domain (PF01923) - Protein of unknown function	UNCLASSIFIED	264686, 284687, 21906767, 21906769, 55811957, 22278995, 35695917, 22278996, 22278997, 285020, 285021, 60170615, 284692, 33657023, 29331822, 284693, 18108384, 29331824, 33657109, 60432289, 29331827, 27486281, 29331828, 284508, 284909, 55811576, 35695855, 285008, 284556, 60433438, 83373044, 18108387, 65274727, 60432113, 285017, 22279000, 265019, 284584, 284682, 284784
3011	94323597 (6021, 6022)	Novel Protein sim. GBank gij5052319[gb]AAD38501.1[AF11883 - (AF118838) citrin; adult-onset type II citrullinemia protein [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	35696052, 58182435, 284756, 21906754, 285018, 284760, 284762, 18108351, 284682, 284448, 21906766, 65274620, 18108374, 284482, 284564
3012	87753087 (6023, 6024)			UNCLASSIFIED	263972

3013	91238799 (6025, 6026)	Novel Protein sim. GBank gij3702286 (AC005787) - R33374_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transcriptfactor	264488, 263994, 35696286, 22278997, 264259, 29331824, 60424289, 66714117, 35698052, 284905, 284906, 284907, 284908, 284909, 58182435, 284511, 284512, 284910, 284591, 284592, 284593, 284594, 33657402, 60433438, 284595, 284596, 55812038, 284758, 33109954, 21908754, 285010, 285016, 284604, 284780, 284682, 284683, 284764, 284389, 284288, 284765, 284766, 284686, 284768, 284687, 21908767, 35695917, 265020, 33657023, 284692, 284693, 33657109, 284628, 264629, 55811576, 35696423, 35695855, 284630, 284631, 284632, 284634, 284635, 284638, 284637, 284638, 284639, 83373044, 284563, 284565, 284566, 284567, 284760
3014	79877263 (6027, 6028)	Novel Protein sim. GBank gij3878374[emb CAA93081] - (Z68879) Similarity to Yeast Chl12p protein (PIR Acc. No. S54453); cDNA EST EMBL:D27950 comes from this gene; cDNA EST EMBL:D27949 comes from this gene; cDNA EST EMBL:D33447 comes from this gene; cDNA EST EMBL:D33316 comes from...		ATPase_associated	
3015	86995468 (6029, 6030)				22278995, 22278996, 22278997, 284259, 29331824, 29331825, 284906, 265007, 265008, 284910, 265011, 265017, 265019, 284691, 33657109, 18108370, 35695855, 284556, 284564
3016	87759945 (6031, 6032)	Novel Protein sim. GBank gij1168819[sp P41733 CC91_YEAST - CELL DIVISION CONTROL PROTEIN 91		UNCLASSIFIED	52644507, 52646842, 56994075, 52645080, 29331822, 29331824, 35698052, 33656970, 52844045, 264596, 33657084, 265017, 265019, 52644229, 21906767, 35695917, 52844150, 33657023, 33657109, 27486261, 27486262, 27486284, 33657349, 27486265, 35695763, 35695855, 87168518
3017	85011154 (6033, 6034)	Novel Protein sim. GBank gij4589658[dbj BAA76851.1] - (AB023224) KIAA1007 protein [Homo sapiens]			284488, 18108397, 22278996, 35696286, 22278999, 284259, 29331822, 60432289, 264908, 29331830, 284909, 56182435, 265006, 265007, 265008, 285009, 284591, 60433356, 60433438, 52846317, 21908754, 55811388, 265010, 265011, 87168559, 265017, 265018, 265019, 264288, 264687, 21906765, 21906766, 21906767, 21908769, 265020, 265022, 65274620, 52845129, 33657109, 33657182, 18108370, 263972, 18108374, 264631, 52844332, 83373044, 18108385, 18108388, 56526486, 87168518, 284404, 80432113, 22279000, 284567

3018	11073891 (6035, 6036)	Novel Protein sim. GBank gjl3219332 (AC004020) - Unknown gene product [Homo sapiens]			264558	264569, 52844507, 18108394, 65274572, 56182575, 22278994, 22278995, 56894075, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331827, 264908, 56182435, 265007, 265008, 60432229, 264593, 60433356, 55812038, 21908754, 87168474, 265011, 87168559, 265017, 265018, 265019, 264681, 18108351, 264448, 264682, 264683, 18108354, 264685, 264687, 264688, 21908766, 21906768, 21906769, 52644150, 264690, 264691, 33657023, 264692, 264693, 33657109, 52645129, 33657349, 264628, 65274791, 264634, 52644332, 56182323, 18108385, 87168518, 22279000, 22279002, 264583
3019	94148231 (6037, 6038)			oncogene		264488, 22278994, 35696286, 264259, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264910, 60174639, 264600, 264603, 264760, 264762, 264682, 264763, 264764, 264288, 264369, 264766, 264687, 264688, 264769, 55811957, 35695917, 33657023, 264628, 35696423, 35695855, 264630, 264632, 264634, 264635, 264636, 264637, 264558, 264557, 264638, 264639, 83373044, 18108385, 264584, 264587, 264488
3020	94318251 (6039, 6040)	Novel Protein sim. GBank gjl3414809 (AF061529) - rjs [Mus musculus]	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)	ATPase-associated		264769, 264628, 264482
3021	80478512 (6041, 6042)	Novel Protein sim. GBank gjl3880889[emb]CAB09005] - (Z95559) cDNA EST yk236d4.5 comes from this gene; cDNA EST EMBL:C13455 comes from this gene; cDNA EST yk329g6.5 comes from this gene; cDNA EST CEMSH45R comes from this gene [Caenorhabditis elegans]				
3022	97718500 (6043, 6044)			UNCLASSIFIED		264259, 29331826, 29331828, 264288, 264586
3023	95305484 (6045, 6046)	Novel Protein sim. GBank gjl416592[sp]P32323JAGA1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR	Contains protein domain (PF00614) - Phospholipase D. Active site motif	UNCLASSIFIED		264488, 22278995, 35696286, 22278997, 29331826, 35696052, 264907, 29331830, 52644045, 56182435, 60432229, 264592, 60433356, 60433438, 264689, 21908767, 55811957, 35695917, 265021, 18108378, 263978, 264635, 264558, 22278000
3024	86675305 (6047, 6048)			UNCLASSIFIED		60432049, 264760, 21906769, 55811957, 35695917, 264890, 264555, 264559
3025	65706629 (6049, 6050)	Novel Protein sim. GBank gjl295671 (L11275) - selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III [Saccharomyces cerevisiae]				264593, 55811576

3026	87643662 (6051, 6052)	Novel Protein sim. GBank gi 3024052 sp P97924 KARI_RAT - KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10)		UNCLASSIFIED	22278996, 22278997, 264490, 29331825, 264111, 265007, 60170831, 265010, 87188559, 265019, 21906765, 29148627, 263987, 20281149, 20281089, 263975, 263977, 20281071, 56528486, 22279000
3027	94844563 (6053, 6054)	Novel Protein sim. GBank gi 4929847 gb AAD34084.1 AF15184 - (AF151847) CGI-89 protein [Homo sapiens]	Contains protein domain (PF01529) - DHHC zinc finger domain	UNCLASSIFIED	18108394, 22278995, 22278996, 35696286, 22278997, 22278998, 60432049, 284259, 29331822, 29331824, 68714117, 29331825, 60432289, 29331828, 29331827, 29331828, 35696052, 284905, 284907, 29331830, 284908, 264909, 264510, 265007, 265008, 265009, 264910, 33857402, 264596, 21906754, 265010, 265011, 87168559, 264800, 265018, 18108351, 264682, 264683, 264764, 264286, 264685, 264687, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 29148629, 35695917, 265020, 265021, 265022, 52844150, 264692, 33857023, 284693, 52845129, 33857109, 27486281, 18108374, 55811576, 35696423, 65274791, 284636, 284556, 284557, 284638, 60170394, 284638, 284558, 83373044, 18108385, 56528486, 22279000, 22279002
3028	94231997 (6055, 6056)	Novel Protein sim. GBank gi 3080521 emb CAA18650 - (AL022598) hypothetical protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 264259, 29331824, 29331827, 35696052, 264908, 265007, 265008, 265009, 60170831, 21906754, 265011, 87168559, 265018, 264762, 264683, 264765, 264689, 21906765, 21906768, 21906769, 29148629, 35695917, 265021, 265022, 33857109, 27486265, 264628, 264629, 18108374, 35696423, 35695855, 264638, 60170394, 22279000, 22279002, 284482, 264584
3029	87619284 (6057, 6058)			UNCLASSIFIED	22278997, 22278999, 29331827, 264905, 264509, 264909, 284510, 284511, 284512, 87168474, 265019, 18108351, 21906768, 284534, 264690, 284693, 263989, 18108370, 284558, 22279000, 22279002, 264482
3030	87544928 (6059, 6060)	Novel Protein sim. GBank gi 3757726 emb CAA18782 - (AL022727) dJ8019.1 (olfactory receptor-like protein [Hs6M1-1]) [Homo sapiens]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	Im7	
3031	91677953 (6061, 6062)	Novel Protein sim. GBank gi 4530587 gb AAD22105.1 - (AF132000) TADA1 protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 35696052, 264908, 265018, 21906765, 21906766, 21906767, 21906768, 265021, 263974, 18108374, 264558, 56528486, 22279000, 22279002

3032	84130124 (6063, 6064)	Novel Protein sim. GBank gi 101951 (U37429) - similar to M. musculus MER5 and other AHPCTSA proteins [Caenorhabditis elegans]	Contains protein domain (PF00534) - synthase Glycosyl transferases group 1	2278996, 35686286, 264259, 29331824, 29331828, 264907, 29331830, 264758, 33109954, 87188474, 87188559, 265019, 264288, 21906769, 265021, 264693, 35686423, 35695855, 264636, 56182323, 83373044, 87188518
3033	85308321 (6065, 6066)	Novel Protein sim. GBank gi 5031573 ref NP_005712.1 pACTR - ARP3 (actin-related protein 3, yeast) homolog	Contains protein domain (PF00022) - struct Actin	35686286, 264259, 29331826, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 265008, 264591, 21906754, 265010, 265019, 264681, 264369, 264768, 21906764, 21906768, 35695917, 33657023, 264628, 35695855, 264632, 264635, 264639, 264482, 264563
3034	80415373 (6067, 6068)		UNCLASSIFIED	264906, 264907, 264510, 264592, 265010, 264762, 264766, 264637, 264638, 264486
3035	91220692 (6069, 6070)	Novel Protein sim. GBank gi 3738207 emb CAA21262 - (AL031853) conserved ATP-GTP binding protein [Schizosaccharomyces pombe]	UNCLASSIFIED	264636
3036	91718323 (6071, 6072)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - III ALU SUBFAMILY SQ WARNING ENTRY!!!!	kinase	264907, 33657402, 265021
3037	95307434 (6073, 6074)	Novel Protein sim. GBank gi 4406590 gb AAD20040 - (AF131768) Similar to Ena-VASP like protein [Homo sapiens]		265017
3038	95421807 (6075, 6076)	Novel Protein sim. GBank gi 5360093 gb AAD42865.1 AF15509 - (AF155099) NY-REN 18 antigen [Homo sapiens]	Contains protein domain (PF00627) - UNCLASSIFIED UBA domain	22278996, 22278997, 264259, 284905, 265007, 265009, 60433356, 21906754, 265016, 265019, 18108351, 264687, 21806765, 265020, 265021, 65274620, 27486262, 264636, 56182323, 16108385, 22279000
3039	87332257 (6077, 6078)	Novel Protein sim. GBank gi 4757128 emb CAB42094.1 - (AJ238717) ZRP protein [Rattus norvegicus]	UNCLASSIFIED	35686286, 29331828, 264108, 264110, 264511, 265007, 21906754, 265011, 264681, 264683, 264687, 21906768, 264691, 18108370, 263972, 284629, 18108374, 263977, 35698423, 264584, 18108391, 264692, 264558, 18108382, 18108385, 264567
3040	90933517 (6079, 6080)	Novel Protein sim. GBank gi 4884278 emb CAB43247.1 - (AL050037) hypothetical protein [Homo sapiens]		
3041	88312357 (6081, 6082)	Novel Protein sim. GBank gi 3876073 emb CAB04122.1 - (Z81505) similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:D28025 comes from this gene; cDNA EST EMBL:D28024 comes from this gene; cDNA EST EMBL:D33210 comes from this gene; cDNA EST EMBL:D33441 comes from this ...	UNCLASSIFIED	56894075, 22278997, 22278998, 29331827, 33656970, 33109954, 21906754, 87188559, 264800, 264683, 21906765, 21906768, 22279002
3042	85749402 (6083, 6084)	Novel Protein sim. GBank gi 790236 (U21156) - sarcolemmal associated protein-2 [Oryctolagus cuniculus]	glycoprotein	264636

3043	87773026 (6085, 6086)	Novel Protein sim. GBank gij854065[emb CAA58337] - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	35696286, 60424269, 35696052, 264508, 264905, 66712502, 56182435, 55811386, 52644286, 55811150, 35695917, 60170615, 33657109, 18108374, 264634, 60431850
3044	87646182 (6087, 6088)	Novel Protein sim. GBank gij4104922 (AF042276) - o251 homolog [Pseudomonas putida]	Contains protein domain (PF01209) - ubiE/COQ5 methyltransferase family	glycoprotein	22278986, 22278988, 22278999, 29331824, 56182435, 264511, 265007, 60170831, 60432229, 60433356, 33109954, 18108351, 264288, 35695917, 18108388, 18108370, 60170394
3045	94127598 (6089, 6090)	Novel Protein sim. GBank gij4589680[dbj BAA76859.1] - (AB023232) KIAA1015 protein [Homo sapiens]	Contains protein domain (PF00095) - Zinc finger, C2H2 type	dna_ma_bind	264488, 264259, 35696052, 264508, 264905, 264509, 264906, 264907, 264909, 264511, 265008, 264591, 264593, 33109954, 264604, 264764, 264683, 264288, 264768, 264768, 21906765, 21906768, 55811957, 35695917, 27486262, 18108370, 264628, 18108374, 35695855, 264630, 264632, 264635, 264563, 264564, 264566
3046	88098247 (6091, 6092)			UNCLASSIFIED	22278999, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264908, 52646317, 55811957, 60432113, 22278000, 22279002, 264482, 264564
3047	95088924 (6093, 6094)			UNCLASSIFIED	264488, 22278998, 22278997, 22278999, 29331824, 29331825, 56182435, 264511, 265008, 265009, 265011, 265017, 264768, 21906768, 21906769, 35695917, 52644150, 33657349, 65274791, 35695855, 264555, 60432113, 22279000, 264566
3048	87629419 (6095, 6096)	Novel Protein sim. GBank gij458034[gb AAD25962.1]AF09287 - (AF092878) zinc RING finger protein SAG [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	284102, 29148784
3049	88229955 (6097, 6098)	Novel Protein sim. GBank gij5454158[re NP_006286.1]pVARS - valyl-IRNA synthetase 1	Contains protein domain (PF01406) - tRNA synthetases class I (C)	UNCLASSIFIED	22278997, 29331826, 264907, 264758, 87168559, 265018, 264448, 21906768, 265020, 33657109, 35695855, 60432113, 22279000
3050	87643679 (6099, 6100)	Novel Protein sim. GBank gij4589642[dbj BAA76843.1] - (AB023216) KIAA0999 protein [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 29331825, 264909, 265007, 264512, 265019, 264288, 21906768, 265020, 264893, 18108385, 56526486, 87168518, 22279002, 264566
3051	87750599 (6101, 6102)				22278997, 264595, 265019, 264288, 264893, 87168518
3052	57108030 (6103, 6104)	Novel Protein sim. GBank gij117528[sp P14755 CRYL_RABIT - LAMBDA-CRYSTALLIN	dehydrogenase		264534

3053	95350373 (6105, 6106)	Novel Protein sim. GBank gi 3947613 emb CAA19465.1 - (AL023828) cDNA EST EMBL:M89008 comes from this gene; cDNA EST yk282d3.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 56181686, 22278995, 35688286, 22278998, 264259, 60432289, 265008, 265009, 60433438, 21908754, 265010, 87168559, 264803, 265018, 265019, 264763, 264764, 264288, 21908765, 21908766, 21908768, 21908769, 35695917, 18108374, 35698423, 264638, 56182323, 22279000, 264563
3054	86943510 (6107, 6108)	Novel Protein sim. GBank gi 1076211 pir S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	35698286, 35696052, 29331830, 264908, 264909, 264512, 264910, 265017, 264804, 264766, 265020, 33657109, 264628, 35695855, 264838, 264584, 264586, 264486
3055	95350537 (6109, 6110)	Novel Protein sim. GBank gi 4680655 gb AAD27717.1 AF13294 - (AF132942) CGI-08 protein [Homo sapiens]		transport	60424178, 55274572, 56182575, 35698286, 22278996, 22278998, 60432049, 264259, 60424289, 60432289, 35696052, 56182435, 265006, 265009, 60170831, 60432229, 60431735, 60433356, 264594, 60433438, 21906754, 55811386, 265011, 87168559, 265019, 18108351, 264883, 264288, 264369, 264689, 21908768, 55811957, 35695917, 60170815, 33657023, 65274620, 33657109, 35695763, 60431528, 18108374, 55810784, 55811576, 35698423, 65274791, 264638, 60431850, 18108381, 56182323, 60170394, 18108385, 60432113, 264584, 264565, 264566
3056	91661636 (6111, 6112)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		glycoprotein	264488, 264569, 18108394, 52646842, 22278997, 22278998, 22278999, 264259, 66714117, 29331826, 29331827, 35696052, 264508, 264509, 264905, 264906, 264807, 264908, 264909, 265006, 264512, 265007, 265008, 265009, 264910, 33657402, 55812038, 264596, 264758, 265010, 265011, 265017, 265019, 264760, 18108351, 264762, 264763, 264764, 264288, 264768, 264687, 18108357, 264768, 264769, 264689, 21908765, 21908766, 21908767, 21908768, 21908769, 35695917, 265020, 265021, 264691, 264693, 33657109, 18108370, 264628, 264629, 18108374, 55811576, 35698423, 35695855, 264630, 264631, 264632, 264634, 264635, 264638, 264637, 264638, 18108381, 83373044, 18108385, 22279000, 22279002, 264563, 264584, 264565, 264566, 264488, 264567

3057	95412746 (6113, 6114)	Novel Protein sim. GBank gjl3878119[embjCAA88860] - (Z49088) similar to GTP-binding protein; cDNA EST EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709 comes from this gene; cDNA EST EMBL:D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST yk353...			264508, 264905, 264907, 264908, 264909, 264510, 264512, 264910, 264592, 264594, 264767, 18108374, 264635, 264555, 264637, 264639, 264563, 264564, 264565, 264486
3058	78646226 (6115, 6116)			UNCLASSIFIED	264693
3059	67629425 (6117, 6118)	Novel Protein sim. GBank gjl4588034[jgb/AAD25982.1]AF09287 - (AF092878) zinc RING finger protein SAG [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HCA type (RING finger)	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264490, 264259, 29331824, 29331825, 29331827, 35696052, 29331828, 265007, 60433438, 265017, 265018, 265019, 264681, 264448, 264288, 264768, 21906765, 21906766, 21906767, 21906769, 28148629, 29148784, 265022, 52644150, 18108370, 264636, 18108385, 264563, 264567
3060	79346691 (6119, 6120)			UNCLASSIFIED	264567
3061	67740964 (6121, 6122)			UNCLASSIFIED	264112, 52644296, 21906768, 33657023, 263974, 18108385
3062	87619465 (6123, 6124)	Novel Protein sim. GBank gjl4454690[jgb/AAD20963] - (AF070657) glutathione S-transferase subunit 13 homolog [Homo sapiens]		transferase	264908, 265008, 18108351, 264566
3063	80078023 (6125, 6126)	Novel Protein sim. GBank gjl2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	18108358, 264558
3064	91241526 (6127, 6128)	Novel Protein sim. GBank gjl4240315[jdbjBAA74936.1] - (AB020720) KIAA0913 protein [Homo sapiens]	Contains protein domain (PF00403) - Heavy-metal-associated domain	UNCLASSIFIED	52646365, 52646842, 65274572, 56182575, 56181886, 22278995, 22278996, 22278997, 22278999, 264259, 60432049, 29331824, 66714117, 264508, 264907, 264908, 56182435, 265009, 60432229, 60433438, 55812038, 52644286, 265018, 264682, 264288, 264686, 264768, 264687, 52644229, 264689, 21906768, 264691, 264692, 264893, 18108370, 18108377, 55811576, 264636, 56182323, 264558, 264639, 18108385, 22279000, 22279002
3065	91639201 (6129, 6130)	Novel Protein sim. GBank gjl5656743[jgb/AAD45960.1]AC00506 - (AC005067) Supported by Human EST H08032.1 (NID:g872854), mouse EST AA870042.1 (NID:g2965487), and gencode [Homo sapiens]		UNCLASSIFIED	22278996, 22278998, 264093, 264094, 264095, 29331824, 60424269, 66714117, 264100, 264907, 265007, 264591, 60432229, 264593, 265011, 265019, 18108351, 264766, 264767, 21906765, 21906768, 264693, 20281089, 22279000, 22279002, 264482, 264566, 264567

3066	91224437 (6131, 6132)	Novel Protein sim. GBank gi 4884268 emb CAB43245.1 - (AL050028) hypothetical protein [Homo sapiens]		UNCLASSIFIED	18108397, 22278995, 56994075, 22278998, 264905, 66712502, 265008, 264512, 264910, 264758, 60174639, 264760, 18108351, 264764, 264683, 18108359, 264692, 18108364, 18108368, 18108370, 18108377, 18108379, 60170394, 264567
3067	95422551 (6133, 6134)	Novel Protein sim. GBank gi 4689258 gb AAD27832.1 AF12185 - (AF121859) sorting nexin 9 [Homo sapiens]	Contains protein domain (PF00787) - struct PX domain		264488, 264489, 35696286, 22278996, 56994075, 264259, 28331822, 28331825, 35696052, 28331828, 264508, 264905, 264509, 264808, 264807, 264908, 264909, 264112, 264510, 264511, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264757, 264595, 264598, 264758, 265010, 265011, 87168559, 264801, 264802, 264603, 264604, 264605, 265019, 264780, 264762, 264448, 264763, 264764, 264288, 264369, 264768, 264768, 264687, 264769, 264689, 21908765, 21906767, 21906768, 35695917, 265020, 265021, 264534, 52644150, 264691, 33857023, 264693, 264628, 60431528, 263977, 35695955, 264630, 264631, 264634, 264635, 264636, 264637, 264638, 264639, 83373044, 56526486, 87168518, 22279000, 22279002, 284563, 284483, 264564, 264565, 264566, 284567, 264486
3068	85360651 (6135, 6136)				284112
3069	95412753 (6137, 6138)	Novel Protein sim. GBank gi 3878119 emb CAA88860 - (Z49088) similar to GTP-binding protein; cDNA EST EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709 comes from this gene; cDNA EST EMBL:D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST yk353...	Contains protein domain (PF01926) - struct GTPase of unknown function		22278996, 56994075, 22278998, 22278999, 264259, 264107, 264905, 28331830, 52644045, 264110, 60170331, 264592, 264594, 33657402, 21906754, 33109954, 87168474, 87168559, 265017, 264448, 264764, 264683, 264768, 52644229, 21908765, 21908768, 21906768, 21908769, 60170615, 33657023, 18108370, 18108376, 264634, 264557, 60170394, 56182323, 18108385, 87168518, 22279000, 264482

3070	94319173 (6139, 6140)	Novel Protein sim. GBank gij3877788[embjCAB05527] - (Z83110) cDNA EST yk472b5.3 comes from this gene; cDNA EST yk474a7.3 comes from this gene; cDNA EST yk472b5.5 comes from this gene; cDNA EST yk468c10.3 comes from this gene; cDNA EST yk468c10.5 comes from this gene; cDNA EST EM...			synthase	264488, 22278994, 22278995, 22278996, 56984075, 22278997, 22278999, 264259, 29331822, 29147820, 29331824, 66714117, 29331826, 29146498, 29146499, 66712502, 29331830, 52844045, 56182435, 264511, 265007, 264512, 264910, 60170831, 264592, 264758, 33109954, 21906754, 87168474, 265019, 18108351, 264448, 264683, 264288, 52844229, 264689, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 265021, 60170815, 52844150, 264691, 33657023, 27486261, 27486284, 264628, 18108370, 18108377, 55811576, 35695855, 264634, 264635, 18108381, 60170394, 56182323, 264558, 83373044, 18108385, 18108387, 56526486, 264404, 264563, 264566
3071	94325573 (6141, 6142)	Novel Protein sim. GBank gij4502425[refNP_001709.1]pBMP6 - bone morphogenetic protein 6 precursor	Contains protein domain (PF00085) - tgf Thioredoxin		tgf	264488, 65274572, 18108398, 22278996, 35698286, 22278997, 22278998, 22278999, 264259, 29331822, 66714117, 29331826, 35696052, 29331828, 29146498, 29146499, 264907, 264908, 29331830, 264909, 52844045, 56182435, 265006, 265007, 264512, 265008, 265009, 60170831, 60432228, 264592, 60433356, 33657402, 60433438, 33109954, 52844296, 87168474, 265010, 265017, 264681, 264288, 264685, 264766, 264687, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 60170815, 52844150, 264690, 264691, 264692, 33657023, 264693, 33657109, 263971, 18108374, 18108377, 35696423, 55811576, 65274791, 35695855, 264630, 264635, 264636, 264557, 60170394, 83373044, 60432113, 22279000, 22279002, 264563, 264564, 264565, 264566, 264567
3072	95115892 (6143, 6144)	Novel Protein sim. GBank gij1263289 (U47856) - fibroin-4 [Araneus diadematus]			transcriptfactor	56182575, 29331822, 29331824, 29331825, 29146498, 264908, 52844045, 56182435, 265008, 60433438, 55812038, 18108351, 264683, 264369, 52844229, 52844150, 33657023, 264693, 33657109, 18108374, 55811576, 65274791, 264555, 56182323, 60432113, 264564

3073	86147248 (6145, 6146)	Novel Protein sim. GBank gi 134840 sp P22528 CORB_HUMAN - CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) (14.8 KD PANCORNULIN)		UNCLASSIFIED	264769
3074	88089351 (6147, 6148)	Novel Protein sim. GBank gi 3419847 (AC004982) - similar to yeast hypothetical protein ybk4; similar to P38164 (PID:g588461) [Homo sapiens]		UNCLASSIFIED	264488, 265019, 284448, 284288, 21906767, 264693, 18108368, 18108370, 18108374, 264587
3075	88095752 (6149, 6150)	Novel Protein sim. GBank gi 4557349 ref NP_000458.1 pBARD - BRCA1 associated RING domain 1	Contains protein domain (PF00023) - Ank repeat	homeobox	264509, 284907, 284689, 284693, 56526486
3076	87819219 (6151, 6152)			UNCLASSIFIED	18108398, 29331822, 29331827, 60432229, 265017, 284681, 284683
3077	88734277 (6153, 6154)	Novel Protein sim. GBank gi 3023956 sp Q00808 HET1_PODAN - VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1	Contains protein domain (PF00400) - WD domain, G-beta repeat	Kinase	65274572, 35896052, 264511, 60170831, 87168474, 284389, 35695917, 33657182, 27486284, 33657349, 35695763, 35695855, 264639
3078	88089355 (6155, 6156)	Novel Protein sim. GBank gi 3900850 (AC004994) - similar to KIAA0600; similar to d1026456 (PID:g3043724) [Homo sapiens]			22278002
3079	87821893 (6157, 6158)	Novel Protein sim. GBank gi 3875410 emb CAB02876 - (Z81052) Similarity to Yeast ABC1P protein (SW:ABC1_YEAST); cDNA EST yk229g8.3 comes from this gene; cDNA EST yk229g8.5 comes from this gene [Caenorhabditis elegans]		transport	29331824, 29331826, 264758, 55811386, 265017, 55811150, 52644229, 21906768, 265020, 285021, 264693, 18108376, 264631, 52644332, 22278002
3080	95288274 (6159, 6160)	Novel Protein sim. GBank gi 5257221 gb AA041265.1 - (AF117887) protein arginine methyltransferase [Mus musculus]		interferon	264488, 52644507, 22278998, 22278998, 264490, 264259, 29331824, 68714117, 29331825, 29331826, 29331827, 29331828, 29148499, 264508, 264905, 264828, 52844045, 58182435, 265008, 284591, 284586, 21906754, 60174639, 285010, 264882, 264448, 264763, 264683, 264764, 284288, 264885, 264769, 264688, 264689, 21908765, 21908767, 21908769, 55811957, 35695917, 265020, 60170615, 52644150, 284692, 33657023, 264693, 65274620, 33657109, 27486261, 35695763, 264628, 18108370, 65274791, 264558, 56182323, 60170394, 264482, 264565, 264484
3081	88094864 (6161, 6162)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - !!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!		UNCLASSIFIED	18108398, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 264585, 264758, 265011, 265018, 264760, 264761, 264763, 264764, 18108394, 264685, 264768, 264628, 264629, 264630, 264631, 264632, 264634, 264635, 264555, 264638, 18108382, 18108385, 264563, 264565, 264566
3082	80310121 (6163, 6164)				264764, 55811957, 264555, 264564

3083	88095758 (6165, 6166)	Novel Protein sim. GBank gjl868241 (U28488) - C56C10.3 gene product [Caenorhabditis elegans]		UNCLASSIFIED	284488, 284259, 29331824, 284108, 285008, 284591, 284592, 21906754, 284288, 284767, 21906768, 21906789, 29148784, 284691, 284632, 22279000
3084	87448568 (6167, 6168)	Novel Protein sim. GBank gjl476774 pir A37475 - probable structural component p38 - borna disease virus			22278995, 60432289, 35898052, 284905, 284906, 284907, 284908, 284909, 285006, 285007, 284910, 284593, 284595, 284758, 284369, 284288, 284768, 35895917, 285020, 18108374, 35898423, 284631, 284556, 284565, 284566, 284587, 284488
3085	87795781 (6169, 6170)	Novel Protein sim. GBank gjl2565057 (U80741) - CAGH44 [Homo sapiens]		UNCLASSIFIED	285011, 284681
3086	87769942 (6171, 6172)	Novel Protein sim. GBank gjl3894189 (AC005662) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	22278998, 284092, 284259, 29331822, 29331825, 284108, 284112, 18108351, 284687, 263987, 263974, 55810764, 263981, 18108385, 284487
3087	87462888 (6173, 6174)				52846365, 56894075, 22278997, 22278998, 29331824, 29331825, 35898052, 60433438, 33109954, 21906754, 52646317, 285017, 284682, 284369, 284684, 21908767, 21906768, 285020, 284691, 33857023, 33657109, 52645129, 33857182, 27486262, 35895855, 87168518
3088	91224441 (6175, 6176)	Novel Protein sim. GBank gjl3355304 (AF001549) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	284591
3089	95361242 (6177, 6178)	Novel Protein sim. GBank gjl4889148 AAD27782.1 AF07704 - (AF077049) lambda-crystallin [Homo sapiens]	Contains protein domain (PF00725) - dehydrogenase 3-hydroxyacyl-CoA dehydrogenase		18108397, 65274572, 56182575, 56181686, 56894075, 35898286, 22278997, 22278998, 284259, 29331824, 29331825, 29331826, 29331828, 284907, 29331830, 284909, 58182435, 284510, 285007, 60170831, 60432229, 21906754, 55811388, 285017, 285018, 285019, 284760, 55811150, 284288, 284768, 58181582, 21906765, 21906766, 21906767, 21906768, 285021, 60170615, 27486262, 18108370, 60431528, 35898423, 284558, 284559, 60432113, 284486

3090	95342371 (6179, 6180)	Novel Protein sim. GBank gi 1354050 (U47024) - MEM3 [Mus musculus]	UNCLASSIFIED	60424179, 52845156, 65274572, 56182575, 56181686, 22278995, 35896286, 56994075, 22278996, 22278998, 22278999, 264259, 29331822, 56182181, 29331824, 29331825, 29331826, 29331827, 29331828, 35896052, 33656970, 264906, 264908, 52644045, 264828, 265008, 265007, 265008, 60170831, 60432229, 60433358, 33657402, 55812038, 264758, 21906754, 33109954, 52846317, 55811386, 52844296, 87168474, 265011, 87168559, 265017, 265018, 265019, 55811150, 18108351, 264681, 264448, 264288, 264369, 18108357, 264768, 52644229, 56181562, 21906764, 21906765, 21906766, 21906767, 21906768, 21906769, 35895917, 265020, 265022, 60170615, 264690, 52644150, 264691, 33657023, 18108385, 65274820, 33657109, 18108388, 33657182, 27486261, 27486285, 35895763, 18108374, 18108376, 55810784, 35896423, 55811576, 65274791, 35895855, 264557, 56182323, 83373044, 18108387, 18108388, 87168518, 22279000, 22279002, 264563, 264482
3091	95317424 (6181, 6182)	Novel Protein sim. GBank gi 3873932 emb CAB01859 - (Z79596) Similarity to Bovine aspartyl beta hydroxylase (TR:G182694); cDNA EST EMBL:D27916 comes from this gene; cDNA EST EMBL:D27915 comes from this gene; cDNA EST EMBL:D64881 comes from this gene; cDNA EST EMBL:D68139 comes f...	UNCLASSIFIED	35896286, 29331822, 35896052, 264508, 264509, 264905, 264906, 264908, 264909, 264510, 264758, 265010, 265011, 264683, 264685, 264760, 264768, 264769, 264693, 264626, 35896423, 35895855, 264632, 264635, 264639, 264482, 264563, 264486

3092	95314592 (6183, 6184)	Novel Protein sim. GBank gil1710756 sp P15880 RS2_HUMAN - 40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN)	Contains protein domain (PF00333) - Ribosomal protein S5	ribosomal prot	284488, 60424179, 18108398, 22278995, 56994075, 22278998, 35898288, 22278997, 22278998, 60432048, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35898052, 29331828, 28146488, 28146488, 284508, 284509, 284905, 284906, 264907, 29331830, 284908, 284909, 284113, 264510, 264511, 265006, 284512, 265007, 265008, 264910, 265009, 60170831, 284591, 284592, 60431735, 284593, 264594, 60433438, 284595, 284758, 21908754, 285010, 265011, 264601, 284602, 265017, 284603, 284604, 265018, 284605, 265019, 284760, 284762, 284681, 18108351, 284763, 284682, 264448, 284764, 284683, 284288, 284389, 284785, 284786, 284686, 284787, 284687, 284788, 284789, 284688, 21908784, 284689, 21908785, 21908786, 21908787, 21908788, 21908789, 29148629, 29148784, 35895917, 285020, 285021, 264534, 60170815, 284690, 284691, 284692, 65274820, 33657109, 27486282, 284628, 284629, 18108374, 263978, 18108377, 35896423, 264630, 284631, 284632, 284634, 284635, 284555, 264636, 284637, 284556, 284638, 284557, 264558, 284639, 60170394, 18108385, 284259, 29331824, 35898052, 264905, 265008, 60432229, 60431735, 284684, 284389, 284288, 284786, 21908787, 35898423, 83373044, 18108385
3093	94318457 (6185, 6186)	Novel Protein sim. GBank gil5002587 emb CAB44347.1 - (Y17454) LSFR1 protein [Homo sapiens]		UNCLASSIFIED	
3094	94316675 (6187, 6188)	Novel Protein sim. GBank gil400734 sp P31044 PBP_RAT - PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN (23 KD MORPHINE-BINDING PROTEIN) (P23K)	Contains protein domain (PF01161) - Phosphatidylethanolamine-binding protein	collagen	18108398, 284259, 60432289, 29331827, 284511, 284763, 284288, 284787, 265022, 284691, 284693, 65274791, 56182323, 284584, 284585

3095	84848162 (6189, 6180)	Novel Protein sim. GBank gi 4877759 gb AAD31421.1 AF12444 - (AF124440) MAGE tumor antigen D1 [Homo sapiens]	Contains protein domain (PF01454) - MAGE family	UNCLASSIFIED	18108397, 56182575, 22278995, 35698286, 56994075, 22278997, 22278999, 264259, 60432049, 66714117, 29331825, 60432289, 35698052, 33656970, 29146499, 264508, 264905, 264509, 29331830, 264909, 264510, 264511, 264512, 265007, 265008, 265009, 60170831, 264758, 21906754, 85658542, 265010, 265011, 87188559, 265017, 265018, 265019, 264780, 264681, 264682, 264683, 264764, 264368, 264288, 264686, 264768, 264769, 264689, 21906765, 21906766, 21906767, 55811957, 35695917, 265020, 265021, 265022, 52644150, 264691, 264692, 33657023, 264693, 263972, 18108376, 55811576, 35698423, 264952, 60170394, 264639, 83373044, 18108385, 18108387, 65274727, 87188518, 60432113, 264482, 264563, 264564, 264566, 264487, 18108391, 22278995, 22278996, 22278997, 22278998, 29331824, 29331825, 29331826, 29331827, 33656970, 264905, 264908, 265008, 264910, 33657402, 265011, 265017, 265018, 264369, 21906766, 21906767, 21906768, 35695917, 265020, 60170615, 264691, 264692, 264693, 27486261, 27486262, 18108370, 60431528, 264634, 264636, 264639, 22279000, 264566 264488, 29331822, 29331825, 60432289, 29331826, 35698052, 29331828, 29331830, 264594, 55812038, 33109954, 33657084, 87188474, 87188559, 52644228, 21906765, 21906767, 18108376, 35698423, 52644332, 264638, 60432113, 22279002
3096	87756128 (6191, 6192)	Novel Protein sim. GBank gi 3882221 dbj BAA34470.1 - (AB018293) KIAA0750 protein [Homo sapiens]	Contains protein domain (PF00307) - struct Calponin homology (CH) domain		
3097	88264895 (6193, 6184)	Novel Protein sim. GBank gi 4468288 emb CAB37981 - (AL022395) dJ273N12.1 (PUTATIVE protein based on EST matches) [Homo sapiens]	Contains protein domain (PF00646) - F-box domain.	UNCLASSIFIED	
3098	80258024 (6195, 6186)				264634, 264637, 264565
3099	91243325 (6197, 6188)	Novel Protein sim. GBank gi 303603 dbj BAA02145.1 - (D12621) cytochrome P-450L TBV [Homo sapiens]		Cyto450	264488, 35698286, 29331822, 29331824, 29331825, 29331827, 265007, 265008, 265010, 265011, 265018, 265019, 18108357, 21906766, 265020, 265022, 55811576, 56182323, 22279002, 264563
3100	87502421 (6199, 6200)	Novel Protein sim. GBank gi 1083764 pir B48013 - proline- rich proteoglycan 2 precursor, parolid - rat		UNCLASSIFIED	29331825, 60432289, 35698052, 264910, 60432229, 264582, 264288, 264693, 263967, 264635
3101	79502134 (6201, 6202)			UNCLASSIFIED	264908, 264693, 264628, 264630, 264632

3102	91220892 (6203, 6204)	Novel Protein sim. GBank gi 5305706 gb AAD41781.1 AF12853 - (AF128536) cytoplasmic phosphoprotein PACSIN2 [Homo sapiens]	Contains protein domain (PF00018) - struct SH3 domain	35696288, 22278996, 22278999, 29331827, 35696052, 264909, 264512, 265008, 60170831, 60433358, 33109954, 18108351, 264684, 264689, 21906767, 60170615, 264692, 33657023, 264638, 22279000, 264482, 264564 35695917, 264565
3103	90838004 (6205, 6206)	Novel Protein sim. GBank gi 464564 sp P35292 RB17_MOUSE - RAS-RELATED PROTEIN RAB-17	UNCLASSIFIED	
3104	87340833 (6207, 6208)	Novel Protein sim. GBank gi 5032207 ref NP_005698.1 pTSSC - tumor-suppressing STF cDNA 6	UNCLASSIFIED	264259, 264684, 264532, 33857182, 264558
3105	94148603 (6209, 6210)			22278997, 264259, 29331824, 35696052, 29331828, 264508, 264509, 264905, 264908, 264907, 264908, 264511, 264910, 264591, 264594, 264758, 264760, 264681, 264762, 264764, 264288, 264766, 264768, 264687, 264769, 21906768, 21906768, 35695917, 33857023, 264692, 264693, 264628, 264629, 35695855, 264630, 264631, 264632, 264634, 264635, 264637, 264638, 264639, 83373044, 264404, 22279002, 264563, 264565, 264566, 264486, 264567
3106	95361416 (6211, 6212)	Novel Protein sim. GBank gi 1938574 (U97190) - B0025.2 gene product [Caenorhabditis elegans]		22278996, 22278997, 22278998, 22278999, 264092, 264093, 264094, 29331822, 264908, 264907, 264908, 52644045, 58182435, 264112, 265008, 265009, 55812038, 265017, 265018, 264883, 264888, 264887, 264788, 52844228, 21906765, 21906768, 21906769, 55811957, 265020, 265022, 264690, 52644150, 264692, 264693, 18108370, 18108377, 55811576, 58182323, 18108385, 18108388, 22279000, 264563
3107	95343272 (6213, 6214)	Novel Protein sim. GBank gi 3341441 emb CAA76851 - (Y17794) winged-helix transcription factor [Gallus gallus]		22278995, 22278996, 35696286, 22278997, 22278998, 264091, 264093, 264259, 29331822, 29331825, 29331826, 60432289, 29331827, 29331828, 33656970, 264105, 264512, 265009, 60433358, 60433438, 265011, 265017, 265018, 21906765, 21906766, 21906767, 21906769, 265021, 264691, 33657108, 27486261, 27486265, 18108370, 263972, 18108374, 55811576, 18108385, 56526488, 264482, 264487 56182435, 264288, 264690, 264564
3108	87340835 (6215, 6216)	Novel Protein sim. GBank gi 5032207 ref NP_005698.1 pTSSC - tumor-suppressing STF cDNA 6	UNCLASSIFIED	

3109	94318461 (6217, 6218)	Novel Protein sim. GBank gi 5002587 emb CAB44347.1 - (Y17454) LSFR1 protein [Homo sapiens]	Contains protein domain (PF00098) - struct Zinc finger, C2H2 type		284480, 284908, 285007, 284910, 284593, 284883, 284884, 284887, 21906767, 21906768, 284693, 18108370, 284628, 18108374, 284632, 284638, 22279000
3110	95080716 (6219, 6220)	Novel Protein sim. GBank gi 1076211 pir S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii	UNCLASSIFIED		284488, 65274572, 22278995, 22278987, 60432049, 284259, 29331822, 29331824, 29331825, 60432289, 29331828, 29331827, 29331828, 284808, 284510, 265006, 265007, 285008, 265009, 60432229, 33857402, 60433356, 285011, 87168559, 284800, 285017, 265018, 265019, 18108351, 284288, 284369, 21906768, 21906767, 21906768, 285020, 60170815, 284693, 65274620, 18108370, 284639, 18108384, 22279000, 284583, 18108390
3111	87754512 (6221, 6222)	Novel Protein sim. GBank gi 3282231 (U75454) - C2H2 type zinc finger protein [Homo sapiens]	Contains protein domain (PF00096) - struct Zinc finger, C2H2 type	transcriptfactor	284488, 18108398, 66712502, 285017, 285018, 285019, 284448, 21906767, 285020, 33857023, 18108365, 18108368, 35698423, 52844332, 18108385, 18108388
3112	88043639 (6223, 6224)	Novel Protein sim. GBank gi 3900848 (AC005023) - match to EST AA381117 (NID:G2013438) [Homo sapiens]	Contains protein domain (PF00046) - homeobox	homeobox	
3113	88207098 (6225, 6226)	Novel Protein sim. GBank gi 2459910 (AF005856) - anon2A5 [Drosophila yakuba]		lm7	18108397, 22278999, 284259, 29331824, 35698052, 284907, 284757, 60433438, 87168559, 284763, 284448, 18108354, 284288, 21906767, 21906769, 35695917, 284690, 284691, 284692, 284693, 18108365, 18108381, 18108384, 18108385, 18108388, 87168518, 22279000, 22279002
3114	79843167 (6227, 6228)	Novel Protein sim. GBank gi 4866270 gb AAB52261.2 - (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh). Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (Hydrolase), Score=57.4, E-value=1e-13, N=1 [C...]	Contains protein domain (PF00702) - hydrolase haloacid dehalogenase-like hydrolase	hydrolase	284509, 56182435, 284910, 21906754
3115	94117896 (6229, 6230)	Novel Protein sim. GBank gi 5032225 ref NP_005876.1 pWBS - Williams-Beuren syndrome chromosome region 11		transcriptfactor	60424179, 56182575, 284259, 29331824, 60424269, 29331826, 66712502, 284510, 285007, 60431735, 60433356, 55812038, 55811388, 285019, 284288, 284689, 21906769, 284691, 33857023, 284693, 60431528, 283974, 60431850, 56182323, 284559, 22279000, 22279002
3116	79842855 (6231, 6232)		UNCLASSIFIED	UNCLASSIFIED	284905, 284758, 21906784, 284690
3117	87771288 (6233, 6234)		UNCLASSIFIED	UNCLASSIFIED	284510, 285011, 18108351, 284288, 284689, 284691, 18108368, 18108372, 283981, 284558, 284564

3118	94665848 (6235, 6236)	Novel Protein sim. GBank gi 3880563 emb CAB01444.1 - (Z78018) predicted using GeneFinder; similar to serine/threonine kinase; cDNA EST yk353d10.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00008) - EGF-like domain	tgf	52645156, 52646842, 65274572, 56182575, 22278985, 56994075, 22278998, 35698286, 22278997, 22278998, 22278998, 264259, 29331822, 29331824, 66714117, 29331826, 29331827, 35698052, 29331828, 264905, 264908, 29331830, 52644045, 56182435, 264510, 264511, 265007, 265008, 265009, 264757, 52646317, 21906754, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 264605, 265019, 264762, 264448, 264682, 264684, 264288, 264766, 56181562, 21906765, 21906766, 21906768, 21908769, 265020, 265022, 264690, 52644150, 264691, 33657023, 264693, 33657109, 33657349, 264628, 18108370, 60431528, 18108374, 35698423, 65274791, 60170394, 83373044, 87168518, 22279000, 22279002, 264486, 265008, 264288
3119	85728796 (6237, 6238)		Contains protein domain (PF00328) - Histidine acid phosphatase		
3120	87344040 (6239, 6240)	Novel Protein sim. GBank gi 5019819 gb AAD37863.1 AF14315 - (AF143152) putative NADH oxidoreductase complex I subunit [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264509, 264510, 264511, 264512, 264288, 264486
3121	94110735 (6241, 6242)	Novel Protein sim. GBank gi 4501877 ref NP_001088.1 pACR - acrosin			52644507, 52645156, 52646365, 52646842, 22278994, 56994075, 22278998, 22278999, 264259, 29331824, 29331827, 35698052, 52644045, 265008, 52646317, 87168474, 87168559, 21906765, 52644150, 33657023, 18108374, 264637, 264638
3122	11814528 (6243, 6244)			UNCLASSIFIED	264638
3123	88083003 (6245, 6246)	Novel Protein sim. GBank gi 2439517 (AC002563) - putative RHO/RAC effector protein; 95% similarity to P49205 (PID:g1345860) [Homo sapiens]	Contains protein domain (PF00780) - CNH domain	kinase	18108382, 29331822, 29331824, 29331825, 264905, 265007, 55812038, 265019, 18108351, 264682, 264288, 264766, 21906764, 21906765, 21906768, 21906769, 55811957, 18108365, 18108368, 27486265, 18108374, 18108381, 18108384, 22279000, 22279002, 264482
3124	87788899 (6247, 6248)			UNCLASSIFIED	264905
3125	91216607 (6249, 6250)	Novel Protein sim. GBank gi 4980828 gb AAD35412.1 AE00171 - (AE001714) oxidoreductase, short chain dehydrogenase/reductase family [Thermotoga maritima]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	56181686, 264259, 66714117, 60432289, 29331828, 29331827, 264907, 264908, 264828, 265009, 60433358, 33657402, 60433438, 264758, 18108351, 264288, 29148627, 29148629, 33657023, 33657109, 18108382, 56526486

3126	95337205 (6251, 6252)			UNCLASSIFIED	22278989, 264480, 264259, 60432049, 29331822, 60432289, 29148498, 52644045, 56182435, 265008, 60433438, 265010, 87168559, 265017, 265018, 55811150, 264763, 264683, 264389, 264685, 29148629, 33657023, 264683, 33657109, 18108374, 55811578, 18108385, 60432113, 22279002, 35696286, 22278986, 22278989, 29331826, 264908, 60433438, 87168559, 264604, 21906765, 21906769, 33657023, 33657349, 264628, 18108374, 18108377, 22279000, 22279002
3127	91639233 (6253, 6254)	Novel Protein sim. GBank gjl2828280[embjCAA16694.1] - (AL021687) putative protein [Arabidopsis thaliana]			22278989, 264259, 52644045, 265008, 21906754, 265017, 265018, 21906768, 18108376, 18108387, 22279000, 22279002, 56182575, 264259, 29331825, 29331828, 52644045, 58182435, 60433356, 264600, 264682, 264763, 264784, 264369, 264288, 264686, 55811957, 264692, 33657023, 33657109, 60432113, 264564, 264568, 264636
3128	87674330 (6255, 6258)	Novel Protein sim. GBank gjl3885828 (AF090133) - lin-7-A (Rattus norvegicus)	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	misc_channel	
3129	87755412 (6257, 6258)	Novel Protein sim. GBank gjl3135273 (AC003058) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	
3130	14993960 (6259, 6260)	Novel Protein sim. GBank gjl3329465 (AF084553) - NSD1 protein [Mus musculus]			
3131	95351469 (6261, 6262)	Novel Protein sim. GBank gjl1848277 (U86136) - telomerase-associated protein TP-1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	56182575, 264259, 29331824, 264807, 56182435, 264594, 60433438, 55812038, 33109954, 21908754, 33657084, 87168474, 264448, 264786, 21908769, 55811957, 265020, 265021, 265022, 60170615, 33657023, 33657109, 33657182, 27486281, 33657349, 65274791, 60170394, 56182323, 83373044, 87168518, 264564

3132	95415459 (6263, 6264)	Novel Protein sim. GBank gi 4680647 gb AAD27713.1 AF13293 - (AF132938) CGI-03 protein [Homo sapiens]	Contains protein domain (PF00789) - UBX domain	ubiquitin	52844507, 52646842, 52646365, 55274572, 58182575, 22278994, 22278995, 35896288, 56994075, 22278998, 22278997, 22278998, 22278999, 80432049, 52645080, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35896052, 284508, 52644045, 58182435, 284910, 60170831, 60432229, 60433356, 33857402, 55812038, 52646317, 21908754, 52644298, 85658542, 87168559, 265017, 265018, 265019, 284448, 264288, 264369, 52644229, 21906769, 21908768, 21906767, 21906768, 21906769, 35895917, 265020, 265021, 60170815, 52644150, 264892, 33857023, 52845129, 33857109, 33857182, 27486261, 27488262, 27486265, 33657349, 35895763, 18108374, 18108376, 55811576, 35895855, 18108385, 18108387, 56528488, 87168518, 60432113, 22279002
3133	87379414 (6265, 6266)	Novel Protein sim. GBank gi 4507613 ref NP_003738.1 pTNKS - TANKYRASE		polymerase	22278998, 22278998, 264905, 265008, 285007, 87168559, 264760, 21908767, 18108374, 22279000, 22279002, 264563
3134	84649816 (6267, 6268)	Novel Protein sim. GBank gi 1729827 sp P54833 TALA_DICDI - FILOPODIN (TALIN HOMOLOG)			284585, 264369, 264685, 264628, 264586
3135	88389356 (6269, 6270)	Novel Protein sim. GBank gi 3093478 (AF012927) - fibrinogen-binding protein [Sireptococcus equi]		struct	22278998, 264095, 29331828, 33857402, 18108348, 263974
3136	84845839 (6271, 6272)	Novel Protein sim. GBank gi 627101 pir S44092 - probable carrier protein c2 - Caenorhabditis elegans	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	22278998, 264259, 264828, 265006, 265008, 60433438, 265019, 264764, 264288, 264769, 264689, 265020, 27488262, 283972, 65274791, 264557, 264558
3137	88257847 (6273, 6274)	Novel Protein sim. GBank gi 3342730 (AC005331) - R31341_1 [Homo sapiens]		UNCLASSIFIED	22278995, 22278998, 22278997, 22278998, 22278999, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264510, 265008, 21908754, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264682, 264769, 21908765, 21908768, 21908767, 21908769, 55811957, 35895917, 265020, 265021, 52844150, 18108370, 18108374, 22279000, 22279002, 264482, 264488

3138	94130186 (6275, 6276)	Novel Protein sim. GBank gj 408759 gb AAD20070 - (AC008836) hypothetical protein [Arabidopsis thaliana]			264569, 264488, 264907, 264511, 264593, 33109854, 87168559, 264681, 264684, 264685, 264686, 264687, 264768, 264688, 264689, 264691, 264692, 264693, 33657109, 264631, 264634, 264635, 264636, 264637, 60170394, 83373044, 18108385, 18108388, 60432113, 22279000, 22279002
3139	87325503 (6277, 6278)	Novel Protein sim. GBank gj 228938 prf 181452C - Hyp-rich glycoprotein [Zea diploperennis]		UNCLASSIFIED	22278997, 22278998, 22278999, 264905, 265018, 265019, 21908765, 265020, 264636, 264557
3140	91222682 (6279, 6280)	Novel Protein sim. GBank gj 932 emb CAA37773 - (X53744) 68kDa subunit of signal recognition particle [Canis familiaris]		struct	22278995, 56994075, 35896286, 264908, 264909, 60433358, 21908754, 52644298, 87168474, 87168559, 264683, 264288, 264885, 264686, 265022, 264693, 27468262, 35895855, 264830, 264555, 264566
3141	87323584 (6281, 6282)	Novel Protein sim. GBank gj 3213227 (AF035209) - putative v-SNARE Vti1a [Mus musculus]		UNCLASSIFIED	56182575, 35896286, 28331828, 264909, 265009, 265018, 18108351, 264369, 21908766, 29148627, 265020, 264628, 264629, 264631, 18108385
3142	95419028 (6283, 6284)	Novel Protein sim. GBank gj 2498187 sp Q95245 C561_PIG - CYTOCHROME B561 (CYTOCHROME B-561)		cytochrome	52845156, 52646365, 22278995, 35896286, 22278998, 22278999, 60432049, 284259, 29331822, 29331824, 29331827, 29148499, 56182435, 265007, 80170831, 60432229, 33657402, 264595, 60433438, 264758, 21908754, 264288, 264768, 264687, 52844229, 21908765, 21908767, 21908768, 60170615, 52644150, 65274620, 33657109, 35895763, 18108370, 18108378, 65274791, 35895855, 264631, 264557, 87168518, 60432113, 22279000
3143	95351475 (6285, 6286)	Novel Protein sim. GBank gj 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264488, 56182575, 22278996, 22278998, 22278999, 29331822, 29331824, 60432289, 35896052, 29331828, 264508, 264905, 264908, 264907, 264908, 264909, 52644045, 56182435, 264511, 264512, 265008, 264910, 60432229, 33657402, 60433358, 60433438, 55812038, 265011, 265019, 264780, 264783, 264448, 264764, 264884, 264288, 264685, 264686, 264768, 264889, 21908765, 21908766, 21908767, 21908769, 35895917, 264690, 33657023, 264693, 263987, 33657109, 264628, 264629, 18108374, 263976, 55811578, 35895855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264558, 87168518, 60432113, 22279000, 22279002, 264563, 264566, 264486

3144	85336329 (6287, 6288)	Novel Protein sim. GBank gij4884468[emb]CAB43322.1] - (AL050225) hypothetical protein [Homo sapiens]			264488, 18108396, 22278996, 35696286, 22278997, 22278999, 29331826, 29331827, 35696052, 29331828, 264106, 265006, 265007, 265009, 33657402, 85658542, 265011, 18108351, 264448, 264369, 21906765, 21908766, 21906767, 265020, 265021, 52844150, 27488261, 18108370, 18108374, 35696423, 56182323, 83373044, 22279000, 22279002, 264567
3145	86611657 (6289, 6290)	Novel Protein sim. GBank gij3679709[emb]CAB03330] - (Z81118) Similarity to Human endosomal protein P182 (TR:Q15075); cDNA EST EMBL:Z14487 comes from this gene; cDNA EST EMBL:Z14556 comes from this gene; cDNA EST EMBL:D27011 comes from this gene; cDNA EST EMBL:D27015 comes from t...	UNCLASSIFIED		18108397, 29331824, 29148499, 20281100, 265006, 55812038, 265010, 21906766, 29148627, 21906789, 29148784, 264692, 33657023, 33657109, 35695763, 263981, 56182323, 87168518
3146	87756314 (6291, 6292)	Novel Protein sim. GBank gij2135746[pir]S69890 - mitogen inducible gene mig-2 - human	Contains protein domain (PF00169) - PH domain	struct	264259, 29331826, 29331828, 29331830, 264510, 264511, 265007, 265009, 264600, 265017, 18108351, 264448, 264369, 21906766, 265021, 264692, 33657109, 18108374, 35696423, 35695855, 60432113, 264564
3147	94848512 (6293, 6294)	Novel Protein sim. GBank gij3674279[emb]CAB07315.1] - (Z92825) predicted using Genefinder. cDNA EST yk315e12.3 comes from this gene; cDNA EST yk315e12.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00702) - haloacid dehalogenase-like hydrolase	UNCLASSIFIED	56181886, 35696286, 60432049, 264259, 56182181, 29331825, 60432289, 35696052, 56182435, 265008, 264910, 60431735, 60433358, 60433436, 265010, 284448, 284288, 265022, 33657023, 33657109, 60431528, 65274791, 264631, 56182323, 264404, 22279002
3148	95352169 (6295, 6296)	Novel Protein sim. GBank gij5225322[gbl]AAD40851.1[AF08310 - (AF083108) sirutin type 3 [Homo sapiens]		UNCLASSIFIED	35696286, 35696052, 264511, 85658542, 87168474, 284764, 35696423, 264555, 264556, 264557, 264558, 83373044, 56526486, 60432113
3149	95308548 (6297, 6298)	Novel Protein sim. GBank gij4200446 (AF102777) - FYVE finger-containing phosphoinositide kinase [Mus musculus]	Contains protein domain (PF01363) - FYVE zinc finger	eph	29331822, 35696052, 264109, 29148629, 18108381
3150	87655472 (6299, 6300)	Novel Protein sim. GBank gij3378454[emb]CAA76893] - (Y17850) ganglioside-induced differentiation associated protein 1 [Mus musculus]	Contains protein domain (PF00043) - Glutathione S-transferases.	transferase	264259, 29331822, 29331824, 29331825, 29331827, 52846317, 264686, 35695855, 56182323, 264639
3151	87772355 (6301, 6302)	Novel Protein sim. GBank gij172591 (M63577) - SFP1 [Saccharomyces cerevisiae]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	oncogene	29331822, 265008
3152	85698108 (6303, 6304)			UNCLASSIFIED	21906754, 87168558, 264605, 21906768, 52844150, 27488264, 35696423, 22279000

3153	95317298 (6305, 6306)	Novel Protein sim. GBank gi 4895041 gb AAD32705.1 AF14395 - (AF143857) coronin-3 [Mus musculus]	Contains protein domain (PF00400) - struct WD domain, G-beta repeat		264488, 52846365, 35686286, 22278996, 22278997, 22278998, 60432048, 264259, 29331826, 60432289, 33658970, 264508, 264908, 33857402, 264595, 60433438, 87168474, 87168559, 264601, 265019, 264448, 264682, 264764, 264288, 264369, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 29148784, 265021, 265022, 60170615, 52644150, 264690, 264691, 33857023, 65274620, 33857109, 18108370, 35695855, 264638, 60170394, 87168516, 60432113, 22279000, 22279002, 22278998, 264259, 29331824, 66712502, 265008, 265010, 265017, 18108354, 264691, 33857023, 264693, 20281149, 18108374, 29331828, 264509, 264905, 264908, 264510, 264511, 264512, 33857402, 264681, 264683, 33857023, 18108370, 264634, 264639, 18108385, 264563, 264486
3154	87718573 (6307, 6308)	Novel Protein sim. GBank gi 4880661 gb AAD27720.1 AF13294 - (AF132945) CGI-11 protein [Homo sapiens]		ATPase associated	
3155	87762394 (6309, 6310)	Novel Protein sim. GBank gi 728837 sp P39184 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		UNCLASSIFIED	
3156	87737449 (6311, 6312)	Novel Protein sim. GBank gi 5630078 gb AAD45821.1 AC00601 - (AC006017) N-acetylglucosaminyltransferase; similar to Q10473 (PID:g1709559) [Homo sapiens]	Contains protein domain (PF00652) - Similarity to lectin domain of ricin beta-chain, 3 copies.	transferase	56182575, 22278986, 22278997, 22278998, 22278999, 60432048, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35898052, 52644045, 265007, 265009, 60170831, 60432229, 60433356, 21908754, 33109954, 87168474, 265010, 265017, 265018, 265019, 18108351, 264448, 264288, 264688, 21906768, 21906769, 35695917, 265020, 265022, 264692, 18108370, 35698423, 56182323, 22279002
3157	88259577 (6313, 6314)				18108396, 264259, 29331828, 35696052, 29148496, 87168559, 265017, 264448, 264288, 264691, 18108366, 52645129, 35698423, 52644332
3158	80034118 (6315, 6316)	Novel Protein sim. GBank gi 5306084 gb AAD41895.1 AF15677 - (AF156778) ASB-3 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	kinase	264488, 263974
3159	94124114 (6317, 6318)	Novel Protein sim. GBank gi 5531272 emb CAB50897.1 - (AJ243800) WSC4 homologue [Kluyveromyces fragilis]		UNCLASSIFIED	56182575, 22278999, 29331824, 264106, 60433356, 264758, 265011, 87168559, 264448, 18108354, 264768, 21906768, 265020, 264691, 264692, 33657109, 18108374, 35698423, 264555, 60170394, 22279000
3160	80221088 (6319, 6320)	Novel Protein sim. GBank gi 3930525 (AF084447) - sex-determination protein homolog Fem1a [Mus musculus]	Contains protein domain (PF00023) - Ank repeat	struct	18108351, 264555, 284556, 264557, 264558, 264559

3161	88074111 (6321, 6322)				264488, 22278985, 22278997, 22278998, 264259, 29331822, 60432289, 29331828, 52644045, 265017, 265018, 264448, 264288, 21908764, 21908767, 265020, 18108374, 284638, 284568
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Table 2

Tissue ID	Tissue Name	Tissue Information	Disease Association
20281069	192xN	Protein-protein Interactions	Any
20281071	192xN	Protein-protein Interactions	Any
20281149	192xN	Protein-protein Interactions	Any
20281152	192xN	Protein-protein Interactions	Any
264111	276xN	Protein-protein Interactions	Any
264112	276xN	Protein-protein Interactions	Any
263966	384xN	Protein-protein Interactions	Any
263967	384xN	Protein-protein Interactions	Any
264110	552xN	Protein-protein Interactions	Any
18108379	SPH 52.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108381	SPH 52.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108383	SPH 52.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108368	SPH 52.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108384	SPH 52.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108394	SPH 53.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108355	SPH 53.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108359	SPH 53.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108361	SPH 53.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108362	SPH 53.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108366	SPH 53.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108354	SPH 54.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108392	SPH 54.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108348	SPH 54.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108382	SPH 54.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108395	SPH 54.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108365	SPH 54.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108397	SPH 55.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108398	SPH 55.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108364	SPH 55.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	
18108388	SPH 55.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108358	SPH 55.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
20281099	SPH 56.2 (MG63)		
20281100	SPH 56.3 (U1SMC)		
264404	SPH.1 (Brain)	Whole Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264510	SPH.10 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264511	SPH.11 (Placenta)	Placenta	Infertility, birth defects
264512	SPH.12 (Thyroid)	Thyroid	Hyperparathyroidism, Hypoparathyroidism
264555	SPH.13 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264556	SPH.14 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264557	SPH.15 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264558	SPH.16 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264559	SPH.17 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264569	SPH.19 (One Fetal tissue and two cell lines)	Mixed	
264687	SPH.19.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, immunodeficiencies
264688	SPH.19.2 (hematopoietic stem cells - CRL2043)	Hematopoietic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264689	SPH.19.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264690	SPH.19.4 (Fetal Liver)	Fetal liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264691	SPH.19.5 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberculous sclerosis, Scleroderma, Obesity, Transplantation
264692	SPH.19.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264693	SPH.19.7 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberculous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264482	SPH.2 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberculous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264600	SPH.21 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264601	SPH.22 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264602	SPH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264603	SPH.24 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264604	SPH.25 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264605	SPH.26 (Placenta)	Placenta	Infertility, birth defects
264634	SPH.28 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis ,Atrial septal defect (ASD),Atrioventricular (A-V) canal defect, Ductus arteriosus , Pulmonary stenosis , Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264635	SPH.29 (Fetal Kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264483	SPH.3 (Bone Marrow)	Bone marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264636	SPH.30 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264637	SPH.31 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264638	SPH.32 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264639	SPH.33 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264484	SPH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264758	SPH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264760	SPH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation

264762	SPH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264764	SPH.44.4 (Prostate)	Prostate	Prostate Cancer
264766	SPH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264768	SPH.44.6 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264769	SPH.44.7 (Uterus)	Uterus	Infertility, birth defects
264905	SPH.48.1 (Burkitt's Lymphoma- Raji)	Burkitt's Lymphoma	Lymphoma, blood cancers
264906	SPH.48.2 (Thalamus- Brain)	Thalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264907	SPH.48.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
264908	SPH.48.4 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
264909	SPH.48.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
264910	SPH.48.6 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
265006	SPH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
265007	SPH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
265008	SPH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
265009	SPH.50.4 (fetal lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
265010	SPH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
265011	SPH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
18108385	SPH.51.1 (MCF-7)	Breast Cancer	Breast Cancer
18108370	SPH.51.2 (CCRF-CEM)	Cancer Cell line	Cancer
18108374	SPH.51.3 (K-562)	Cancer Cell line	Cancer
18108351	SPH.51.4 (OVCAR-3)	Ovarian cancer	Ovarian cancer
18108372	SPH.51.5 (HL-60)	Cancer Cell line	Cancer
264486	SPH.6 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,

264508	SPH.8 (Fetal Brain)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264509	SPH.9 (Lymph Node)	Lymph Node	Lymphedema , Allergies
20798451	SRH 56.3(UtSMC)		
264487	SRH.1 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264534	SRH.11 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264535	SRH.12 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264563	SRH.19 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264488	SRH.2 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264564	SRH.20 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264565	SRH.21 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264566	SRH.22 (Placenta)	Placenta	Infertility, birth defects
264567	SRH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264591	SRH.25 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264592	SRH.26 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264593	SRH.27(thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264594	SRH.28 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264595	SRH.29 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264489	SRH.3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,

264596	SRH.30 (Placenta)	Placenta	Infertility, birth defects
264628	SRH.33 (fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264629	SRH.34 (lymph Node)	Lymph Node	Lymphedema, Allergies
264630	SRH.35 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264631	SRH.36 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264632	SRH.37 (Fetal Brain)	Fetal Brain	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264490	SRH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264681	SRH.43.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, immunodeficiencies
264682	SRH.43.2 (hematopoietic stem cells - CRL2043)	Hematopoietic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264683	SRH.43.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264684	SRH.43.4 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264685	SRH.43.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264686	SRH.43.7 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264757	SRH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264759	SRH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264761	SRH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264763	SRH.44.4 (Prostate)	Prostate	Prostate Cancer
264765	SRH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host

264767	SRH.44.6 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264828	SRH.46.1 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264887	SRH.47.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
18108377	SRH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
18108380	SRH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
18108396	SRH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108391	SRH.50.4 (fetal lung)	Fetal Lung	Airway diseases, infection
18108357	SRH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
18108390	SRH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
264532	SRH.9 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
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263994	cDNA-ORF Selection		
264080	Mx96		
21906754	NQH 6.1 (HH729)		
22278996	NQH 6.10 (PrEC)	Endothelial cells	heart disease, cancer
22278997	NQH 6.11 (CAEC)	Endothelial cells	heart disease, cancer
22278998	NQH 6.12 (CSC)	Cancer Cell line	Cancer
22278999	NQH 6.13 (NHNPC)	Cancer Cell line	Cancer
22279000	NQH 6.14 (NHMC-RM)	Cancer Cell line	Cancer
22279002	NQH 6.15 (Hypothalamus)	Hypothalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
21906764	NQH 6.2 (In Dated Platelets)	Platelets	Clotting diseases, stroke
21906765	NQH 6.3 (HuVec)	Endothelial cells	heart disease, cancer
87168474	NQH 6.3 (Sized-HUVEC)	Endothelial cells	heart disease, cancer
21906766	NQH 6.4 (U1MVEC- myo)	Cancer Cell line	Cancer
21906767	NQH 6.5 (NHEM-neo)	Cancer Cell line	Cancer
21906768	NQH 6.6 (NHEK)	Cancer Cell line	Cancer
21906769	NQH 6.7 (ByCAEC)	Endothelial cells	heart disease, cancer
22278994	NQH 6.8 (NHA)	Cancer Cell line	Cancer

22278995	NQH 6.9 (PrSC)	Cancer Cell line	Cancer
27486261	NQH 7.1 (Jurkat E6-untreated)	Cancer Cell line	Cancer
27486262	NQH 7.2 (TF1-untreated)	Cancer Cell line	Cancer
27486264	NQH 7.3 (U87-untreated)	Cancer Cell line	Cancer
27486265	NQH 7.4 (THP1-untreated)	Cancer Cell line	Cancer
29331822	NQH 8.1 (Brain- amygdala)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331824	NQH 8.2 (Brain-hippocampus)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331825	NQH 8.3 (Brain- substantia nigra)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331826	NQH 8.4 (small intestine)	Small intestine	digestive diseases, obesity, diabetes
29331827	NQH 8.5 (Spinal cord)	Spinal chord	paralysis, neurodegenerative disorders
29331828	NQH 8.6 (stomach)	Stomach	Stomach cancer
29331830	NQH 8.7 (Trachea)	Trachea	Airway diseases, infection
87168518	NQH 9.1 (Sized-MG-63_treatment pool)		
87168559	NQH 9.2 (Sized-HEPG2 untreated)		
35695763	NQH.10.1 (MCF-7untreated)	Cancer Cell line	Cancer
35695855	NQH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
35695917	NQH.10.3 (JAR)	Cancer Cell line	Cancer
35696052	NQH.10.4 (PA-1)	Cancer Cell line	Cancer
35696286	NQH.10.5 (CADMEC)	Endothelial cells	heart disease, cancer
35696423	NQH.10.6 (CADMEC_LA)	Endothelial cells	heart disease, cancer
52644045	NQH.11.1 (SK-PN-DW)	Cancer Cell line	Cancer
52644150	NQH.11.2 (Chorionic Villus Cells)	Chorionic villus	fertility, birth defects
52644229	NQH.11.3 (A549)	Cancer Cell line	Cancer
52644296	NQH.11.4 (U266B1)	Cancer Cell line	Cancer
52644332	NQH.11.5 (Daoy)	Cancer Cell line	Cancer
52644507	NQH.11.6 (SW1783)	Cancer Cell line	Cancer
52645080	NQH.12.1 (U-118MG)	Cancer Cell line	Cancer
52645129	NQH.12.2 (A204)	Cancer Cell line	Cancer
52645156	NQH.12.3 (T24)	Cancer Cell line	Cancer
52646317	NQH.12.4 (G-401)	Cancer Cell line	Cancer
52646365	NQH.12.5 (CaSki)	Cancer Cell line	Cancer
52646842	NQH.12.6 (SHP-77)	Cancer Cell line	Cancer

60424179	NQH.14.1 (Yale75_breast carcinoma)	Breast carcinoma	Breast Cancer
60424269	NQH.14.2 (Yale78B_ovarytumor)	Ovary tumor	Ovarian cancer
60431528	NQH.14.3 (Yale79_prostateBPH)	Prostate	Prostate Cancer
60431602	NQH.14.4 (Yale80_ProstateAdenocarcinoma)	Prostate	Prostate Cancer
60431735	NQH.14.5 (Yale86_UterineMyoma)	Uterine Myoma	Uterine Cancer
60431850	NQH.14.6 (Yale207_Myometrium)	Myometrium	Fertility
60432049	NQH.15.1 (Yale99_cervix)	Cervix	Osteoporosis, cervical cancer
60432113	NQH.15.2 (Yale45_spleenTP)		Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
60432229	NQH.15.3 (Yale16_Skin)	Skin	wound healing, melanoma
60432289	NQH.15.4 (Yale137_Parotid)		
60433356	NQH.15.5 (Yale38_SmallIntestine)	Small intestine	digestive diseases, obesity, diabetes
60433438	NQH.15.6 (Yale28_ColonAscending)	Colon	Colon cancer
65274444	NQH.17.1 (Larynx)	Larynx	Cancer
65274572	NQH.17.2 (Duodenum)	Duodenum	
65274620	NQH.17.3 (Kidney, Primary tumors)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
65274727	NQH.17.4 (Lung Pleura, normal)	Lung	Airway diseases, infection
65274791	NQH.17.5 (Lung, Normal Adult)	Lung	Airway diseases, infection
83373044	NQH.18.230 (Pooled adrenal gland, placenta)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
85658542	NQH.18.560 (Pooled uterus, BeWo pool)	Uterus	Infertility, birth defects
33656970	NQH.9.1 (MG-63_treatment pool)	Cancer Cell line	Cancer
33657023	NQH.9.2 (HEPG2 untreated)		Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
33657084	NQH.9.3 (PC3_untreated)	Cancer Cell line	Cancer
33657109	NQH.9.4 (TF-1_TPA)	Cancer Cell line	Cancer
33657182	NQH.9.5 (TF-1_TPO)	Cancer Cell line	Cancer
33657349	NQH.9.6 (TF-1_Hemin)	Cancer Cell line	Cancer
33657402	NQH.9.7 (HFDPC)	Cancer Cell line	Cancer
264259	NQH1 (Mixture of eight adult & two fetal tissues)		
264288	NQH2 (Ten tissues plus lymphocyte control)		
264448	NQH3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
265017	NQH4.1 (lymph node)	Lymph Node	Lymphedema, Allergies

265018	NQH4.2 (fetal kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
66712502	NQH4.2 (Sized)		
265019	NQH4.3 (pituitary gland)		Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
66714117	NQH4.3 (Sized)		
265020	NQH4.4 (testis)	testis	Infertility, birth defects
265021	NQH4.5 (fetal liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
265022	NQH4.6 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
18108376	NQH5.1 (MCF-7)	Breast cancer	Breast Cancer
18108387	NQH5.2 (CCRF-CEM)	Cancer Cell line	Cancer
264952	NRL1: HPLC FRACTIONATION OF RELIG		
263971	Old BB3 Baits		
263969	Old BB5 Baits		
263975	ORFSEL		
263972	OTHER Baits		
263978	pGALORF		
264106	PPBAITS		
264088	QC-YA7		
264089	QC-YA8		
264102	Resequenced Interactors		
264369	RRH.1		
60170394	RRH.10.1 (MCF-7untreated)	Breast cancer	Breast Cancer
60170615	RRH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
60170831	RRH.10.3 (JAR)	Cancer Cell line	Cancer
60174639	RRH.11.8 (HeLa)	Cancer Cell line	Cancer
264113	rrQEA Baits		
263973	RRQEA_B5 baits		
29146498	SRD 3.1 (SKMC)	Cancer Cell line	Cancer
29146499	SRD 3.2 (SKMC)	Cancer Cell line	Cancer
29147620	SRD 3.3 (RPTEC)	Cancer Cell line	Cancer
29148627	SRD 3.4 (HRCE)	Cancer Cell line	Cancer
29148629	SRD 3.6 (HRE)	Cancer Cell line	Cancer
29148784	SRD 3.7 (HRE)	Cancer Cell line	Cancer
55810764	SRD.7.1 (Lymph Node)	Lymph Node	Lymphedema, Allergies
55811150	SRD.7.2 (pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
55811386	SRD.7.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,

55811576	SRD.7.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
55811957	SRD.7.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
55812038	SRD.7.6 (Fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
56181562	SRD.8.1 (Lymph Node)	Lymph Node	Lymphedema , Allergies
56181686	SRD.8.2 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
56182181	SRD.8.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
56182323	SRD.8.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
56182435	SRD.8.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
56182575	SRD.8.6 (Fetal Kidney)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
32833986	SRD4: HL adapter		
56526486	SRD5.1:rr fragments		
33109954	SRD5: long-RXRJ		
56994075	SRD9.1 (CS/SC)	Cancer Cell line	Cancer
263977	TSC Screen I		

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 Glu Pro Cys Arg Asp Val Met Thr Ser Tyr Val Leu Gly Asn Lys Val
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 Thr Cys Cys Arg Pro Leu Glu Leu Trp Pro Val Lys Thr Pro Gly Asn
 100 105 110
 Pro Met Ala Arg Arg Glu Thr Val Leu
 115 120

<210> 7
 <211> 480
 <212> DNA
 <213> Homo sapiens

<400> 7
 agatcttttc agaagcggtg ggtggggcgt tcatatccac gtgaatgggc ccaaaggca
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 agaaaacca cacctctcct cccctcccca gtggctgtgg ctttcctagg gacaatagga
 120
 tgaatgggct ttcagtgtgg ggacagcaaa acatgcacta gggcccagag tggcagttct
 180
 cttggtgtgg agagtgcctg ccacaggcct tggccagagc ccgtgagggga gtggtgtgtg
 240
 aaaggccacc tccacgtggg taagcgtgag gacttggact tctctggcac tgagatggga
 300
 cctcctgcct gtgggagtca tctggccacc accctggggc cagtaaaggt tggagctaga
 360

agggtcgtcc tccctgactt gagctctgag ggctttgcct gccagccag agcggcaagg
420
cacaggggac cctcggggac gcccatggcc accctgggga agacagggct cctcacgcgt
480

<210> 8
<211> 119
<212> PRT
<213> Homo sapiens

<400> 8
Met Gly Phe Gln Cys Gly Asp Ser Lys Thr Cys Thr Arg Ala Gln Ser
1 5 10 15
Gly Ser Ser Leu Gly Val Glu Ser Ala Cys His Arg Pro Trp Pro Glu
20 25 30
Pro Val Arg Glu Trp Cys Val Lys Gly His Leu His Val Gly Lys Arg
35 40 45
Glu Asp Leu Asp Phe Ser Gly Thr Glu Met Gly Pro Pro Ala Cys Gly
50 55 60
Ser His Leu Ala Thr Thr Leu Gly Pro Val Lys Val Gly Ala Arg Arg
65 70 75 80
Val Val Leu Pro Asp Leu Ser Ser Glu Gly Phe Ala Cys Pro Ala Arg
85 90 95
Ala Ala Arg His Arg Gly Pro Ser Gly Thr Pro Met Ala Thr Leu Gly
100 105 110
Lys Thr Gly Leu Leu Thr Arg
115

<210> 9
<211> 428
<212> DNA
<213> Homo sapiens

<400> 9
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120
tcccagggat gctggatgac ctctttcagt ccatgttcct gtgcgccctg ctgctcttct
180
ggctgtgcgt gtaccacggg attcgtgtcc agggagaaag aaagtgttta actttctatt
240
tgcctaaatt cttcattggt ggactattgt gggtggcttc tgttacgcta ggaatatggc
300
aaacagttaa cgaattacat gatccaatgt accagtatcg agttgatacc ggaaattttc
360
agggaatgaa ggtcttcttc atggtggtgg cagcgggtga cattctgtac ctcttgttct
420
tgatagtg
428

<210> 10
<211> 138
<212> PRT

<213> Homo sapiens

<400> 10

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Met Arg Asp Trp Gly Ile Glu Gln Lys Trp Met Ser Val Leu Leu Pro
 1           5           10           15
Leu Leu Leu Leu Tyr Asn Asp Pro Phe Phe Pro Leu Ser Phe Leu Val
      20           25           30
Asn Ser Trp Leu Pro Gly Met Leu Asp Asp Leu Phe Gln Ser Met Phe
      35           40           45
Leu Cys Ala Leu Leu Leu Phe Trp Leu Cys Val Tyr His Gly Ile Arg
      50           55           60
Val Gln Gly Glu Arg Lys Cys Leu Thr Phe Tyr Leu Pro Lys Phe Phe
65           70           75           80
Ile Val Gly Leu Leu Trp Leu Ala Ser Val Thr Leu Gly Ile Trp Gln
      85           90           95
Thr Val Asn Glu Leu His Asp Pro Met Tyr Gln Tyr Arg Val Asp Thr
      100          105          110
Gly Asn Phe Gln Gly Met Lys Val Phe Phe Met Val Val Ala Ala Val
      115          120          125
Tyr Ile Leu Tyr Leu Leu Phe Leu Ile Val
      130          135

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<210> 11

<211> 453

<212> DNA

<213> Homo sapiens

<400> 11

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gaatgttgca ggcaaactca agaccggtgg ccttggtgaa ggtccaggtc agctcggcgg
120
acttgccccg ctcgaccagc acgctgttgg ggtcgcatg cttcatgccg cccatatcgc
180
catgccccat ggcggcgtgg tccatcttgc ccatgccggt ggccgtgagc atgccgctgg
240
cttgcatctt gagcatttct ttctggtgtt cggcgtgcat cgccgcatca cccagattga
300
attcgtgcag taactggcct ttgttgacca gcacaaagcg cacggtctca ccggctttta
360
catccagagc cttgggcgaa aaggaaatgt cctgcagggt gacttccacg gtgcgcgtgg
420
ctttatcggc cggtgccggg tggccaaacg cgt
453

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<210> 12

<211> 130

<212> PRT

<213> Homo sapiens

<400> 12

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Met Leu Gln Ala Asn Ser Arg Pro Val Ala Leu Val Lys Val Gln Val
 1           5           10           15
Ser Ser Ala Asp Leu Pro Gly Ser Thr Ser Thr Leu Leu Gly Ser Ser

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<400> 13
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120
tgggccctac catgctggca ttttcctcca tgtgtcaaac acatggggttc agccagcgaa
180
gattccatgg gacctcctcg tgtgggacgt gtgctcccca ccacaaatgg aacgttcctt
240
gtttgcatct ggaggggttg gtggtcctgc tggctggagc agcctggggc cagaggaagc
300
cgtatcaacc ggctctgcag cgcttcagcg agggtgccct ggagtaccta gccaacctgg
360
accgagcccc agaccccacg gtcaggaagg acgcctttgc caccgacatc ttcagcgcct
420
acgatgttct cttccatcag tggctgcaga gtcgagaagc caagctccgt cttgccgtgg
480
tggaggctct ggggcctatg agccatctgc tgcccagtga gaggctggaa gagcagctgc
540
ccaagctect ccctgggatt ctgcacctct acaagaagca cgcagagacc ttctacttgt
600
ccaagagcct gggccagatc ctcgaggcag ctgtgagtgt gggcagccgc aactggaga
660
cccagctgga tgccctcttg gctgcactgc actcccagat ctgtgtgcct gtggagtect
720
caagccccct ggtgatgagt aaccagaagg aggtgctgcg ctgcttcact gtgctggcct
780
gcagctcgcc tgaccgccta ctggccttcc tgctgcccag gctggacacc accaatgaga
840
ggacccgcgt gggcaccctg cagggggcca aacatgtcat caactcaact gctgctcaaa
900
tggaagataa aaagcccttt atcctgtctt ccatgaggct tcctctcctg aacaccaaca
960

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gcaaggtgaa gcgggcagtg gtgcaggtga ttagcgccca tggcccacca cggctacctg
 1020
 gagcagcctg gaggtgaggc gatgatcgag taaatcgtgc agcagtgcgc gctgcccccc
 1080
 gagcaggagc ctgagaagcc aggccccggc agcaaggacc ccaaggccga cagcgtgcgg
 1140
 gccatcagcg tgcgcaccct ctacctggtc agcaccaccg tggacaggat gagtcacgtc
 1200
 ctctggccat acctgctcca gttcctcacc cctgtgcgct tcaactggggc cctgactccg
 1260
 ctctgcagga gcctcgtgca tctggcgcag aagaggcagg aggccggggc cgacgccttc
 1320
 ctcattccagt acgacgcca tgcgagcctc ccgtctccct atgctgtaac cggaagactg
 1380
 ttggttgtgt cttccagccc ctacctaggg gacggacgtg gggcagcggc gctgcgcctc
 1440
 ctcaagtgtc tgcacccaaa cattcaccct ttgctgggtc agcattggga aacgactgtc
 1500
 ccgctgctgc tgggggtacct ggatgagcac acagaagaga ccctgccaca ggaggagtgg
 1560
 gaggagaagc tgttgatggt gagggccggg gtacggccca tcctgggcct taaggtgttg
 1620
 tctggcctgg ggggtgctgg ggtggcagag gctgggccac ctgcctcgac ctacacctgt
 1680
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 1740
 agcgggggccc ttgctgtgac aaggcaccgg ccctctagca gtcgcagccc caagcgtcgg
 1800
 gggcaacctc tcacctgcc tggtagacca actgtggcat ggctgtcccc tgagggttgg
 1860
 ctctgccgcc cccggcctcc gctggaaggc ggtctgcagc ccctgcagcc acagcacatg
 1920
 gggatgtgcc caggctccag ccagccctgt gaggggtcgg gctcccagcc cctcagtggc
 1980
 atcttgccct gcagttcctg cgagacaccc tggccatcat ttctgacaac gcgt
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<210> 14

<211> 222

<212> PRT

<213> Homo sapiens

<400> 14

Ile	Val	Gln	Gln	Cys	Ala	Leu	Pro	Pro	Glu	Gln	Glu	Pro	Glu	Lys	Pro
1				5					10					15	
Gly	Pro	Gly	Ser	Lys	Asp	Pro	Lys	Ala	Asp	Ser	Val	Arg	Ala	Ile	Ser
			20					25					30		
Val	Arg	Thr	Leu	Tyr	Leu	Val	Ser	Thr	Thr	Val	Asp	Arg	Met	Ser	His
		35					40				45				
Val	Leu	Trp	Pro	Tyr	Leu	Leu	Gln	Phe	Leu	Thr	Pro	Val	Arg	Phe	Thr
	50					55					60				
Gly	Ala	Leu	Thr	Pro	Leu	Cys	Arg	Ser	Leu	Val	His	Leu	Ala	Gln	Lys
65					70					75				80	
Arg	Gln	Glu	Ala	Gly	Ala	Asp	Ala	Phe	Leu	Ile	Gln	Tyr	Asp	Ala	His

				85					90					95				
Ala	Ser	Leu	Pro	Ser	Pro	Tyr	Ala	Val	Thr	Gly	Arg	Leu	Leu	Val	Val			
				100					105					110				
Ser	Ser	Ser	Pro	Tyr	Leu	Gly	Asp	Gly	Arg	Gly	Ala	Ala	Ala	Leu	Arg			
				115					120					125				
Leu	Leu	Ser	Val	Leu	His	Pro	Asn	Ile	His	Pro	Leu	Leu	Gly	Gln	His			
				130					135					140				
Trp	Glu	Thr	Thr	Val	Pro	Leu	Leu	Leu	Gly	Tyr	Leu	Asp	Glu	His	Thr			
				145					150					155				
Glu	Glu	Thr	Leu	Pro	Gln	Glu	Glu	Trp	Glu	Glu	Lys	Leu	Leu	Met	Val			
				165					170					175				
Arg	Ala	Gly	Val	Arg	Pro	Ile	Leu	Gly	Leu	Lys	Val	Leu	Ser	Gly	Leu			
				180					185					190				
Gly	Gly	Ala	Gly	Val	Ala	Glu	Ala	Gly	Pro	Pro	Ala	Ser	Thr	Ser	Pro			
				195					200					205				
Arg	Gly	Leu	Ala	Gly	Glu	Pro	Arg	Ile	Arg	Gln	His	Gln	Gly					
				210					215					220				

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<210> 15
<211> 363
<212> DNA
<213> Homo sapiens
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<400> 15
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gtgggttcga tccttgccctc gtgctggaac cagccgatca tggaccgggc gttggtgccg
120
ttgcaggaca ccaatgacac cttcatggcc aacatgcaga agaacgggtac ctattcgatc
180
atcccgcgta tcgccggcgg cgagatcacc ccggacaaac tgatcgccct cggcgcggtg
240
gcgaagaaat acgatctgta caccaagatc accggcggcc agcgggatcga cctgttcggc
300
gccagttgc acgaattgcc gcagatctgg ggcgagctgg tggatgccgg attcgagacc
360
ggt
363
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<210> 16
<211> 121
<212> PRT
<213> Homo sapiens
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<400> 16
Xaa Ala Leu Leu Ala Arg His Gly Lys Gly His Val Gly Cys Asp Ile
  1             5             10             15
Cys Lys Pro Ala Val Gly Ser Ile Leu Ala Ser Cys Trp Asn Gln Pro
      20             25             30
Ile Met Asp Pro Ala Leu Val Pro Leu Gln Asp Thr Asn Asp Thr Phe
      35             40             45
Met Ala Asn Met Gln Lys Asn Gly Thr Tyr Ser Ile Ile Pro Arg Ile
      50             55             60
Ala Gly Gly Glu Ile Thr Pro Asp Lys Leu Ile Ala Leu Gly Ala Val

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65		70		75		80									
Ala	Lys	Lys	Tyr	Asp	Leu	Tyr	Thr	Lys	Ile	Thr	Gly	Gly	Gln	Arg	Ile
				85					90					95	
Asp	Leu	Phe	Gly	Ala	Gln	Leu	His	Glu	Leu	Pro	Gln	Ile	Trp	Gly	Glu
			100					105					110		
Leu	Val	Asp	Ala	Gly	Phe	Glu	Thr	Gly							
		115					120								

<210> 17
 <211> 682
 <212> DNA
 <213> Homo sapiens

<400> 17
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 120
 tctagcatcc tccagtatgg aggctgcatt aagactgcat gaaggagagg gagagaaggg
 180
 agaaacagag cagctggaca agaggacagg tatagggaat aagggagaag ccagtaaggc
 240
 aggaaagacc ctccgtgaca aaggggcagg gaacagaact caaacattta atggcaggta
 300
 acccaggtta gaatggtaaa ttgaaagggtg aatataaagg gagaatgggtg aaatgaattt
 360
 tctgaaatta attgctgtgt ttatagtttt tagccatgca tcggaatcac ctcaggactc
 420
 cactcccaat caattatata tctggggggag gaccaaggcg ttggtatttt tcagaagctc
 480
 cactggtgat tctgacagca cagctaggat taagaaactg atcaatggga acagcatgcc
 540
 tgttgcagag gagcttccct gggaaatgtc acacacagaa catcaatctt ccttccccac
 600
 tcctgagatc cctcattctt tggcaccagg aacagttgca attagtaaac cctggttccc
 660
 tgctgtctca caaatcgcaa ga
 682

<210> 18
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 18
Met Asn Phe Leu Lys Leu Ile Ala Val Phe Ile Val Phe Ser His Ala
1 5 10 15
Ser Glu Ser Pro Gln Asp Ser Thr Pro Asn Gln Leu Tyr Ile Trp Gly
20 25 30
Arg Thr Lys Ala Leu Val Phe Phe Arg Ser Ser Thr Gly Asp Ser Asp
35 40 45
Ser Thr Ala Arg Ile Lys Lys Leu Ile Asn Gly Asn Ser Met Pro Val
50 55 60
Ala Glu Glu Leu Pro Trp Glu Met Ser His Thr Glu His Gln Ser Ser

65					70					75				80	
Phe	Pro	Thr	Pro	Glu	Ile	Pro	His	Ser	Leu	Ala	Pro	Gly	Thr	Val	Ala
				85					90					95	
Ile	Ser	Lys	Pro	Trp	Phe	Pro	Ala	Val	Ser	Gln	Ile	Ala	Arg		
			100					105					110		

<210> 19
 <211> 515
 <212> DNA
 <213> Homo sapiens

<400> 19
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 ccccatctc aactatgtta gccagtctgg ctgttcactt agtcactaca gtttgcttct
 120
 cgtctgcagt gcagtcttgg gctataagaa acactgggccc actcaatacc tcccccttt
 180
 tggcccttct cctcctctgg tccatgggtg gggttggggg gagcccagtt tcagcaccag
 240
 cagctggagc ccataccaca ctcatttttc agttctggct gtgggagccc ctcccacagg
 300
 tttcagttcc ccaagcccca ggctgagtt ttttttattg caaaagctgg ttgttgttgt
 360
 ggctagctcc caggcgtgtg aggtgcagct tgctaagtaa gagctaggaa agagaatagg
 420
 gtctgtctgt aggtgtccag tctgaaggaa tgcctgggat acttcctcaa gcagttcctt
 480
 ctcacagtct cctggctgct ccgcatgtca gatct
 515

<210> 20
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 20
 Met Gly Pro Ala Ser Leu Leu His Pro Ser Leu Gly Lys Asp His Ala
 1 5 10 15
 Pro Ile Ser Thr Met Leu Ala Ser Leu Ala Val His Leu Val Thr Thr
 20 25 30
 Val Cys Phe Ser Ser Ala Val Gln Ser Trp Ala Ile Arg Asn Thr Gly
 35 40 45
 Pro Leu Asn Thr Ser Pro Leu Leu Ala Leu Leu Leu Leu Trp Ser Met
 50 55 60
 Gly Gly Val Gly Gly Ser Pro Val Ser Ala Pro Ala Ala Gly Ala His
 65 70 75 80
 Thr Thr Leu Ile Phe Gln Phe Trp Leu Trp Glu Pro Leu Pro Gln Val
 85 90 95
 Ser Val Pro Gln Ala Pro Gly Leu Ser Phe Phe Tyr Cys Lys Ser Trp
 100 105 110
 Leu Leu Leu Trp Leu Ala Pro Arg Arg Val Arg Cys Ser Leu Leu Ser
 115 120 125
 Lys Ser

130

<210> 21
 <211> 390
 <212> DNA
 <213> Homo sapiens

<400> 21
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 tagacgcggt gcctatgggt gcggaggacc atggagtga gcgagtaaga ctagatgatg
 120
 caacaaatgt gcctgagggt gaaatggcac gagccagtgc caatgagggc atgacacctg
 180
 ttaaccacga caaataccct tctgtccttt taaatgaagc ggcccaggct tcattactgg
 240
 atacaatgac tgcttgcaact gatgggttca caattgagca attggagctt acacgatctc
 300
 tatgttatga aagagtatta gcacatcgat cctcatggga tcgttcagcc ctgggtcaag
 360
 aattaaagca agttgtccaa ggcattccatn
 390

<210> 22
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 22
 Met Val Ala Glu Asp His Gly Val Lys Arg Val Arg Leu Asp Asp Ala
 1 5 10 15
 Thr Asn Val Pro Glu Gly Glu Met Ala Arg Ala Ser Ala Asn Glu Gly
 20 25 30
 Met Thr Pro Val Asn His Asp Lys Tyr Pro Ser Val Leu Leu Asn Glu
 35 40 45
 Ala Ala Gln Ala Ser Leu Leu Asp Thr Met Thr Ala Cys Thr Asp Gly
 50 55 60
 Phe Thr Ile Glu Gln Leu Glu Leu Thr Arg Ser Leu Cys Tyr Glu Arg
 65 70 75 80
 Val Leu Ala His Arg Ser Ser Trp Asp Arg Ser Ala Leu Ala Gln Glu
 85 90 95
 Leu Lys Gln Val Val Gln Gly Ile His
 100 105

<210> 23
 <211> 385
 <212> DNA
 <213> Homo sapiens

<400> 23
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 ctgggcctgt tcgccgtgct gctgtcctgc tgcgcctcgg ccatgtacac cagcgtggag
 120

ggctgggact acgtggactc gctctacttc tgcttcgtca ccttcagcac catcggcttc
 180
 ggggacctgg tgagcagcca gcacgccgcc taccggaacc aggggctcta ccgcctgggc
 240
 aacttcctct tcatactgct cggcgtgtgc tgcatttact cgctcttcaa cgtcatctcc
 300
 atcctcatca agcaggtgct caactggatg ctgcgcaagc tgagctgccg ctgctgcgcg
 360
 cgctgctgcc cggctcctgg cgcgc
 385

<210> 24
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 24
 Xaa Ser Glu Ala Asp Ser Leu Ala Gly Trp Lys Pro Ser Val Tyr His
 1 5 10 15
 Val Leu Leu Ile Leu Gly Leu Phe Ala Val Leu Leu Ser Cys Cys Ala
 20 25 30
 Ser Ala Met Tyr Thr Ser Val Glu Gly Trp Asp Tyr Val Asp Ser Leu
 35 40 45
 Tyr Phe Cys Phe Val Thr Phe Ser Thr Ile Gly Phe Gly Asp Leu Val
 50 55 60
 Ser Ser Gln His Ala Ala Tyr Arg Asn Gln Gly Leu Tyr Arg Leu Gly
 65 70 75 80
 Asn Phe Leu Phe Ile Leu Leu Gly Val Cys Cys Ile Tyr Ser Leu Phe
 85 90 95
 Asn Val Ile Ser Ile Leu Ile Lys Gln Val Leu Asn Trp Met Leu Arg
 100 105 110
 Lys Leu Ser Cys Arg Cys Cys Ala Arg Cys Cys Pro Ala Pro Gly Ala
 115 120 125

<210> 25
 <211> 337
 <212> DNA
 <213> Homo sapiens

<400> 25
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 aggaggggag ttcccagctc tgtatttttg aagggtcagt cttggtgctt ggaccagtga
 120
 ggagccccgt gggatccaga ctcgagtggg tggagccggg gcaggtggga gcagagacac
 180
 tggaggaaag ctggtcgaat gcactgtgta tttggaggca gaaccagcag agggctctct
 240
 gggttgagtg tagggcaaaa gagaaagaag gcaccaagcc tggggtctgg gttttctctc
 300
 ttacacttgc tgggtggacg gtggtgccac tgaatga
 337

<210> 26

<211> 111
 <212> PRT
 <213> Homo sapiens

<400> 26
 Met Gly Glu Thr Val His Phe Leu Leu Gly Leu Arg Gly Lys Ser Leu
 1 5 10 15
 Gln Ser Phe Glu Glu Gly Ser Ser Gln Leu Cys Ile Phe Glu Gly Ser
 20 25 30
 Val Leu Leu Leu Gly Pro Val Arg Ser Pro Val Gly Ser Arg Leu Glu
 35 40 45
 Trp Val Glu Pro Gly Gln Val Gly Ala Glu Thr Leu Glu Glu Ser Trp
 50 55 60
 Ser Asn Ala Leu Cys Ile Trp Arg Gln Asn Gln Gln Arg Val Leu Trp
 65 70 75 80
 Val Glu Cys Arg Ala Lys Glu Lys Glu Gly Thr Lys Pro Gly Val Trp
 85 90 95
 Val Phe Ser Leu Thr Leu Ala Gly Trp Thr Val Val Pro Leu Asn
 100 105 110

<210> 27
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 27
 ccgacgtcga atatccatgc agccgcgccg aggatggaga gagcgatgga gcaactcaac
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 cgcctgacgc gctcgctgcg ccgcgcgcgc accgtggagt tgcccagagga taatgaaact
 120
 gctgtttata cattaatgcc aatggttatg gctgatcaac acaggtctgt ttctgaacta
 180
 ctatcaaatt caaaatttga tgtcaattat gcattcggac gtgtgaaaag aagcttgctt
 240
 cacattgcag caaattgtgg atcgggtggaa tgcttggttt tgctgttaaa gaaaggagca
 300
 aatcctaact atcaagatat ttcaggctgt aca
 333

<210> 28
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 28
 Pro Thr Ser Asn Ile His Ala Ala Ala Pro Arg Met Glu Arg Ala Met
 1 5 10 15
 Glu Gln Leu Asn Arg Leu Thr Arg Ser Leu Arg Arg Ala Arg Thr Val
 20 25 30
 Glu Leu Pro Glu Asp Asn Glu Thr Ala Val Tyr Thr Leu Met Pro Met
 35 40 45
 Val Met Ala Asp Gln His Arg Ser Val Ser Glu Leu Leu Ser Asn Ser
 50 55 60
 Lys Phe Asp Val Asn Tyr Ala Phe Gly Arg Val Lys Arg Ser Leu Leu

65		70		75		80									
His	Ile	Ala	Ala	Asn	Cys	Gly	Ser	Val	Glu	Cys	Leu	Val	Leu	Leu	Leu
		85		90		95									
Lys	Lys	Gly	Ala	Asn	Pro	Asn	Tyr	Gln	Asp	Ile	Ser	Gly	Cys	Thr	
		100		105		110									

<210> 29
 <211> 375
 <212> DNA
 <213> Homo sapiens

<400> 29
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 gagagctatt tgagcgccgt gacgccgctg agtcccaaag agattcgtca gctgccccgc
 120
 tacaatatca cgatcaagcg cgtcgtgaac atgacgggca agggccgcac gccgagctgg
 180
 tactcgctcg tcgtggctgg caatggtcgg ggcctcgtgg gctatggcga aggcaaagat
 240
 actaacatca gccgcgcgaa caaaaaggcg ttccacgccg cggtgaaaaa catggacttg
 300
 gtatcgggcc accggtcgaa gagtggcgcc aacacgctcg agccccccgt cgagggccgc
 360
 tggggcgcta cgcgt
 375

<210> 30
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 30
Xaa Pro Ser Val Leu Ala Ile Met Thr Ala Gly Ser Asp Gln Gly Glu
1 5 10 15
Glu Val Asn Ser Glu Ser Tyr Leu Ser Ala Val Thr Pro Leu Ser Pro
20 25 30
Lys Glu Ile Arg Gln Leu Pro Arg Tyr Asn Ile Thr Ile Lys Arg Val
35 40 45
Val Asn Met Thr Gly Lys Gly Arg Thr Pro Ser Trp Tyr Ser Leu Val
50 55 60
Val Ala Gly Asn Gly Arg Gly Leu Val Gly Tyr Gly Glu Gly Lys Asp
65 70 75 80
Thr Asn Ile Ser Arg Ala Asn Lys Lys Ala Phe His Ala Ala Val Lys
85 90 95
Asn Met Asp Leu Val Ser Val His Arg Ser Lys Ser Gly Ala Asn Thr
100 105 110
Leu Glu Pro Pro Val Glu Gly Arg Trp Gly Ala Thr Arg
115 120 125

<210> 31
 <211> 375
 <212> DNA
 <213> Homo sapiens

<400> 31
 accggtcttg gcctcagctt tgctctgaaa ttgaagtcgg tgccaaaagt ggggaagagc
 60
 gggagcaggc acttacgagc ctgcgcgtca gggatgcttc ctgggcccct gagagtgcag
 120
 agattcctgg atccagagct gcggctgggc ggctgcagct gcgcctggga gtgcagggt
 180
 cccgccctgc cagctcaaaa ggaaatgggg gctcctgcct gttcctggct cctgttggcc
 240
 ctgcagagtg cacaaaccta gccgcgcttc ctccactgca gcttacgtct ttgcagcagc
 300
 cactcccgat gggctgccac tgccatctgt gagaccataa tgtgtgcaat ttgagactca
 360
 tggcctgcat tgttt
 375

<210> 32
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 32
 Met Gln Ala Met Ser Leu Lys Leu His Thr Leu Trp Ser His Arg Trp
 1 5 10 15
 Gln Trp Gln Pro Ile Gly Ser Gly Cys Cys Lys Asp Val Ser Cys Ser
 20 25 30
 Gly Gly Ser Ala Ala Arg Phe Val His Ser Ala Gly Pro Thr Gly Ala
 35 40 45
 Arg Asn Arg Gln Glu Pro Pro Phe Pro Phe Glu Leu Ala Gly Arg Glu
 50 55 60
 Pro Cys Thr Pro Arg Arg Ser Cys Ser Arg Pro Ala Ala Ala Leu Asp
 65 70 75 80
 Pro Gly Ile Ser Ala Leu Ser Gly Ala Gln Glu Ala Ser Leu Thr Arg
 85 90 95
 Arg Leu Val Ser Ala Cys Ser Arg Ser Ser Pro Leu Leu Ala Pro Thr
 100 105 110
 Ser Ile Ser Glu Gln Ser
 115

<210> 33
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 33
 ccatgcagcc caaccgttgg cgataaagtc cgtttaggcg ataccaattht atgggcaacc
 60
 attgaacaag atttattaac caaagggtgat gagtgtaaat ttggtggcgg taaaagtgtg
 120
 cgtgatggta tggcgcaaag cggcaccgca actcgcgaca atccaaatgt attggatttt
 180
 gtgattacca atgtgatgat cattgatgcc aaattaggca ttatcaaagc cgatattgggt
 240

attcgcgatg gtcgtattgt cggatcggga caagcaggta accctgacac catggatgac
300

gtcacgcaa acatgattat cggtgctagc acagaagtac ataacgggtgc a
351

<210> 34

<211> 117

<212> PRT

<213> Homo sapiens

<400> 34

Pro	Cys	Ser	Pro	Thr	Val	Gly	Asp	Lys	Val	Arg	Leu	Gly	Asp	Thr	Asn
1				5				10					15		
Leu	Trp	Ala	Thr	Ile	Glu	Gln	Asp	Leu	Leu	Thr	Lys	Gly	Asp	Glu	Cys
		20						25					30		
Lys	Phe	Gly	Gly	Gly	Lys	Ser	Val	Arg	Asp	Gly	Met	Ala	Gln	Ser	Gly
	35					40						45			
Thr	Ala	Thr	Arg	Asp	Asn	Pro	Asn	Val	Leu	Asp	Phe	Val	Ile	Thr	Asn
	50				55						60				
Val	Met	Ile	Ile	Asp	Ala	Lys	Leu	Gly	Ile	Ile	Lys	Ala	Asp	Ile	Gly
65				70					75					80	
Ile	Arg	Asp	Gly	Arg	Ile	Val	Gly	Ile	Gly	Gln	Ala	Gly	Asn	Pro	Asp
			85					90					95		
Thr	Met	Asp	Asp	Val	Thr	Pro	Asn	Met	Ile	Ile	Gly	Ala	Ser	Thr	Glu
			100					105					110		
Val	His	Asn	Gly	Ala											
			115												

<210> 35

<211> 355

<212> DNA

<213> Homo sapiens

<400> 35

nngctagctg caccaccacc tgttcatgca ggcagagcgg ccaccctca tggaagaaga
60
ggaatccact gtattgggca caggcttcct gctggacctt ggcaagcagg tgcttggtg
120
gtaccaggaa gtccagcgtg tacctcagtg cgtcctcccg ataagtcctc tccaccacct
180
ggaacacctg gcccaacagg gtgggggctg ttgcctcaaa ggggtggatac agggcggcga
240
gagtgtctg cacacagtec tccactggct caggctecat ggctcggcgc cgggcccgt
300
ccgacgcttg gtcgggaggg cggggccggg cgcgccaccg cctcccttca cgcgt
355

<210> 36

<211> 118

<212> PRT

<213> Homo sapiens

<400> 36

Xaa Leu Ala Ala Pro Pro Pro Val His Ala Gly Arg Ala Ala Thr Pro

```

      1             5             10             15
His Gly Arg Arg Gly Ile His Cys Ile Gly His Arg Leu Pro Ala Gly
      20             25             30
Pro Trp Gln Ala Gly Ala Trp Leu Val Pro Gly Ser Pro Ala Cys Thr
      35             40             45
Ser Val Arg Pro Pro Asp Lys Ser Ser Pro Pro Pro Gly Thr Pro Gly
      50             55             60
Pro Thr Gly Trp Gly Leu Leu Pro Gln Arg Val Asp Thr Gly Arg Arg
      65             70             75             80
Glu Cys Ser Ala His Ser Pro Pro Leu Ala Gln Ala Pro Trp Leu Gly
      85             90             95
Ala Gly Pro Arg Pro Thr Leu Gly Arg Ala Gly Gly Ala Gly Arg Ala
      100             105             110
Thr Ala Ser Leu His Ala
      115

```

<210> 37
 <211> 492
 <212> DNA
 <213> Homo sapiens

```

<400> 37
acgcgtggcc ttcgtctgcc accaggaccg actcagcccc accgggtttc cggaccgcgc
60
gcaaccatga caagggcgat gttgtgatct ggggtggattc cttctccgac atgctcgagg
120
gateggatct ctgggcggta gtcacgggtgc ttgccgaggc cggctatcgc ccacgggtcc
180
tcgccgacga cgtctgctgc gggttgacgt ggatcactac cggtcagctc gacggtgctc
240
ggcgtcggct gcgcgctggc ctcgacgtgc tggcaccctt gtcagacgcc agcgtcccag
300
tcgttgggct agagccgtcc tgcactaccg tctggcgtga tgacgcactc cgcctcctgc
360
cagatgatcc gcgcgtccac cgggtagcca gaaacatgca taccgtcgcc gagatgcttg
420
aggcagcaca gtggacccca ccctcgctag caggccacac cctcgtcgct cagccccatt
480
gtcatcccgc gg
492

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<210> 38
 <211> 127
 <212> PRT
 <213> Homo sapiens

```

<400> 38
Met Leu Glu Gly Ser Asp Leu Ser Ala Val Val Thr Val Leu Ala Glu
      1             5             10             15
Ala Gly Tyr Arg Pro Arg Val Leu Ala Asp Asp Val Cys Cys Gly Leu
      20             25             30
Thr Trp Ile Thr Thr Gly Gln Leu Asp Gly Ala Arg Arg Arg Leu Arg
      35             40             45
Ala Gly Leu Asp Val Leu Ala Pro Leu Ser Asp Ala Ser Val Pro Val

```


50	55	60
Val Gly Leu Glu Pro Ser Cys Thr Thr Val Trp Arg Asp Asp Ala Leu		
65	70	75
Arg Leu Leu Pro Asp Asp Pro Arg Val His Arg Val Ala Arg Asn Met		80
	85	90
His Thr Val Ala Glu Met Leu Glu Ala Ala Gln Trp Thr Pro Pro Ser		95
	100	105
Leu Ala Gly His Thr Leu Val Ala Gln Pro His Cys His Pro Ala		110
	115	120
		125

<210> 39
 <211> 412
 <212> DNA
 <213> Homo sapiens

<400> 39
 aacgaaggtn ccgtacgcgc tctgaaagcc ctgcgtaaag agcggtccga tcgccgggaa
 60
 gtgatgngca ccgcaaaaat gcaggtgggc gaagccgcga gttcaggcaa gattgtcttt
 120
 gaaatggaag acgtttatta cagcattgcc ggaaaacaac tggtgagcaa cttctctgcg
 180
 caagtcatgc gtggtgataa aattgcgctg attggcccga acggttgtgg taaaacgacg
 240
 ttgctgaaac tgatgttaag taagattcag gcagacagcg gccgtgttca ctgcggtact
 300
 aaactggaag ttgcgtactt cgaccagcac cgtgctgagc tggatcctga gcgtacggcg
 360
 atggataacc tggccgaagg taagcaggaa gtgatggtaa atggccgtgt an
 412

<210> 40
 <211> 137
 <212> PRT
 <213> Homo sapiens

<400> 40
Asn Glu Gly Xaa Val Arg Ala Leu Lys Ala Leu Arg Lys Glu Arg Ser
1 5 10 15
Asp Arg Arg Glu Val Met Xaa Thr Ala Lys Met Gln Val Val Glu Ala
20 25 30
Ala Ser Ser Gly Lys Ile Val Phe Glu Met Glu Asp Val Tyr Tyr Ser
35 40 45
Ile Ala Gly Lys Gln Leu Val Ser Asn Phe Ser Ala Gln Val Met Arg
50 55 60
Gly Asp Lys Ile Ala Leu Ile Gly Pro Asn Gly Cys Gly Lys Thr Thr
65 70 75 80
Leu Leu Lys Leu Met Leu Ser Lys Ile Gln Ala Asp Ser Gly Arg Val
85 90 95
His Cys Gly Thr Lys Leu Glu Val Ala Tyr Phe Asp Gln His Arg Ala
100 105 110
Glu Leu Asp Pro Glu Arg Thr Val Met Asp Asn Leu Ala Glu Gly Lys
115 120 125
Gln Glu Val Met Val Asn Gly Arg Val

130

135

<210> 41
 <211> 1080
 <212> DNA
 <213> Homo sapiens

<400> 41
 gaattcaagt ggacacaggc tccacgcccg cgtctcaccg ataagagcta caagcacaac
 60
 tactatgacg agcgggtttc gtcgaagag cgtcttgagc gcaactgtggc taaggatttc
 120
 gtcacgacgg aggtcgagcc catgtgggat gcggtgatg tcatgcggat gggtaaggat
 180
 ctcttcatcc agcacggtct gacgacaaat cggaagtcaa tggagtgggt taagcgttac
 240
 taccctgatt tccgcgttca cgcggtgaat ttccctgggg atccgtaccc gatccatc
 300
 gacgcgacct ttgtgccgct tcgtccgggg ctcacatca acaacccgaa tcgtccactg
 360
 ccgcaggagc agaggaagat cttcgaggcc aatgactggc agatcggtga tgctgctcag
 420
 ccggcgcacg acacgcctcc agaattgtgc tactcgtctg tgtggctatc aatgaactgc
 480
 ttggtacttg atccgaagac ggtcatctgc gaggcttcgg aagttcatca gatggagcag
 540
 atggacaagc tgggtatgaa cgtcatcccc gtcgccttcc gtgacgcgta cccattcggt
 600
 ggaggtctcc actgcgccac agctgatgta tatcgogaag gtacctgtga ggactacttc
 660
 ccgaatcagg tcgacgaccc gaccttgggt tgagaaaacc ccgtgggtcat gtcacgactg
 720
 acgcatctcg gtggctcggg acggaactta cgttgctcgt taccgggccg ccgggtctga
 780
 tatggcagta tcacgcctag caaaaaggag catgtcatgg acatggagcc gggcatcatc
 840
 aacgtcaaac aggaagtcc aggcgtcggg acgatgaacc agaaagtggg attcgtgtcc
 900
 atgcttcttt ctgcaacggg tatgggggtg gtgggtactt tcgggcgtct cagcactcct
 960
 gtggatccca cgacgggcag taagtacatc atcggtgatt ttttggccac tggtaggatg
 1020
 atagtcgggg tcctgggatt tctgcttatt atcgtcatac ttggaaaatg gtctgagctc
 1080

<210> 42
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 42
 Glu Phe Lys Trp Thr Gln Ala Pro Arg Pro Arg Leu Thr Asp Lys Ser
 1 5 10 15
 Tyr Lys His Asn Tyr Tyr Asp Glu Arg Val Ser Leu Glu Glu Arg Leu

```
<210> 43
<211> 358
<212> DNA
<213> Homo sapiens
```

```
<210> 44
<211> 105
<212> PRT
<213> Homo sapiens
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441

1				5					10					15			
Leu	Gly	His	Arg	Gly	Cys	Leu	Pro	Ala	Ala	Pro	Gly	Arg	Ala	Val	Asp		
			20					25					30				
Thr	Thr	Ala	Trp	Ser	Ala	Val	Pro	Gly	His	Cys	His	Ala	His	Arg	Cys		
		35					40				45						
Pro	Leu	Arg	Met	Asp	Leu	Gly	Phe	Arg	Ile	Arg	Val	Ala	Tyr	Gln	Arg		
	50					55				60							
Glu	Ser	Gln	Ile	Leu	Lys	Glu	Val	Gln	Ser	Pro	Glu	Gly	Met	Ile	Ser		
65					70					75					80		
Leu	Arg	Asp	Thr	Ala	Ala	Ser	Leu	Arg	Leu	Glu	Arg	Asp	Thr	Arg	Gln		
			85					90						95			
Leu	Pro	Leu	Leu	Thr	Ser	Ala	Leu	His									
			100					105									

<210> 45
 <211> 905
 <212> DNA
 <213> Homo sapiens

<400> 45
 gtcgacgata aaggagtatt tgcgcagcag cagtatgatg ctctcggtga ggcggtttc
 60
 gcggctcctg gaatcccaga gcagtatggt ggcgacggtg cggatgcatg tgcgtccgca
 120
 ataatcatgg aagaggtcgc tcgagtctgt gcgtcgctgt ccaccgtcat atcgtccaat
 180
 gagcttggtg ccgtccctct cctcaaatac ggtagcgagg agcagaggaa acgttatctt
 240
 tctgaagttg cttcgggtaa ggcacttttc ggatatgcgc tctccgagge tgatgctgga
 300
 tcagatccag ctgcacttaa gtgtcgagcc gacgaagatg gggacagttt cgtcctgaat
 360
 ggcgttaagg cttgggtcac ggaggctggc gaggccaagt acctggtgat atttgcggtt
 420
 actgaccag acgatccgcg ccacagaatc agcgcggtga tgggccatgc agatgaccgc
 480
 ggcattagct acggggctcc ggagcacaaa atggggatac gcgggtcagt taccagggaa
 540
 gtggttttca agaatacgcg tatccccaag gaacgagtaa ttggccgtcg agggcacggt
 600
 ctgagtgttg ctctaggtac gcttgataac tctcgtgtct cgattgctgc tcaagcagtg
 660
 ggaattgccc aaggagcttt agacattgcc acggattacg tccagaagcg caagcagttt
 720
 ggccagccac tgtccaattt tgagggaatc cagttcatgc tcgcagacat ggcaatgcgt
 780
 ttggaggcgg cgcgagcgt gacatactct gcagctgac gtagtgggcg ccagactgac
 840
 gatgtgagtt acttcggcgc ggcgccaaa tgtttcgctt ccgacacagc gatggcagtg
 900
 tgcac
 905

<210> 46

<211> 301
 <212> PRT
 <213> Homo sapiens

<400> 46

Val	Asp	Asp	Lys	Gly	Val	Phe	Ala	Gln	Gln	Gln	Tyr	Asp	Ala	Leu	Val
1				5					10					15	
Glu	Ala	Gly	Phe	Ala	Ala	Pro	Gly	Ile	Pro	Glu	Gln	Tyr	Gly	Gly	Asp
			20					25					30		
Gly	Ala	Asp	Ala	Ile	Ala	Ser	Ala	Ile	Ile	Met	Glu	Glu	Val	Ala	Arg
		35					40					45			
Val	Cys	Ala	Ser	Ser	Ser	Thr	Val	Ile	Ser	Ser	Asn	Glu	Leu	Gly	Thr
	50					55					60				
Val	Pro	Leu	Leu	Lys	Tyr	Gly	Ser	Glu	Glu	Gln	Arg	Lys	Arg	Tyr	Leu
65					70					75				80	
Ser	Glu	Val	Ala	Ser	Gly	Lys	Ala	Leu	Phe	Gly	Tyr	Ala	Leu	Ser	Glu
			85						90					95	
Ala	Asp	Ala	Gly	Ser	Asp	Pro	Ala	Ala	Leu	Lys	Cys	Arg	Ala	Asp	Glu
			100					105					110		
Asp	Gly	Asp	Ser	Phe	Val	Leu	Asn	Gly	Val	Lys	Ala	Trp	Val	Thr	Glu
		115					120					125			
Ala	Gly	Glu	Ala	Lys	Tyr	Leu	Val	Ile	Phe	Ala	Val	Thr	Asp	Pro	Asp
	130					135					140				
Asp	Pro	Arg	His	Arg	Ile	Ser	Ala	Leu	Met	Val	His	Ala	Asp	Asp	Pro
145				150					155					160	
Gly	Ile	Ser	Tyr	Gly	Ala	Pro	Glu	His	Lys	Met	Gly	Ile	Arg	Gly	Ser
			165						170					175	
Val	Thr	Arg	Glu	Val	Val	Phe	Lys	Asn	Thr	Arg	Ile	Pro	Lys	Glu	Arg
		180						185					190		
Val	Ile	Gly	Arg	Arg	Gly	His	Gly	Leu	Ser	Val	Ala	Leu	Gly	Thr	Leu
	195						200					205			
Asp	Asn	Ser	Arg	Val	Ser	Ile	Ala	Ala	Gln	Ala	Val	Gly	Ile	Ala	Gln
	210					215					220				
Gly	Ala	Leu	Asp	Ile	Ala	Thr	Asp	Tyr	Val	Gln	Lys	Arg	Lys	Gln	Phe
225					230					235				240	
Gly	Gln	Pro	Leu	Ser	Asn	Phe	Glu	Gly	Ile	Gln	Phe	Met	Leu	Ala	Asp
			245						250					255	
Met	Ala	Met	Arg	Leu	Glu	Ala	Ala	Arg	Ala	Leu	Thr	Tyr	Ser	Ala	Ala
		260						265					270		
Asp	Arg	Ser	Gly	Arg	Gln	Thr	Asp	Asp	Val	Ser	Tyr	Phe	Gly	Ala	Ala
	275						280					285			
Ala	Lys	Cys	Phe	Ala	Ser	Asp	Thr	Ala	Met	Ala	Val	Cys			
	290					295					300				

<210> 47
 <211> 379
 <212> DNA
 <213> Homo sapiens

<400> 47

aagcttgtag agctagtccg aagcggactg tcggtacgcc aagctgctaa aagatgtggg
 60
 atgcacctta ccgctgcgta tgccgtagct acggaagctg ggtgccatat ccggttaagt
 120

cagtatgctc ggaaagtccg ccagacgcag ttaagagtgg aatacctgcg ccttcggctg
 180
 gcgagcctgc ctggtggtga tgctggcgcg gcagtaggaa ttgatcgctg actgcgttta
 240
 gatttcgaaa aaggactcac caaatcccag ggctgcagag aagagttcat acccgtcggc
 300
 gaagacgcca gcacgtataa cagacttatg aaagcgctgc gccaacgcca tgatgtcatc
 360
 aaatccggaa agcttgccc
 379

<210> 48
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 48
 Met His Leu Thr Ala Ala Tyr Ala Val Ala Thr Glu Ala Gly Cys His
 1 5 10 15
 Ile Arg Leu Ser Gln Tyr Ala Arg Lys Val Arg Gln Thr Gln Leu Arg
 20 25 30
 Val Glu Tyr Leu Arg Leu Arg Leu Ala Ser Leu Pro Gly Gly Asp Ala
 35 40 45
 Gly Ala Ala Val Gly Ile Asp Arg Arg Leu Arg Leu Asp Phe Glu Lys
 50 55 60
 Gly Leu Thr Lys Ser Gln Gly Arg Arg Glu Glu Phe Ile Pro Val Gly
 65 70 75 80
 Glu Asp Ala Ser Thr Tyr Asn Arg Leu Met Lys Ala Leu Arg Gln Arg
 85 90 95
 His Asp Val Ile Lys Ser Gly Lys Leu Ala
 100 105

<210> 49
 <211> 309
 <212> DNA
 <213> Homo sapiens

<400> 49
 tgatcatgat gctggcatgg actattctgg tccctgttcc tctctcacct gctgaaggac
 60
 atccctctaa tttttgtgtc tccttctgta tcatcaaatt ttccctctct actgagtctc
 120
 ttgcatctcc ttggaagcat gctgtactat gtcccatcct taaagaactc cccttgtctg
 180
 cacattaccc tctgccagct ggctcatttt tctgctcccc ttacagggga aactcttcaa
 240
 aaagttatct ccacctcctt ccattctcatg ttctcttgaa cctgcagtac tgggtgctcc
 300
 ctcccttttg
 309

<210> 50
 <211> 101
 <212> PRT

<213> Homo sapiens

<400> 50

Met	Met	Leu	Ala	Trp	Thr	Ile	Leu	Val	Pro	Val	Pro	Leu	Ser	Pro	Ala
1				5					10					15	
Glu	Gly	His	Pro	Ser	Asn	Phe	Cys	Val	Ser	Phe	Cys	Ile	Ile	Lys	Phe
			20					25					30		
Ser	Leu	Ser	Thr	Glu	Ser	Leu	Ala	Ser	Pro	Trp	Lys	His	Ala	Val	Leu
		35					40					45			
Cys	Pro	Ile	Leu	Lys	Glu	Leu	Pro	Leu	Ser	Ala	His	Tyr	Pro	Leu	Pro
	50					55					60				
Ala	Gly	Ser	Phe	Phe	Cys	Ser	Pro	Leu	Gln	Gly	Asn	Ser	Ser	Lys	Ser
65					70				75					80	
Tyr	Leu	His	Leu	Leu	Pro	Ser	His	Val	Leu	Leu	Asn	Leu	Gln	Tyr	Trp
			85					90					95		
Val	Leu	Pro	Pro	Phe											
			100												

<210> 51

<211> 512

<212> DNA

<213> Homo sapiens

<400> 51

agatccttga agaattgcca cactgtcttc ctccctgctt ataatttcct tattccctag
60
gatgtgatcc ttgttcttgg ggctcacat ggcagctgga tctctggcga ttgcatctga
120
gttccagaca ccaggatgga aaagaaaaga aggaggggca agaggaaccc ccagatgctc
180
cttaagagct actgctgggc attcccactt gcatctcatt tgctcgatcg ctgtcactgt
240
gccctaacga gctgcaagga cactggggaa atgagtctgt cttgtacttc atgtgccctt
300
caaatcttc tggtgctgag ggagaagagg ccagccggta ttgaggaaca actagcactt
360
tctgcttccg cgtcccaggg ggacgtgggt gtgttgaatc cacaccgggg gtgcggacct
420
ctgaggctgg gctggatggg acatcaggtg ggccctctgt ttcatttatg tgacctcca
480
tcaggtcttc tggttggatc ctgctttcta ga
512

<210> 52

<211> 125

<212> PRT

<213> Homo sapiens

<400> 52

Met	Glu	Lys	Lys	Arg	Arg	Arg	Gly	Lys	Arg	Asn	Pro	Gln	Met	Leu	Leu
1				5					10					15	
Lys	Ser	Tyr	Cys	Val	Ala	Phe	Pro	Leu	Ala	Ser	His	Leu	Leu	Asp	Arg
			20					25				30			
Cys	His	Cys	Ala	Leu	Thr	Ser	Cys	Lys	Asp	Thr	Gly	Glu	Met	Ser	Leu

```

          35          40          45
Ser Cys Thr Ser Cys Ala Pro Gln Asn Leu Leu Leu Leu Arg Glu Lys
          50          55          60
Arg Pro Ala Gly Ile Glu Glu Gln Leu Ala Leu Ser Ala Ser Ala Ser
65          70          75          80
Gln Gly Asp Val Gly Val Leu Asn Pro His Arg Gly Cys Gly Pro Leu
          85          90          95
Arg Leu Gly Trp Met Gly His Gln Val Gly Pro Leu Phe His Leu Cys
          100          105          110
Asp Leu Pro Ser Gly Leu Leu Val Gly Ser Cys Phe Leu
          115          120          125

```

<210> 53
 <211> 474
 <212> DNA
 <213> Homo sapiens

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<400> 53
accggtacac ctacgtcacc cgtaaaaacc gacgcaatac ccg gatcgcc tcgtcctcaa
60
aaaattcgat cccgtcgtgc gtcgtcacat tgagttcaag gagggccgct aatggccaaa
120
aagtccaaga ttgtcgccca gaagaaacgt gagaagctcg tagcccaata cgccgaaagg
180
cgcgccgaac tcaaggccat catgaagtgc ccaactgcct cattggacga acgcatggag
240
gcacgcgta agctgtctcg cctgccgcgc gattcatccc ccgtgcgggtt acgtaaccgt
300
gaccaagtcg acgggcgctcc ccgcggctac gttggcaagg ccggtgtgtc ccgtatccgt
360
ttccgtgaga tggcccaccg cggcgaactc cccggaatcg cgaagtcaag ctggtgaagc
420
catggcagta ccgaagcgaa agaagtcccg ttcgaccacg cgtcataggc gggc
474

```

<210> 54
 <211> 101
 <212> PRT
 <213> Homo sapiens

```

<400> 54
Met Ala Lys Lys Ser Lys Ile Val Ala Gln Lys Lys Arg Glu Lys Leu
1          5          10          15
Val Ala Gln Tyr Ala Glu Arg Arg Ala Glu Leu Lys Ala Ile Met Lys
          20          25          30
Cys Pro Thr Ala Ser Leu Asp Glu Arg Met Glu Ala Ser Arg Lys Leu
          35          40          45
Ser Arg Leu Pro Arg Asp Ser Ser Pro Val Arg Leu Arg Asn Arg Asp
          50          55          60
Gln Val Asp Gly Arg Pro Arg Gly Tyr Val Gly Lys Ala Gly Val Ser
65          70          75          80
Arg Ile Arg Phe Arg Glu Met Ala His Arg Gly Glu Leu Pro Gly Ile
          85          90          95
Ala Lys Ser Ser Trp

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100

<210> 55
<211> 378
<212> DNA
<213> Homo sapiens

<400> 55
ccatggccca ggacagccgg catatcggct acgactacgg tacaccggtg gcgccacagt
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tcggcgcagc caagcccgcg gcgtgctgcc aggcgcaagc gacaaacacc ggcccgtggg
120
tggtgttcga ccatgtgcgt tgcacccacg acacctttct gatcgacgtc tttctcaacc
180
agcccgatgc caccgcgcag caggtcaatg ccgacaaccc gcactacgtc gggcgtttca
240
gccgcatcgg catgggcctg gtggatgaca agggccggtg cattaccagc ggcgtatcgc
300
gcgcgttgaa tgcggcgcgc agcaccaagg cgctgaacct gggaccgagt gacgcggcgc
360
agttatcggg gaggcgta
378

<210> 56
<211> 125
<212> PRT
<213> Homo sapiens

<400> 56
Met Ala Gln Asp Ser Arg His Ile Gly Tyr Asp Tyr Gly Thr Pro Val
1 5 10 15
Ala Pro Gln Phe Gly Ala Ala Lys Pro Ala Ala Cys Cys Gln Ala Gln
20 25 30
Ala Thr Asn Thr Gly Pro Trp Val Val Phe Asp His Val Arg Cys Thr
35 40 45
His Asp Thr Phe Leu Ile Asp Val Phe Leu Asn Gln Pro Asp Ala Thr
50 55 60
Ala Gln Gln Val Asn Ala Asp Asn Pro His Tyr Val Gly Arg Phe Ser
65 70 75 80
Arg Ile Gly Met Gly Leu Val Asp Asp Lys Gly Arg Cys Ile Thr Gln
85 90 95
Gly Val Ser Arg Ala Leu Asn Ala Ala Arg Ser Thr Lys Ala Leu Asn
100 105 110
Leu Gly Pro Ser Asp Ala Ala Gln Leu Ser Val Arg Arg
115 120 125

<210> 57
<211> 388
<212> DNA
<213> Homo sapiens

<400> 57
agaccacccc gacacagatc aggagtcgtc atgtccagaa agaagaaggt cggcatcctc
60

accgcaggcg gtgattgccc cgggctcaac gccgctatcc gcggatttgg caaggctgcc
 120
 atccgccagc acgacatgga gctcatcggt attcaggacg gctttcttgg attggcggga
 180
 aaccgcacca tctcccttgg cccgcgtgcc ctctcaggca tcttgacggt cggcgggacc
 240
 atcctgggaa ctagccgtga caaggtcaat cacatgatta tcgacggcga ggaacgggat
 300
 atggtcccca ccaccgtcga gaattacgag aagctggggc ttgacgcttt ggtgactttg
 360
 ggtggcgggtg gcaccgccaa gaacgcgt
 388

<210> 58
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 58
 Arg Pro Thr Arg His Arg Ser Gly Val Val Met Ser Arg Lys Lys Lys
 1 5 10 15
 Val Gly Ile Leu Thr Ala Gly Gly Asp Cys Pro Gly Leu Asn Ala Ala
 20 25 30
 Ile Arg Gly Phe Gly Lys Ala Ala Ile Arg Gln His Asp Met Glu Leu
 35 40 45
 Ile Gly Ile Gln Asp Gly Phe Leu Gly Leu Ala Gly Asn Arg Thr Ile
 50 55 60
 Ser Leu Gly Pro Arg Ala Leu Ser Gly Ile Leu Thr Val Gly Gly Thr
 65 70 75 80
 Ile Leu Gly Thr Ser Arg Asp Lys Val Asn His Met Ile Ile Asp Gly
 85 90 95
 Glu Glu Arg Asp Met Val Pro Thr Thr Val Glu Asn Tyr Glu Lys Leu
 100 105 110
 Gly Leu Asp Ala Leu Val Thr Leu Gly Gly Gly Gly Thr Ala Lys Asn
 115 120 125
 Ala

<210> 59
 <211> 417
 <212> DNA
 <213> Homo sapiens

<400> 59
 ggtaccatcg gagctcgaca agaaatgggtt ggggtgaagtc gtggcttctg ctccacccag
 60
 tgccctcatg ggtcagccca cctgaatatc ttcatgcctg tgcatttctc ctgatgttca
 120
 cgtgtgccct gtgtttttac gcatctgtga tcgtgcaccc acgcgtctca gagaggagcc
 180
 cgtttgggaa tccggagaat gtgcgctggc ggaagagcgt cacacactgg aagcaaacct
 240
 cagaccgcgt ggacaagacc aaggatgaaa tggaacacga ggccttggtg gaagggaacc
 300

tggcaaccga ggcaagccta gtggttctgg acacactgga gatcatcgtg cagacgggtga
360

tgctttcaga agcccgggag agcgtcttgg gggcagtgct gaaggttgtg ctgtaca
417

<210> 60
<211> 101
<212> PRT
<213> Homo sapiens

<400> 60
Met Phe Thr Cys Ala Leu Cys Phe Tyr Ala Ser Val Ile Val His Pro
1 5 10 15
Arg Val Ser Glu Arg Ser Pro Phe Gly Asn Pro Glu Asn Val Arg Trp
20 25 30
Arg Lys Ser Val Thr His Trp Lys Gln Thr Ser Asp Arg Val Asp Lys
35 40 45
Thr Lys Asp Glu Met Glu His Glu Ala Leu Val Glu Gly Asn Leu Ala
50 55 60
Thr Glu Ala Ser Leu Val Val Leu Asp Thr Leu Glu Ile Ile Val Gln
65 70 75 80
Thr Val Met Leu Ser Glu Ala Arg Glu Ser Val Leu Gly Ala Val Leu
85 90 95
Lys Val Val Leu Tyr
100

<210> 61
<211> 304
<212> DNA
<213> Homo sapiens

<400> 61
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gcacacatat ttgcaggctt ggagagagtg tgtgggggca tgtactttcg gtgggtcaag
120
tatgaagaag caggccttat aaacacatat tctgacctta acctgtactt cagaagagga
180
ccgctgactc accaaggagg cctgaaggac aaggcagcat ctctgtcttc acatgagtcc
240
tcccctagac cgggcccattg gccaggcctg accacagagc tcccattgcc tttcctgcac
300
gcgt
304

<210> 62
<211> 92
<212> PRT
<213> Homo sapiens

<400> 62
Met Gly Ala Leu Gln Phe Trp Arg Ser Leu Ser Ala His Ile Phe Ala
1 5 10 15

Gly Leu Glu Arg Val Cys Gly Gly Met Tyr Phe Arg Trp Val Lys Tyr
 20 25 30
 Glu Glu Ala Gly Leu Ile Asn Thr Tyr Ser Asp Leu Asn Leu Tyr Phe
 35 40 45
 Arg Arg Gly Pro Leu Thr His Gln Gly Gly Leu Lys Asp Lys Ala Ala
 50 55 60
 Ser Leu Ser Ser His Glu Ser Ser Pro Arg Pro Gly Pro Trp Pro Gly
 65 70 75 80
 Leu Thr Thr Glu Leu Pro Leu Pro Phe Leu His Ala
 85 90

<210> 63
 <211> 577
 <212> DNA
 <213> Homo sapiens

<400> 63
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 ctgacggtgc tagctgggtg gctcacccta gccgggcgta tcagtgtcgg ggaactcgtc
 120
 accgtggtcg ggctggcca aaccctcggc cctccgctgc gagcactggg cgtcgacacc
 180
 gcgacgatgt tggccaccgc ccacgcctcc ggggaccgat tctgtgagtt gcgtgatagc
 240
 ccggcagcct ggcagatcca ccccgacgac ggtgcccgc caacaccggg tgatggcccg
 300
 gtggagttgc acatcccggg cagggatttc cagcttgacg tcgccggcgg caccatgtg
 360
 ggtatcatgg cgcctcaatc ggtctgtgac gccttggccg aggcgataga ccacggctcc
 420
 gagaccgtct tgaatggggg tcccgcagc cgcctcaacc ctgcccacg gcgtcgtctg
 480
 gtgctgggtg ctccccgctc ccccgaaactg ttcgacgata ctgcccgtgc gaacatcgtg
 540
 cttgacagcc agacgactgt cgccaggctg aatgcat
 577

<210> 64
 <211> 192
 <212> PRT
 <213> Homo sapiens

<400> 64
 Arg Val Lys Gly Val Tyr Thr Gly Thr Ile Asn Ala Ser Val Gly Val
 1 5 10 15
 Phe Ile Thr Ala Leu Thr Val Leu Ala Gly Trp Leu Thr Leu Ala Gly
 20 25 30
 Arg Ile Ser Val Gly Glu Leu Val Thr Val Val Gly Leu Ala Gln Thr
 35 40 45
 Leu Gly Pro Pro Leu Arg Ala Leu Gly Val Asp Thr Ala Thr Met Leu
 50 55 60
 Ala Thr Ala His Ala Ser Gly Asp Arg Phe Cys Glu Leu Arg Asp Ser
 65 70 75 80

Pro Ala Ala Trp Gln Ile His Pro Asp Asp Gly Ala Arg Thr Thr Pro
 85 90 95
 Gly Asp Gly Pro Val Glu Leu His Ile Pro Val Arg Asp Phe Gln Leu
 100 105 110
 Asp Val Ala Gly Gly Thr His Val Gly Ile Met Ala Pro Gln Ser Val
 115 120 125
 Cys Asp Ala Leu Ala Glu Ala Ile Asp His Gly Ser Glu Thr Val Leu
 130 135 140
 Asn Gly Val Pro Ala Ser Arg Leu Asn Pro Ala Gln Arg Arg Arg Leu
 145 150 155 160
 Val Leu Val Ala Pro Arg Ser Pro Glu Leu Phe Asp Asp Thr Ala Arg
 165 170 175
 Ala Asn Ile Val Leu Asp Ser Gln Thr Thr Val Ala Arg Leu Asn Ala
 180 185 190

<210> 65
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 65
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 60
 aagaaggccg ctttcaagat caccgcgcgc gggcaactag tgggcacccat ggcctccgag
 120
 cgccttggcg tacccttcgg catcatcgac ctttcgcttg ccctactgc cgaattggga
 180
 gattcggggg cccacatcct tgagcatatg ggattggacc aagtaggcac gcacggcaca
 240
 actgctgctt tggctctgct taacgacgcc gtaaagaaag gcggcatgat ggcctgcccc
 300
 cgcgtcggcg gtttgtctgg ctcttccatc ccgggctcc
 339

<210> 66
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 66
 Val Asp Arg Ala Leu Gly Ser Leu Glu Gly Ala Ser Leu Asp Gln Val
 1 5 10 15
 Ala Glu Glu Val Lys Lys Ala Ala Phe Lys Ile Thr Arg Ala Gly Gln
 20 25 30
 Leu Val Gly Thr Met Ala Ser Glu Arg Leu Gly Val Pro Phe Gly Ile
 35 40 45
 Ile Asp Leu Ser Leu Ala Pro Thr Ala Glu Leu Gly Asp Ser Gly Ala
 50 55 60
 His Ile Leu Glu His Met Gly Leu Asp Gln Val Gly Thr His Gly Thr
 65 70 75 80
 Thr Ala Ala Leu Ala Leu Leu Asn Asp Ala Val Lys Lys Gly Gly Met
 85 90 95
 Met Ala Cys Pro Arg Val Gly Gly Leu Ser Gly Ser Phe Ile Pro Gly
 100 105 110

Ser

<210> 67

<211> 446

<212> DNA

<213> Homo sapiens

<400> 67

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 60
 cgcacaggca cgggtcaggg gcgttcgcgg cgccagctgg cacaacttcg cgaccggtga
 120
 caaggggtcc ttcgacgcca acgagcttgc cgtaactcct gatactgaca ccgtcatcca
 180
 gggagtcggg cccgccctag ccctcctcga ttcagcgtgg ggacgccaga tccacgtgga
 240
 gacaacaggg tgtcccagtg ccgtgggtctg gaatccacgc tcctcgtcga cacatgccga
 300
 taacccgaca gcccaggcat ggcgcgattt cgtatgcgtc gagaccgggg cctgcaagga
 360
 caatgcggtc attgttgccc cacacagcga cctcaccatg tccacacgga ttagcgtcga
 420
 aacgttgtga tcgctgcatg gatatt
 446

<210> 68

<211> 133

<212> PRT

<213> Homo sapiens

<400> 68

Met	Trp	His	Thr	Tyr	Leu	Arg	Val	Ala	Asp	Ala	Ala	Gln	Ala	Arg	Val
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Arg	Gly	Val	Arg	Gly	Ala	Ser	Trp	His	Asn	Phe	Ala	Thr	Gly	Asp	Lys
			20					25					30		
Gly	Ser	Phe	Asp	Ala	Asn	Glu	Leu	Ala	Val	Thr	Pro	Asp	Thr	Asp	Thr
		35					40					45			
Val	Ile	Gln	Gly	Val	Gly	Pro	Ala	Leu	Ala	Leu	Leu	Asp	Ser	Ala	Trp
	50					55					60				
Gly	Arg	Gln	Ile	His	Val	Glu	Thr	Thr	Gly	Cys	Pro	Ser	Ala	Val	Val
65					70					75				80	
Trp	Asn	Pro	Arg	Ser	Ser	Ser	Thr	His	Ala	Asp	Asn	Pro	Thr	Ala	Gln
			85						90					95	
Ala	Trp	Arg	Asp	Phe	Val	Cys	Val	Glu	Thr	Gly	Ala	Cys	Lys	Asp	Asn
			100					105					110		
Ala	Val	Ile	Val	Ala	Pro	His	Ser	Asp	Leu	Thr	Met	Ser	Thr	Arg	Ile
		115					120					125			
Ser	Val	Glu	Thr	Leu											

<210> 69

<211> 552

<212> DNA

<213> Homo sapiens

<400> 69

nnaagggtaa ggagaaaagc aaggaccttg caaagagagc ctctgtgccg gagaggctgg
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ccctcaagga ggagccaaaa gaagacccca gtggagcagc tgtgcccag atgccaaaaa
120
agtcctccaa gattgccagc ttcattccca aaggggggaa gctcaacagt gccagaagg
180
agcnccatgg ccccttcctt cagtggata ccaaaaccag gaatgaaaag catgcccggg
240
aaatcccaaa gtgcccagc gccttccaag gaaggggagc ggagccggag tgggaagctg
300
agctcaggac tccccagca gaagccccag ctggacggca gacactccag ttcctcttcc
360
agcctggcgt cctcagaagg aaaaggccca ggagggacca ccctgaacca cagcatcagc
420
agccagactg tcagtgggtc tgtcgggacc acccagacca caggaagcaa tnnaccgtca
480
gtgttcagct acctcagccc cagcagcaat acaaccatcc caacactgcc acggttgac
540
ctttcctgta ca
552

<210> 70

<211> 184

<212> PRT

<213> Homo sapiens

<400> 70

Xaa	Arg	Val	Arg	Arg	Lys	Ala	Arg	Thr	Leu	Gln	Arg	Glu	Pro	Leu	Cys
1				5					10					15	
Arg	Arg	Gly	Trp	Pro	Ser	Arg	Arg	Ser	Gln	Lys	Lys	Thr	Pro	Val	Glu
			20					25					30		
Gln	Leu	Cys	Pro	Arg	Cys	Gln	Lys	Ser	Pro	Pro	Arg	Leu	Pro	Ala	Ser
		35					40					45			
Ser	Pro	Lys	Gly	Gly	Ser	Ser	Thr	Val	Pro	Arg	Arg	Ser	Xaa	Met	Ala
	50					55					60				
Pro	Ser	Leu	Ser	Gly	Ile	Pro	Lys	Pro	Gly	Met	Lys	Ser	Met	Pro	Gly
65					70				75					80	
Lys	Ser	Pro	Ser	Ala	Pro	Ala	Pro	Ser	Lys	Glu	Gly	Glu	Arg	Ser	Arg
				85					90					95	
Ser	Gly	Lys	Leu	Ser	Ser	Gly	Leu	Pro	Gln	Gln	Lys	Pro	Gln	Leu	Asp
			100					105					110		
Gly	Arg	His	Ser	Ser	Ser	Ser	Ser	Ser	Leu	Ala	Ser	Ser	Glu	Gly	Lys
		115						120					125		
Gly	Pro	Gly	Gly	Thr	Thr	Leu	Asn	His	Ser	Ile	Ser	Ser	Gln	Thr	Val
	130					135						140			
Ser	Gly	Ser	Val	Gly	Thr	Thr	Gln	Thr	Thr	Gly	Ser	Asn	Xaa	Pro	Ser
145					150					155				160	
Val	Phe	Ser	Tyr	Leu	Ser	Pro	Ser	Ser	Asn	Thr	Thr	Ile	Pro	Thr	Leu
				165					170					175	
Pro	Arg	Leu	His	Leu	Ser	Cys	Thr								
				180											

<210> 71
 <211> 316
 <212> DNA
 <213> Homo sapiens

<400> 71
 cgcgttgaaa tggcgttcga acttaaactg ttacatattg actccgtgcc attaaacatt
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 ttgaatcctg ttaaagggac tccatttgaa agcaacgaag ctttacgtcc tttaaataac
 120
 ttacgtacct tcgccgtatt ccgtttcatc ttgccaaacg cattgatacg aactgcaggt
 180
 ggccgcgaag taaatctacg agacttacaa gcttatgctc taaaagggtg cctaaacggt
 240
 atcatgggtg gtggctactt aactactggc ggtcgttcac ctcaagacga tctccaaatg
 300
 attcaagact tggagt
 316

<210> 72
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 72
 Arg Val Glu Met Ala Phe Glu Leu Lys Arg Leu His Ile Asp Ser Val
 1 5 10 15
 Pro Leu Asn Ile Leu Asn Pro Val Lys Gly Thr Pro Phe Glu Ser Asn
 20 25 30
 Glu Ala Leu Arg Pro Leu Asn Ile Leu Arg Thr Phe Ala Val Phe Arg
 35 40 45
 Phe Ile Leu Pro Asn Ala Leu Ile Arg Thr Ala Gly Gly Arg Glu Val
 50 55 60
 Asn Leu Arg Asp Leu Gln Ala Tyr Ala Leu Lys Gly Gly Leu Asn Gly
 65 70 75 80
 Ile Met Val Gly Gly Tyr Leu Thr Thr Gly Gly Arg Ser Pro Gln Asp
 85 90 95
 Asp Leu Gln Met Ile Gln Asp Leu Glu
 100 105

<210> 73
 <211> 384
 <212> DNA
 <213> Homo sapiens

<400> 73
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 gcttggtatg tcgaccgagc cgaggagctc gagggcgctc acggtgcccc gtttgtgccg
 120
 ccacgagtga ccgtcgtcac cccgccgtgg aacttcgccc tgtctattac cgccggatcc
 180

acccttgccg ctctggccgc cggatcgtca gtactactca agcccgtcc acaggcccgc
 240
 cactgtgctg ccgtcatctc tgaatgcctg tgggaggctg ggatcccgcg ggacgttctg
 300
 cagctcgtcg atgttgagga aaatgaggct ggtaaaccac tggtagacca ccccgaggtc
 360
 gatcgggtca tcctcacggg aggt
 384

<210> 74
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 74
 Xaa Thr Gly Lys Ile Leu Ala Glu Gly Asp Val Glu Val Ser Glu Ala
 1 5 10 15
 Ile Asp Phe Ala Ala Trp Tyr Val Asp Arg Ala Glu Glu Leu Glu Gly
 20 25 30
 Val Asp Gly Ala Gln Phe Val Pro Pro Arg Val Thr Val Val Thr Pro
 35 40 45
 Pro Trp Asn Phe Ala Leu Ser Ile Thr Ala Gly Ser Thr Leu Ala Ala
 50 55 60
 Leu Ala Ala Gly Ser Ser Val Leu Leu Lys Pro Ala Pro Gln Ala Arg
 65 70 75 80
 His Cys Ala Ala Val Ile Ser Glu Cys Leu Trp Glu Ala Gly Ile Pro
 85 90 95
 Arg Asp Val Leu Gln Leu Val Asp Val Glu Glu Asn Glu Ala Gly Lys
 100 105 110
 His Leu Val Ser His Pro Glu Val Asp Arg Val Ile Leu Thr Gly Gly
 115 120 125

<210> 75
 <211> 405
 <212> DNA
 <213> Homo sapiens

<400> 75
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 60
 cgcattgagg cgctggccga gctctatgcc gatcccaaga ccagggtggt gagcttctgg
 120
 accatgggct tcaaccagca caccgcgggc gtctggtgca acaatctcgt ctacaacatc
 180
 cacctgctga ccggaaaaat ctgcagcccc ggcaacagcc cgttctcgct gaccgggagc
 240
 ccatcggcct gcggcacggc gcgcgaggtc ggtaccttct cgcacgcct gcccgccgac
 300
 atggtggtca ccagcaaggc gcaccgcgac atcgccgaga agatctggca gctgccggaa
 360
 ggaccagtcc ccgacaagcc cggctaccac gccgtgctgc agagc
 405

<210> 76

<211> 135
 <212> PRT
 <213> Homo sapiens

<400> 76
 Glu Phe Val Ser Glu Tyr Thr Leu Glu Asn Ser Ala Glu Met Ser Gly
 1 5 10 15
 Val Arg Ser Xaa Arg Ile Glu Ala Leu Ala Glu Leu Tyr Ala Asp Pro
 20 25 30
 Lys Thr Arg Val Val Ser Phe Trp Thr Met Gly Phe Asn Gln His Thr
 35 40 45
 Arg Gly Val Trp Cys Asn Asn Leu Val Tyr Asn Ile His Leu Leu Thr
 50 55 60
 Gly Lys Ile Ser Thr Pro Gly Asn Ser Pro Phe Ser Leu Thr Gly Gln
 65 70 75 80
 Pro Ser Ala Cys Gly Thr Ala Arg Glu Val Gly Thr Phe Ser His Arg
 85 90 95
 Leu Pro Ala Asp Met Val Val Thr Ser Lys Ala His Arg Asp Ile Ala
 100 105 110
 Glu Lys Ile Trp Gln Leu Pro Glu Gly Pro Val Pro Asp Lys Pro Gly
 115 120 125
 Tyr His Ala Val Leu Gln Ser
 130 135

<210> 77
 <211> 5816
 <212> DNA
 <213> Homo sapiens

<400> 77
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 cggcgtgcgc gccgcgcagc ctcaggcccc gggttacttg attgcagctc cctctgtttt
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 180
 ggtccaggct cagctggtgg cccagggtga gccggtggtg cagagccagg gagccatcct
 240
 ggataaaggg acaatcaaac tcaaggtgcc cacgggcctc cggggccaag cgcttctgaa
 300
 agtgtggggc cgcggctggc aggcggagga ggggcccctc tttcacaacc agacctcgtt
 360
 gaccgtggac ggccggggcg cttctgtatt catccagacg gacaagcctg tgtacagacc
 420
 ccagcaccga gtgctcataa gcatcttcac cgtctctcca aatctgaggc ctgtcaacga
 480
 gaagctggaa gcctacatcc tggacccccg aggctctcgg atgatagagt ggagacactt
 540
 aaagccgttc tgctgcggca tcaccaacat gagcttcccc ttgtccgacc agcctgtgtt
 600
 gggagaatgg ttcatttttg ttgaaatgca aggccacgcg tacaacaagt cttttgaagt
 660
 tcagaagtat gtgttgccca agtttgagct tctgattgac ccgccccggt atatccaaga
 720

cctggacgcc tgtgagacag gcactgtgcg ggccaggtat acctttggga aacctgtggc
780
tggtgcctta atgatcaaca tgactgttaa tgggtgtaggg tactacagcc acgaggtggg
840
acgccctgtc ctcagaacaa ccaagatcct cggtccccgg gacttcgaca tctgcgtgag
900
ggacatgac ccagcggacg tccctgagca cttccggggc agggtcagca tctgggcat
960
ggtgaccagt gtggacggga gccagcaggt cgcgttcgat gactccaccc ccgtgcagag
1020
gcagctggtg gacatccggt actccaagga cacgaggaag cagttcaagc cgggcctggc
1080
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1140
ccagattaag gcagagctga caccaaagga taacatctac accagtgaag ttgtgtccca
1200
gcgtggacta gtggggtttg aaatccccct catccccacg tcagcccagc acgtgtggct
1260
ggagaccaag gtgatggcac tgaacgggaa gcccgtaggg gctcagtacc tgcccagcta
1320
cctctcccc ggcagctggt actccccag ccagtgtac ctgcagctgc agccaccctc
1380
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1440
ctttaccctg tactacgagg tggctgcacg gggcaatatt gtgctatcgg gccagcagcc
1500
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1560
tttaacacac ctttctgaga cagagcccc accagcccca gaagctgagg tcgacgtgtg
1620
tgtgacctct cttcatctgg ccgtgacccc cagcatggtc ccccttggtc gcctgctggt
1680
cttctacgtc agggagaatg gagaaggggt cgccgacagc cttcagtttg cagtcgagac
1740
cttcttcgaa aaccaggttt cagtgcgta ttcagcaaag gagacccaac ctggggagggt
1800
tgtcgacctg cggatcaggg ctgcaagggg cagctgtgtg tgcgtcgccg cagttgataa
1860
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1980
ggctgggctg acggcacaac gacgccggcg ctcctctgtc ttcccgtggc cttggggcat
2040
caccaaggac tctggggttg ctttcaccga aacgggactg gtggtgatga ccgaccgagt
2100
gagcctgaac caccggcagg acggtggcct ctacaccgat gaggtgtcc ccgctttcca
2160
gccccacaca gggagcctgg tggcagtggc tccttccagg cccccccca gaacagagaa
2220
gagaaaaagg actttcttcc ccgaaacatg gatttggtcat tgtctcaaca tcagtgaccc
2280
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2340

ggccgtggcc ctgtccacct ctcagggctt aggcacgcc gagccctccc tgctgaagac
2400
cttcaagccc ttcttcgtgg acttcatgct ccccgctctc atcatccgtg gggagcaggt
2460
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 <211> 799
 <212> PRT
 <213> Homo sapiens

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 50 55 60
 His Phe Ala Pro Asn Val Phe Val Leu Lys Tyr Leu Gln Lys Thr Gln
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 Gly Tyr Gln Arg Gln Leu Thr Tyr Lys Arg Gln Asp Gly Ser Tyr Ser
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 Arg Glu Leu Ala Ala Ala Lys Ser Trp Ile Ile Gln Gln Gln Gln Ala
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 Asp Gly Ser Phe Leu Ala Val Gly Arg Val Leu Asn Lys Asp Ile Gln
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 Gly Gly Ile His Gly Ile Val Pro Leu Thr Ala Tyr Val Val Val Ala
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 195 200 205
 Lys Ala Arg His Phe Leu Glu Ser Ala Ala Pro Leu Ala Met Asp Pro
 210 215 220
 Tyr Ser Cys Ala Leu Thr Thr Tyr Ala Leu Thr Leu Leu Arg Ser Pro
 225 230 235 240
 Ala Ala Pro Glu Ala Leu Arg Lys Leu Arg Ser Leu Ala Ile Met Arg
 245 250 255
 Asp Gly Val Thr His Trp Ser Leu Ser Asn Ser Trp Asp Val Asp Lys
 260 265 270
 Gly Thr Phe Leu Ser Phe Ser Asp Arg Val Ser Gln Ser Val Val Ser
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 Gly Asp Val Ala Ala Ala Leu Pro Val Val Lys Trp Leu Ser Gln Gln

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Cys	Leu	Met	Gln	Ile	Asp	Val	Thr	Tyr	Asn	Val	Pro	Asp	Pro	Val	Ala
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Lys	Pro	Ala	Phe	Gln	Leu	Leu	Val	Ser	Leu	Gln	Glu	Pro	Glu	Ala	Gln
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Glu	Asp	Arg	Val	Thr	Ala	Gly	Pro	Arg	Pro	Pro	Val	Ser	Ser	Gly	Asn
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 <211> 346
 <212> DNA
 <213> Homo sapiens

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<210> 80
 <211> 101
 <212> PRT
 <213> Homo sapiens

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 Asp Val Gly Leu Ser Glu Gly Ala Val Lys Tyr Phe Gln Ser Arg Thr
 35 40 45
 Asn Asp Phe Met Ala Leu Ser Ile Asp Ala Val Ala Ser Ala Asp Ala
 50 55 60
 Tyr Ser Val Gly Phe Pro Gly Phe Gly Gly Met Asn Leu Ala Pro Ile
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 Ser Glu Glu Ala Ala Ala Glu Met Glu Glu Pro Tyr Ile Tyr His Phe
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 Pro Asp Gly Asn Ala
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<210> 81
 <211> 429
 <212> DNA
 <213> Homo sapiens

<400> 81

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<210> 82
 <211> 79
 <212> PRT
 <213> Homo sapiens

<400> 82
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 20 25 30
 Met Cys Pro Cys Ala Cys Leu Cys Cys Val Cys Ala Cys Met Cys Ala
 35 40 45
 Cys Leu Cys Val Xaa Val Cys Val Arg Ala Cys Val Cys Thr Cys Val
 50 55 60
 His Val His Val Cys Ala Pro Val Cys Met Ser Val Cys Thr Arg
 65 70 75

<210> 83
 <211> 411
 <212> DNA
 <213> Homo sapiens

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<210> 84
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 84
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 20 25 30
 Asn Asp Leu Ile Gly Leu Gly Ile Asp Lys Ala Lys Ile Glu Ile Ile
 35 40 45
 His Asn Gly Ile Asp His Arg Pro Phe Phe Pro Gln Leu Gln Ile Asp
 50 55 60
 Ala Glu Thr Val Thr Ile Lys Pro Phe Ala Ile Lys Arg Pro Tyr Phe
 65 70 75 80
 Ile Tyr Gly Ser Arg Leu Ser Gly Pro Glu Lys Lys His Ile Glu Leu
 85 90 95
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<210> 85
 <211> 333
 <212> DNA
 <213> Homo sapiens

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<210> 86
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 86
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 Phe Lys Val Ile Ala Thr Ser Gly Thr Gln Arg Phe Leu Val Glu Asn

ATTORNEY DOCKET NO.: 15966-543

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65				70				75						80	
Thr	Glu	Gly	Pro	Gln	Ala	Leu	Ala	Asp	Ser	Arg	Ser	Leu	Arg	Arg	Ala
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 <211> 355
 <212> DNA
 <213> Homo sapiens

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<210> 88
 <211> 96
 <212> PRT
 <213> Homo sapiens

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Cys	Pro	Val	Val	Leu	Leu	Ser	Asp	Val	His	Ser	Val	Gly	Val	Gln	Gly
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Asp	Gly	Arg	Thr	Tyr	Gly	Ser	Pro	Ile	Val	Leu	Arg	Pro	Val	Thr	Ser
		35				40				45					
Glu	Asp	Ala	Met	Thr	Ala	Asp	Trp	Ala	Arg	Ile	Pro	Tyr	Asp	Val	Leu
	50				55					60					
Glu	Lys	Ile	Ser	Thr	Arg	Ile	Thr	Asn	Ala	Cys	Pro	Gln	Ile	Asn	Arg
65				70				75					80		
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<210> 89
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 89

ATTORNEY DOCKET NO.: 15966-543

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<210> 90
 <211> 61
 <212> PRT
 <213> Homo sapiens

<400> 90
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<210> 91
 <211> 327
 <212> DNA
 <213> Homo sapiens

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<210> 92
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 92
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ATTORNEY DOCKET NO.: 15966-543

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Leu Gly Val Gly Ala Phe Pro Gly Lys Ala Ala Gly Arg Glu Ser Thr			
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Ala Pro Ser Gly Thr Leu Cys Val Leu Ala Ala Pro Gly Thr Cys Arg			
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Arg Pro Cys Trp Ala Ser Thr Cys Arg Ala Pro Gly Ser Cys Val Gly			
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<210> 93

<211> 394

<212> DNA

<213> Homo sapiens

<400> 93

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394

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<210> 94

<211> 109

<212> PRT

<213> Homo sapiens

<400> 94

Met Leu Ala Gly Asn Asp Asn Phe His Cys His Pro Leu Ala Val Ile			
1	5	10	15
Thr Val Val Asp Thr Gln Pro Asp Ser Leu Glu Ile Glu Arg Phe Arg			
20	25	30	
Phe Arg Thr Leu Gly His Asp Gln Val Ala Pro Gly Ile Tyr Arg Tyr			
35	40	45	
Lys Arg Arg Gly Ala Ser Leu Ala Arg Pro Pro Leu Leu His Pro Arg			
50	55	60	
Gly Arg Arg Ala Arg Arg Leu Pro Leu Ala Val Leu Trp Arg Pro Ile			
65	70	75	80
Ala His Val Arg Arg Pro Ile Arg Ala Cys Cys Ser Gly Met Gly Pro			
85	90	95	
His Arg Asn Ala Pro Arg Gly Thr Ala Cys Arg Thr Arg			

100

105

<210> 95
 <211> 531
 <212> DNA
 <213> Homo sapiens

<400> 95
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 tgcttgatc ctaaaatgga ctggtcttgg gtgtgtaacc ccggtgaagt tatagcctcc
 120
 ccaaattgag gtgacagaag gaagacaaga ggtgtaagct ggagagggaa gggaagaaat
 180
 cagtggcttt ggccagcctc tgtgccaccc agtacgacag aggagtggga actggccctc
 240
 tggggctctg cttggccata ggcactgcac attgtgccac ctgctcatca cctcctctag
 300
 tctcacactg agcatcggag tacctgttgt gcagacagga aaactgagga gctctgagag
 360
 gctgagcatg gagctcacc ccatgcatag ggtgtgggaa gagggcacag gaggcctcat
 420
 ccatggggga aagggttgag gatggacatg ggtggggaga gggcatagac atcccttcct
 480
 aatctctgtt cccaccacat ttcataggag atgagttagg agatgacagc t
 531

<210> 96
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 96
 Met Arg Pro Pro Val Pro Ser Ser His Thr Leu Trp His Gly Val Ser
 1 5 10 15
 Ser Met Leu Ser Leu Ser Glu Leu Leu Ser Phe Pro Val Cys Thr Thr
 20 25 30
 Gly Thr Pro Met Leu Ser Val Arg Leu Glu Glu Val Met Ser Arg Trp
 35 40 45
 His Asn Val Gln Cys Leu Trp Pro Ser Arg Ala Pro Glu Gly Gln Phe
 50 55 60
 Pro Leu Leu Cys Arg Thr Gly Trp His Arg Gly Trp Pro Lys Pro Leu
 65 70 75 80
 Ile Ser Ser Leu Pro Ser Pro Ala Tyr Thr Ser Cys Leu Pro Ser Val
 85 90 95
 Thr Ser Ile Trp Gly Gly Tyr Asn Phe Thr Gly Val Thr His Pro Arg
 100 105 110
 Pro Val His Phe Arg Ile Gln Ala Lys Phe Pro Glu
 115 120

<210> 97
 <211> 405
 <212> DNA
 <213> Homo sapiens

<400> 97

ggtcggggcca gtcgaacttc attcccgcctt cgaggggtctt gctgcggatg ggccgtacgc
 60
 tcgcggtgcc ttgcgcgcgg gctggttaggt ggagaagccg cgcgagtacg cgccgtagag
 120
 cgacatcgtg tctgagacgt cgaagctcag gccagctttt ggcgctccagg cgcgctcggt
 180
 cggctccgcc tcttgccgga attgattcag cgcaatcccc gccatcacat gccagcgctt
 240
 gtccagggtc atgaaatcct gggcataggc gcgcgaggag cgcagcggcg aattggacag
 300
 gcgctcgata ttgggcgtga tgtccgaaga cgggaacggg acccgggggg agaagacgtt
 360
 gcccgggaaa agatcccccg acgccatcgt ggtgtcgacc gagat
 405

<210> 98

<211> 122

<212> PRT

<213> Homo sapiens

<400> 98

Met	Ala	Ser	Gly	Asp	Leu	Phe	Pro	Gly	Asn	Val	Phe	Ser	Pro	Arg	Val
1				5					10					15	
Pro	Phe	Pro	Ser	Ser	Asp	Ile	Thr	Pro	Asn	Ile	Glu	Arg	Leu	Ser	Asn
			20					25					30		
Ser	Pro	Leu	Arg	Ser	Ser	Arg	Ala	Tyr	Ala	Gln	Asp	Phe	Met	Thr	Leu
		35					40				45				
Asp	Lys	Arg	Trp	His	Val	Met	Ala	Gly	Ile	Ala	Leu	Asn	Gln	Leu	Pro
	50					55					60				
Gln	Glu	Gly	Gly	Pro	Thr	Glu	Arg	Ala	Trp	Thr	Pro	Lys	Leu	Gly	Leu
65					70					75				80	
Ser	Phe	Asp	Val	Ser	Asp	Thr	Met	Ser	Leu	Tyr	Gly	Ala	Tyr	Ser	Arg
			85						90				95		
Gly	Phe	Ser	Thr	Tyr	Gln	Pro	Ala	Arg	Lys	Ala	Pro	Arg	Ala	Tyr	Gly
			100					105					110		
Pro	Ser	Ala	Ala	Arg	Pro	Ser	Lys	Arg	Glu						
		115					120								

<210> 99

<211> 545

<212> DNA

<213> Homo sapiens

<400> 99

acgcgtccgc tcccgatgtc gttgacgagc tgcgctcagc gatgacggta ctcacccatc
 60
 tgccccgacg acccagcaaa cgtccccggc tgttcctcat tgaccacgcc gaccggatcg
 120
 tcgatcccat cactcgggat ttgctggaat ccctgggttcg cgaagccggc gaggctgcgg
 180
 tgatcttggg tgcccagcgt cgcggtcgca tcgattgggt ctccccacag atcatccaca
 240

acctggccga acaccatttt gagtcgtcct ctggagggtac tcgatgatga ctgaacgttc
 300
 ccattccacg atcagggttaa ggtggccggc ggtgggtggtt ctggtcctcg ttccgctgct
 360
 ggtggtcgcc ggattggtcc gggacgacct ggcataccac cgaccgggtg ggccgggtga
 420
 aagcggccgt cgtcaacgag gacaaggccg tcaagggtgcg tggacaactg gttccgatgg
 480
 gccgccaact caccgccgcc ttgatggact ctggctcgca caccactgat ggccacaccg
 540
 tcgac
 545

<210> 100
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 100
 Met Gly Thr Phe Ser His His Arg Val Pro Pro Glu Asp Asp Ser Lys
 1 5 10 15
 Trp Cys Ser Ala Arg Leu Trp Met Ile Cys Gly Glu Ser Gln Ser Met
 20 25 30
 Arg Pro Arg Arg Trp Ala Pro Lys Ile Thr Ala Ala Ser Pro Ala Ser
 35 40 45
 Arg Thr Arg Asp Ser Ser Lys Ser Arg Val Met Gly Ser Thr Ile Arg
 50 55 60
 Ser Ala Trp Ser Met Arg Asn Ser Arg Gly Arg Leu Leu Gly Arg Arg
 65 70 75 80
 Gly Arg Trp Val Ser Thr Val Ile Ala Glu Arg Ser Ser Ser Thr Thr
 85 90 95
 Ser Gly Ala Asp Ala
 100

<210> 101
 <211> 619
 <212> DNA
 <213> Homo sapiens

<400> 101
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 60
 tcatgcacga tccggacttc gatccgatcc ccatgggtgaa caaggagctt gacgccttcg
 120
 aagctgccgg gggtgactat ctcatcctcg ccacggattc cggacgcaag ggatacacga
 180
 ccgcccgtcc tcacgaggcc ggcggaanaac gctattacca acctggacca gatccgcgaa
 240
 gtctgcgcca gccgcaacgt caccgcctgt ctacaccccc attggggaac gatggtccag
 300
 aaccgtgacg aagtgatccg cgtgctcgag aactcctcga tcgggctgtg cctggacact
 360
 ggtcatctgg cctgtgggtgg taccgatgtc gttgagctgg tgcgtaagta cgccaaccgc
 420

gtcgacattg tccacgccaa agatgtccat aaggagatgg ccgacaagct tttgcctggc
 480
 gagatcacct ggtccgaagg cattcgcgcc gggatgttcg caccatcgg cgacggtgat
 540
 atcgactttg cagccatcgt gaggtcctt gatgaagccg ggttcgatgg ttattacgtc
 600
 ctagagcagg acatcatga
 619

<210> 102
 <211> 173
 <212> PRT
 <213> Homo sapiens

<400> 102
 Thr Arg Ser Leu Thr Pro Ser Lys Leu Pro Gly Val Thr Ile Ser Ser
 1 5 10 15
 Ser Pro Arg Ile Pro Asp Ala Arg Asp Thr Arg Pro Pro Val Leu Thr
 20 25 30
 Arg Pro Ala Glu Asn Ala Ile Thr Asn Leu Asp Gln Ile Arg Glu Val
 35 40 45
 Cys Ala Ser Arg Asn Val Thr Ala Cys Leu His Pro His Trp Gly Thr
 50 55 60
 Met Val Gln Asn Arg Asp Glu Val Ile Arg Val Leu Glu Asn Ser Ser
 65 70 75 80
 Ile Gly Leu Cys Leu Asp Thr Gly His Leu Ala Cys Gly Gly Thr Asp
 85 90 95
 Val Val Glu Leu Val Arg Lys Tyr Ala Asn Arg Val Asp Ile Val His
 100 105 110
 Ala Lys Asp Val His Lys Glu Met Ala Asp Lys Leu Leu Pro Gly Glu
 115 120 125
 Ile Thr Trp Ser Glu Gly Ile Arg Ala Gly Met Phe Ala Pro Ile Gly
 130 135 140
 Asp Gly Asp Ile Asp Phe Ala Ala Ile Val Arg Leu Leu Asp Glu Ala
 145 150 155 160
 Gly Phe Asp Gly Tyr Tyr Val Leu Glu Gln Asp Ile Met
 165 170

<210> 103
 <211> 321
 <212> DNA
 <213> Homo sapiens

<400> 103
 nnccatgggg gaagacaaca gccatgtggg ggagaccgga gccattgggg ggagaccctt
 60
 gccattgggg ggagaccctt gccgtgggga aagaccctg ccatggggga gaccctgcc
 120
 actgggggga gaccctgcc gctgggggga gaccgagcc attgggggga gaccctgcc
 180
 atggggaaag accctgccca ttgggggaga ntacctgcca ttgggggaga tccctgccgt
 240
 tggggggaga tccctgctgt tggggggaga ntccctcctg taggggaaga cccctgcagg
 300

agtgggttggg gcgaagaccc c
321

<210> 104
<211> 107
<212> PRT
<213> Homo sapiens

<400> 104
Xaa His Gly Gly Arg Gln Gln Pro Cys Gly Gly Asp Pro Ser His Trp
1 5 10 15
Gly Glu Thr Pro Ala Ile Gly Gly Arg Pro Leu Pro Trp Gly Lys Thr
20 25 30
Pro Ala Met Gly Gln Thr Pro Ala Thr Gly Gly Arg Pro Leu Pro Leu
35 40 45
Gly Gly Asp Pro Ser His Trp Gly Glu Thr Pro Ala Met Gly Lys Asp
50 55 60
Pro Cys His Trp Gly Arg Xaa Pro Ala Ile Gly Gly Asp Pro Cys Arg
65 70 75 80
Trp Gly Glu Ile Pro Ala Val Gly Gly Arg Xaa Pro Pro Val Gly Glu
85 90 95
Asp Pro Cys Arg Ser Gly Trp Gly Glu Asp Pro
100 105

<210> 105
<211> 344
<212> DNA
<213> Homo sapiens

<400> 105
nnntctctcc gaccgcgtcc agatccaccg tggcccgcac gaaccagtcg ttgttgccctt
60
ccgggtcaac gagggtttgg cgcacgggtcc actccgtggc gcccggggtg atgtgcaaca
120
gggcggggccc gcgcgcggcc gggcctgatt ccagcctctc gtgctcgtcc cagtacccat
180
ccagcgcacg gccccagcgg tcggcaccac agccgtggtc gccgtcgagc gccccaggg
240
cctcaatgtc gtcacggcg gccagttcca cccggcgga catctcgttg cggaccatga
300
cccgggaagg gcgggaattc tcggtcagtt tcggcggtgc cggc
344

<210> 106
<211> 62
<212> PRT
<213> Homo sapiens

<400> 106
Cys Ala Thr Gly Arg Ala Arg Ala Arg Pro Gly Leu Ile Pro Ala Ser
1 5 10 15
Arg Ala Arg Pro Ser Thr His Pro Ala His Arg Pro Ser Gly Arg His
20 25 30
Pro Ser Arg Gly Arg Arg Arg Ala Pro Pro Gly Pro Gln Cys Arg His

35 40 45
 Arg Arg Pro Val Pro Pro Gly Gly Thr Ser Arg Cys Gly Pro
 50 55 60

<210> 107
 <211> 549
 <212> DNA
 <213> Homo sapiens

<400> 107
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 60
 gccgcttaat aaccgaccaa catgaaactc aagggtgccc ccttcctagc ggggaccctg
 120
 cacagaccgc aaaataagggt gttttgctct gccctcctca gttcacgtgg gcaccttgga
 180
 acactgaaga aggcattttc cgaactcact gtcctacgga cttattctcc gcaactgtttt
 240
 cgcttccttc gccctgttct cgtgactgac aggagcaggg gtcacaagca ggcagcccga
 300
 gagctctgct cacctggaaa agcatttttg ttagcttaa atgtgaaggc ctcaggcagt
 360
 ggctgttgt cctcctccac atgcgcccat cttcactctt tcatgtgact ggctgtttt
 420
 tgaaggcaag gccctgtca cccttggtta ggccaggtat gttctgcacc gaaaatggcc
 480
 ctgccctctg cattggatgg ctagctctta ggttggttta ttttagcaaa taagcgttac
 540
 agggtaggc
 549

<210> 108
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 108
 Met Lys Leu Lys Gly Cys Pro Phe Leu Ala Gly Thr Leu His Arg Pro
 1 5 10 15
 Glu Asn Lys Gly Phe Cys Ser Ala Leu Leu Ser Ser Arg Gly His Leu
 20 25 30
 Gly Thr Leu Lys Lys Ala Phe Ser Glu Leu Thr Val Leu Arg Thr Tyr
 35 40 45
 Ser Pro His Cys Phe Arg Leu Leu Arg Pro Val Leu Val Thr Asp Arg
 50 55 60
 Ser Arg Gly His Lys Gln Ala Ala Arg Glu Leu Cys Ser Pro Gly Lys
 65 70 75 80
 Ala Phe Leu Cys Ser Leu Asn Val Lys Ala Ser Gly Ser Gly Leu Leu
 85 90 95
 Ser Ser Ser Thr Cys Ala His Leu His Ser Phe Met
 100 105

<210> 109
 <211> 748

<212> DNA

<213> Homo sapiens

<400> 109

nngaattcag atttactttt tgcatttcct tgaatataaa ataggcagta aactaaccta
 60
 aagtcagaag acttatttgt tctggtacct attctgctgt taataaattg ataaatgagt
 120
 gatattgggg taagttacca atttacttta cagcccttaa gtaaataatc tgctttcctc
 180
 agcatcatag acttttgaag aggattaatt aagcgcttaa aaaacctgta gactctatta
 240
 cagtcagtga aaggaataat tctctttaca aagtaaagtc agttgtttta ttttagacaa
 300
 gagtgttcta aacttcgtga agagttaagg cttcaacatg aagaggataa gaagtcagca
 360
 atgtctcaac ttttgcagtt gaaagatcga gagaaaaatg cagcaagaga ttcatggcag
 420
 aagaaagtag aagatctctt aaaccagatt tccttgctga aacagaatct ggagatacag
 480
 ctttcccagt ctcagacttc tttgcaacaa ctgcaagccc agtttacgca agaacgacag
 540
 cggcttacgc aagagcttga agaattagag gagcaacatc agcaaagaca caaatcatta
 600
 aaagaagcac atgtccttgc atttcaaact atggaagagg aaaaggaaaa ggagcaaaga
 660
 gctcttgaaa atcatttaca acagaagcat tctgcagagc ttcaatcact aaaagatgca
 720
 cacagagagt caatggaggg cttccgga
 748

<210> 110

<211> 157

<212> PRT

<213> Homo sapiens

<400> 110

Met	Gln	Leu	Phe	Tyr	Phe	Arg	Gln	Glu	Cys	Ser	Lys	Leu	Arg	Glu	Glu
1				5					10					15	
Leu	Arg	Leu	Gln	His	Glu	Glu	Asp	Lys	Lys	Ser	Ala	Met	Ser	Gln	Leu
			20					25					30		
Leu	Gln	Leu	Lys	Asp	Arg	Glu	Lys	Asn	Ala	Ala	Arg	Asp	Ser	Trp	Gln
		35					40					45			
Lys	Lys	Val	Glu	Asp	Leu	Leu	Asn	Gln	Ile	Ser	Leu	Leu	Lys	Gln	Asn
	50					55					60				
Leu	Glu	Ile	Gln	Leu	Ser	Gln	Ser	Gln	Thr	Ser	Leu	Gln	Gln	Leu	Gln
65					70					75				80	
Ala	Gln	Phe	Thr	Gln	Glu	Arg	Gln	Arg	Leu	Thr	Gln	Glu	Leu	Glu	Glu
			85					90					95		
Leu	Glu	Glu	Gln	His	Gln	Gln	Arg	His	Lys	Ser	Leu	Lys	Glu	Ala	His
			100				105						110		
Val	Leu	Ala	Phe	Gln	Thr	Met	Glu	Glu	Glu	Lys	Glu	Lys	Glu	Gln	Arg
		115					120						125		
Ala	Leu	Glu	Asn	His	Leu	Gln	Gln	Lys	His	Ser	Ala	Glu	Leu	Gln	Ser

130	135	140
Leu Lys Asp Ala His Arg	Glu Ser Met Glu Gly Phe Arg	
145	150	155

<210> 111
 <211> 429
 <212> DNA
 <213> Homo sapiens

<400> 111
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 cgtgaaccgc tcgccccgca ggtcaacgac ttcgggatca ccgggttcga cggcattctc
 120
 tcggcttatn nacgccacca gcatncgact ttggctgaga tcatcgcacc gttcggacat
 180
 ctggtcatga tcgacggaac cgactcattc gatctcatgg ccttcaagtc aaagtcgtta
 240
 acggtgacca gcgagtcgat gttcagccgt ccacagttcg cgacgcccga cgtcgccgaa
 300
 caaggccggg cactggccag catcgccgac ctcgtcgaga aggggcagat ccgtccgacg
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 atgaccgccc atatcgaggg tctgacaacc cagcatgtgc gtgaggccac cgcagccgtc
 420
 ggtccggc
 429

<210> 112
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 112
 Ala Arg Pro Glu Ser Ala Gln Trp Cys Gln Asp Met Gly Ala Thr Gly
 1 5 10 15
 Ile Ile Asn His Arg Glu Pro Leu Ala Pro Gln Val Asn Asp Phe Gly
 20 25 30
 Ile Thr Gly Phe Asp Gly Ile Leu Ser Ala Tyr Xaa Arg His Gln His
 35 40 45
 Xaa Thr Leu Ala Glu Ile Ile Ala Pro Phe Gly His Leu Val Met Ile
 50 55 60
 Asp Gly Thr Asp Ser Phe Asp Leu Met Ala Phe Lys Ser Lys Ser Leu
 65 70 75 80
 Thr Val Thr Ser Glu Ser Met Phe Ser Arg Pro Gln Phe Ala Thr Pro
 85 90 95
 Asp Val Ala Glu Gln Gly Arg Ala Leu Ala Ser Ile Ala Asp Leu Val
 100 105 110
 Glu Lys Gly Gln Ile Arg Pro Thr Met Thr Arg His Ile Glu Gly Leu
 115 120 125
 Thr Thr Gln His Val Arg Glu Ala Thr Ala Ala Val Glu Ser Gly
 130 135 140

<210> 113
 <211> 382

<212> DNA

<213> Homo sapiens

<400> 113

gtgcactgga cggatgctgg ggaactgagg cctgcccttc tccactcctg ctgcctctgt
 60
 gtggaccgcc tgccacctgg cttcaacgat gtggacgctc tgtgccgggc gctgtcagct
 120
 gtccacagcc ccaccttctg ccagctggcg tgcggccagg atgggcagct gaagggttc
 180
 gcggtgctgg agtatgagac ggctgagatg gcggaggagg cacagcagca ggcggacggc
 240
 ctgtccctgg ggggcagcca cctgcgagtc tccttctgcg cccctgggac ccccgggcgc
 300
 agtatgctgg ccgctctcat cgttgcccag gccacggccc tcaatcgggg gcagggagtc
 360
 ctccccgagc ccaacatcct gc
 382

<210> 114

<211> 125

<212> PRT

<213> Homo sapiens

<400> 114

Met	Leu	Gly	Ser	Gly	Arg	Thr	Pro	Cys	Pro	Arg	Leu	Arg	Ala	Val	Ala
1				5				10					15		
Trp	Ala	Thr	Met	Arg	Ala	Ala	Ser	Ile	Leu	Arg	Pro	Gly	Val	Pro	Gly
			20				25					30			
Ala	Gln	Lys	Glu	Thr	Arg	Arg	Trp	Leu	Pro	Pro	Arg	Asp	Arg	Pro	Ser
		35				40					45				
Ala	Cys	Cys	Cys	Ala	Ser	Ser	Ala	Ile	Ser	Ala	Val	Ser	Tyr	Ser	Ser
	50				55			60							
Thr	Ala	Lys	Pro	Phe	Ser	Cys	Pro	Ser	Trp	Pro	His	Ala	Ser	Trp	Gln
65				70			75						80		
Lys	Val	Gly	Leu	Trp	Thr	Ala	Asp	Ser	Ala	Arg	His	Arg	Ala	Ser	Thr
			85			90							95		
Ser	Leu	Lys	Pro	Gly	Gly	Arg	Arg	Ser	Thr	Gln	Arg	Gln	Gln	Glu	Trp
			100			105							110		
Arg	Arg	Ala	Gly	Leu	Ser	Ser	Pro	Ala	Ser	Val	Gln	Cys			
		115				120						125			

<210> 115

<211> 4798

<212> DNA

<213> Homo sapiens

<400> 115

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 catttcactc cctgtttgga gccatgagtg gccccctgtt gccttcaaga ctgaagccat
 120
 ccccatcctt cctcccacca acctagaggc tttgcttcgt aaatgctggc cctttccttc
 180

atgggctcca ccctctgagt gtgtcatgaa ctcttccact tccttgcctt ggctcgtatt
240
gggtcctctg cccgaggtca gagatttgga cgagcccttc tcctccatct tcacagtctc
300
catttaccat tagatgccag gccagacag ttgatgaaa atgtaagaaa cggacccaag
360
tataagaaaa agctagatct gtccatttta tttctagttt ttggaagaga tgtggatata
420
gagaaatatt actctactat tgaaaaaat atatatcagt ctgattataa atgtcaactc
480
atactaagtc aatatcaggg aagcagtgtg gagaaggatg tggcaaactg gagattgctg
540
tttccataga aagagggcag ctaatgctta tctccagacc attgttatgc agtaatgtag
600
actccatttc accagattta attcttaagg agaaactgga aacttgtatt attatttgat
660
tattactttt ggcagttaat tttaaaaatc accgttttagg ccaaaacaac atgacatttg
720
tctgggctac aagggactct tagcgactct tagcttgcaac ttacctttct aatctcaggg
780
ctttttacaa agcccttctc tgaattccct gaagatatgc tagcttgaag gctcactgca
840
tactctcaac ttcccagcca cttccctggt tccctcttat accagttaat actttgatgt
900
tattttttca gtctatttta atctttttaga ctggagggtc cttgaggggtg gggcctaatt
960
cttgttttta tcttcccat agcaattatc aagttatctg ctcccttttg cacctaagaa
1020
atattagttg gggtgataac tgaatggctg tccttctgcc ttcgttactg cttttgtgga
1080
tgttattttc tttgaccctt attccaccctg tgtgcagtgg agaggatggg tgttgatatt
1140
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1260
tctacccctt gccacctctc accttcttcc ctttcacctt tttctgtagc tgaacggaaa
1320
ccaccgtctt ttaacatgaa tgcgatgagt gccttatacc acattgcaca gaacgaatcc
1380
cccgtgctcc agtcaggaca ctgggtctgag tacttccgga attttgtcga ctctgtctt
1440
cagaaaatcc ctcaagacag accaacctca gaggttctcc tgaagcaccg ctttgtgctc
1500
cgaggagcggc caccacagt catcatggac ctgatccaga ggaccaagga tgccgtgcgg
1560
gagctggaca acctgcagta ccgcaagatg aagaagatcc tgttccaaga ggcaccaac
1620
ggccctggtg ccgaggcccc agaggaggaa gaggaggccg agccctacat gcaccgggccc
1680
gggactctga ccagcctcga gagtagccac tcagtgccca gcatgtccat cagcgcctcc
1740
agccagagca gctccgtcaa cagcctagca gatgcctcag acaacgagga agaggaggag
1800

gaggaggagg aagaggagga ggaggaagaa ggcctgaag cccgggagat ggccatgatg
1860
caggaggggg agcacacagt cacctctcac agctccatta tccaccggct gccgggctct
1920
gacaacctat atgatgacct ctaccagcca gagataacct ccagccctct ccagccgct
1980
gcagccccag ctcccacttc caccacctct tccgcccgc gccgggccta ctgccgtaac
2040
cgagaccact ttgccaccat ccgaaccgcc tccctgggtca gccgtcagat ccaggagcat
2100
gagcaggact ctgcgctgcg ggagcagctg agcggctata agcggatgcg acgacagcac
2160
cagaagcagc tgctggccct ggagtcacgg ctgaggggtg aacgggagga gcacagtgc
2220
cggctgcagc gggagcttga ggcgcagcgg gctggctttg gggcagaggc agaaaagctg
2280
gcccgggcgc accaggccat aggtgagaag gaggcacgag ctgcccaggc cgaggagcgg
2340
aagttccagc agcacatcct tgggcagcag aagaaggagc tggctgccct gctggaggca
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4798

<210> 116
<211> 1062
<212> PRT
<213> Homo sapiens

<400> 116
Met Met Gly Thr Ser Gln Gly His Val Ala Arg Lys Ser Arg Asn Trp

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			20					25					30				
Cys	His	Leu	Ser	Pro	Ser	Ser	Leu	Ser	Pro	Phe	Ser	Val	Ala	Glu	Arg		
		35					40					45					
Lys	Pro	Pro	Leu	Phe	Asn	Met	Asn	Ala	Met	Ser	Ala	Leu	Tyr	His	Ile		
	50					55					60						
Ala	Gln	Asn	Glu	Ser	Pro	Val	Leu	Gln	Ser	Gly	His	Trp	Ser	Glu	Tyr		
65					70					75					80		
Phe	Arg	Asn	Phe	Val	Asp	Ser	Cys	Leu	Gln	Lys	Ile	Pro	Gln	Asp	Arg		
			85					90					95				
Pro	Thr	Ser	Glu	Val	Leu	Leu	Lys	His	Arg	Phe	Val	Leu	Arg	Glu	Arg		
			100					105					110				
Pro	Pro	Thr	Val	Ile	Met	Asp	Leu	Ile	Gln	Arg	Thr	Lys	Asp	Ala	Val		
		115				120						125					
Arg	Glu	Leu	Asp	Asn	Leu	Gln	Tyr	Arg	Lys	Met	Lys	Lys	Ile	Leu	Phe		
	130					135					140						
Gln	Glu	Ala	Pro	Asn	Gly	Pro	Gly	Ala	Glu	Ala	Pro	Glu	Glu	Glu	Glu		
145					150					155					160		
Glu	Ala	Glu	Pro	Tyr	Met	His	Arg	Ala	Gly	Thr	Leu	Thr	Ser	Leu	Glu		
			165					170					175				
Ser	Ser	His	Ser	Val	Pro	Ser	Met	Ser	Ile	Ser	Ala	Ser	Ser	Gln	Ser		
		180						185					190				
Ser	Ser	Val	Asn	Ser	Leu	Ala	Asp	Ala	Ser	Asp	Asn	Glu	Glu	Glu	Glu		
	195					200					205						
Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gly	Pro	Glu	Ala	Arg		
	210					215					220						
Glu	Met	Ala	Met	Met	Gln	Glu	Gly	Glu	His	Thr	Val	Thr	Ser	His	Ser		
225					230					235					240		
Ser	Ile	Ile	His	Arg	Leu	Pro	Gly	Ser	Asp	Asn	Leu	Tyr	Asp	Asp	Pro		
			245					250					255				
Tyr	Gln	Pro	Glu	Ile	Thr	Pro	Ser	Pro	Leu	Gln	Pro	Pro	Ala	Ala	Pro		
		260						265					270				
Ala	Pro	Thr	Ser	Thr	Thr	Ser	Ser	Ala	Arg	Arg	Arg	Ala	Tyr	Cys	Arg		
	275					280						285					
Asn	Arg	Asp	His	Phe	Ala	Thr	Ile	Arg	Thr	Ala	Ser	Leu	Val	Ser	Arg		
	290					295				300							
Gln	Ile	Gln	Glu	His	Glu	Gln	Asp	Ser	Ala	Leu	Arg	Glu	Gln	Leu	Ser		
305					310					315					320		
Gly	Tyr	Lys	Arg	Met	Arg	Arg	Gln	His	Gln	Lys	Gln	Leu	Leu	Ala	Leu		
			325					330					335				
Glu	Ser	Arg	Leu	Arg	Gly	Glu	Arg	Glu	Glu	His	Ser	Ala	Arg	Leu	Gln		
		340				345						350					
Arg	Glu	Leu	Glu	Ala	Gln	Arg	Ala	Gly	Phe	Gly	Ala	Glu	Ala	Glu	Lys		
	355					360					365						
Leu	Ala	Arg	Arg	His	Gln	Ala	Ile	Gly	Glu	Lys	Glu	Ala	Arg	Ala	Ala		
	370				375						380						
Gln	Ala	Glu	Glu	Arg	Lys	Phe	Gln	Gln	His	Ile	Leu	Gly	Gln	Gln	Lys		
385					390					395					400		
Lys	Glu	Leu	Ala	Ala	Leu	Leu	Glu	Ala	Gln	Lys	Arg	Thr	Tyr	Lys	Leu		
		405						410				415					
Arg	Lys	Glu	Gln	Leu	Lys	Glu	Glu	Leu	Gln	Glu	Asn	Pro	Ser	Thr	Pro		
		420						425				430					
Lys	Arg	Glu	Lys	Ala	Glu	Trp	Leu	Leu	Arg	Gln	Lys	Glu	Gln	Leu	Gln		

481

865 870 875 880
 Pro Gly Leu Ala Leu Pro Leu Val Ala Met Ala Ala Gly Gly Arg Trp
 885 890 895
 Val Arg Gln Gln Gly Pro Arg Val Arg Arg Gly Ile Ser Arg Leu Trp
 900 905 910
 Leu Arg Val Leu Leu Arg Leu Ser Pro Met Ala Phe Arg Ala Leu Gln
 915 920 925
 Gly Cys Gly Ala Val Gly Asp Arg Gly Leu Phe Ala Leu Tyr Pro Lys
 930 935 940
 Thr Asn Lys Asp Gly Phe Arg Ser Arg Leu Pro Val Pro Gly Pro Arg
 945 950 955 960
 Arg Arg Asn Pro Arg Thr Thr Gln His Pro Leu Ala Leu Leu Ala Arg
 965 970 975
 Val Trp Val Leu Cys Lys Gly Trp Asn Trp Arg Leu Ala Arg Ala Ser
 980 985 990
 Gln Gly Leu Ala Ser His Leu Pro Pro Trp Ala Ile His Thr Leu Ala
 995 1000 1005
 Ser Trp Gly Leu Leu Arg Gly Glu Arg Pro Thr Arg Ile Pro Arg Leu
 1010 1015 1020
 Leu Pro Arg Ser Gln Arg Gln Leu Gly Pro Pro Ala Ser Arg Gln Pro
 1025 1030 1035 1040
 Leu Pro Gly Thr Leu Ala Gly Arg Arg Ser Arg Thr Arg Gln Ser Arg
 1045 1050 1055
 Ala Leu Pro Pro Trp Arg
 1060

<210> 117
 <211> 471
 <212> DNA
 <213> Homo sapiens

<400> 117
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 ctgctcgacc ttctgcctt ggccaaggca gctggccagg tattagcggc cggcatcgtc
 120
 gtcacgggcg gagtgcgaat gttttggatc ccgctgccga actccatcat tgctttgggg
 180
 acgcctactt cgatcttggt gacgggtgttc ttcatgtgt tgtgcgcaa tgcggtgaat
 240
 ttcatgatg gacttgacgg cctggcatcc ggtgtggtgg ccatcgggtc cttggctttc
 300
 ttctcataca cctacctgct ggctcacgaa caggactttg ttgttgcgac gactaccagt
 360
 ctcattacgg ctgcgacggc gggcgctgt ctcgggtttt tgccccacaa ctggcatccg
 420
 gcgaggatgt tcatgggtga ttccggagct ctgctacttg gcttattgct a
 471

<210> 118
 <211> 157
 <212> PRT
 <213> Homo sapiens

<400> 118

Xaa Ala Leu Thr Ile Cys Leu Ala Gly Val Val Ile Cys Ala Val Gly
 1 5 10 15
 Val Val Asp Asp Leu Leu Asp Leu Pro Ala Leu Ala Lys Ala Ala Gly
 20 25 30
 Gln Val Leu Ala Ala Gly Ile Val Val Thr Gly Gly Val Arg Met Phe
 35 40 45
 Trp Ile Pro Leu Pro Asn Ser Ile Ile Ala Leu Gly Thr Pro Thr Ser
 50 55 60
 Ile Leu Val Thr Val Phe Phe Ile Val Leu Cys Ala Asn Ala Val Asn
 65 70 75 80
 Phe Ile Asp Gly Leu Asp Gly Leu Ala Ser Gly Val Val Ala Ile Gly
 85 90 95
 Ser Leu Ala Phe Phe Ser Tyr Thr Tyr Leu Leu Ala His Glu Gln Asp
 100 105 110
 Phe Val Val Ala Thr Thr Thr Ser Leu Ile Thr Ala Ala Thr Ala Gly
 115 120 125
 Ala Cys Leu Gly Phe Leu Pro His Asn Trp His Pro Ala Arg Met Phe
 130 135 140
 Met Gly Asp Ser Gly Ala Leu Leu Leu Gly Leu Leu Leu
 145 150 155

<210> 119

<211> 302

<212> DNA

<213> Homo sapiens

<400> 119

ntcaaacatg agcagtcgtg gcggccgagg ccgcggtggc tattatcgcg agctttatgg
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 tagccgaggt cgaggcagta aatctaataa aactttcgca aaaaattcgg atgtctactc
 120
 tcagaaaaag actcgaacag tacgaggcac ctccgaagat ttagcacgat cgctccataa
 180
 gcttcatatg cgcccgtacc ctgcgtatca tgacattgag ggtatgtggg ctttcccagc
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 ctttactttt tatctggatc atgcacaagc agacccatac gctgcccacaa ataaggcagc
 300
 cn
 302

<210> 120

<211> 98

<212> PRT

<213> Homo sapiens

<400> 120

Met Ser Ser Arg Gly Gly Arg Gly Arg Gly Gly Tyr Tyr Arg Glu Leu
 1 5 10 15
 Tyr Gly Ser Arg Gly Arg Gly Ser Lys Ser Asn Glu Thr Phe Ala Lys
 20 25 30
 Asn Ser Asp Val Tyr Ser Gln Lys Lys Thr Arg Thr Val Arg Gly Thr
 35 40 45
 Ser Glu Asp Leu Ala Arg Ser Leu His Lys Leu His Met Arg Pro Tyr

50		55		60											
Pro	Ala	Tyr	His	Asp	Ile	Glu	Gly	Met	Trp	Ala	Phe	Pro	Ala	Phe	Thr
65					70					75					80
Phe	Tyr	Leu	Asp	His	Ala	Gln	Ala	Asp	Pro	Tyr	Ala	Ala	Pro	Asn	Lys
				85					90					95	
Ala Arg															

<210> 121
 <211> 318
 <212> DNA
 <213> Homo sapiens

<400> 121
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 cctaaaggat ttgccgcatt acaggaaagt tttttggtaa gtttgggggtt gtttctgtgc
 120
 tgtgtgagaa ggagtagaag cagctccagt agagtgggcc ttttcatttt tatccagagg
 180
 aaatttgtag gctgtggcta ttacttcttt ttttttcttt tttttttttg ttttagagaca
 240
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 300
 tgcctcccag gttcaagc
 318

<210> 122
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 122
Xaa Met Gly Gly Pro Gly Thr Ala Leu Val Pro Leu Phe Phe Leu Gly
1 5 10 15
Lys Lys Leu Ser Pro Lys Gly Phe Ala Ala Leu Gln Glu Ser Phe Leu
20 25 30
Val Ser Leu Gly Leu Phe Leu Cys Cys Val Arg Arg Ser Arg Ser Ser
35 40 45
Ser Ser Arg Val Gly Leu Phe Ile Phe Ile Gln Arg Lys Phe Val Gly
50 55 60
Cys Gly Tyr Tyr Phe Leu Phe Phe Leu Phe Phe Phe Cys Leu Glu Thr
65 70 75 80
Glu Ser Xaa Ser Val Ala Arg Leu Glu
85

<210> 123
 <211> 338
 <212> DNA
 <213> Homo sapiens

<400> 123
 acgcgtctag ggtagaaatc aactccagta actgtcattc aacctcagca atgctgggga
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cgggcagagg cagggcagct gtgtgccaca ttctgccag ggctggtcag gccccggctc
 120
 tcaccactcc tcctccctgc tttgaacctg tggaacaaag ggcccctgca ccccaactca
 180
 ttctcttttg ccacataagg gcctcaagtc atgtgtccc ctctgctgg gttgcttttt
 240
 ctccctctgc ttgggtcact gttcacacca ctggccactt tcctcagga agggccctca
 300
 ctgcccacac acctaaacat gcccctgct cctccata
 338

<210> 124
 <211> 96
 <212> PRT
 <213> Homo sapiens

<400> 124
 Met Leu Gly Thr Gly Arg Gly Arg Ala Ala Val Cys His Ile Pro Ala
 1 5 10 15
 Arg Ala Gly Gln Ala Pro Ala Leu Thr Thr Pro Pro Pro Cys Phe Glu
 20 25 30
 Pro Val Glu Gln Arg Ala Pro Ala Pro Gln Leu Ile Pro Leu Cys His
 35 40 45
 Ile Arg Ala Ser Ser His Ala Val Pro Ser Ala Trp Val Ala Phe Ser
 50 55 60
 Pro Ser Ala Trp Val Thr Val His Thr Thr Gly His Phe Pro Gln Gly
 65 70 75 80
 Arg Ala Leu Thr Ala His Thr Pro Lys His Ala Pro Cys Ser Ser Ile
 85 90 95

<210> 125
 <211> 280
 <212> DNA
 <213> Homo sapiens

<400> 125
 ccatggacct ggccagccac catcacctgc ctctgcctc acccaccctg ggtgcctgcc
 60
 ggcaaggatt ggagggcaga ctgctggagc gtgagaccag gccaatctgt ctttctggga
 120
 accttcagcc tccaactgga gctgactgtc aactttcggg tgagaagtca cttttctgca
 180
 ttcccaccac actatctatc tgtgcaatac ggcagcgtga cagcactcac cttattgagg
 240
 gcttctgctg tcctggccca ttctggatag gcctgatcta
 280

<210> 126
 <211> 92
 <212> PRT
 <213> Homo sapiens

<400> 126
 Met Asp Leu Ala Ser His His His Leu Pro Pro Ala Ser Pro Thr Leu

1		5		10		15									
Gly	Ala	Cys	Arg	Gln	Gly	Leu	Glu	Gly	Arg	Leu	Leu	Glu	Arg	Glu	Thr
		20			25			30							
Arg	Pro	Ile	Cys	Leu	Ser	Gly	Asn	Leu	Gln	Pro	Pro	Thr	Gly	Ala	Asp
		35			40			45							
Cys	Gln	Leu	Ser	Gly	Glu	Lys	Ser	Leu	Phe	Cys	Ile	Pro	Thr	Thr	Leu
	50				55			60							
Ser	Ile	Cys	Ala	Ile	Arg	Gln	Arg	Asp	Ser	Thr	His	Leu	Ile	Glu	Gly
65				70				75						80	
Phe	Cys	Cys	Pro	Gly	Pro	Phe	Trp	Ile	Gly	Leu	Ile				
			85					90							

<210> 127
 <211> 444
 <212> DNA
 <213> Homo sapiens

<400> 127
 cgcgatgatcg ccgtggcgga gggccgcggc gccgactcga tcgcccagct gacaaccgag
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 ctgcaaagcc gtcactgccc tgcggagcag atcacgtccg tcagcatcga catgtcgcca
 120
 gcgttcatca ggggctgcgc cgagcacctg cccaacgcgc gcgtcacctt cgacaagtcc
 180
 cacgtcatcg ggcacgcca tgcggccgtg gacaggatgc gccgcatcga gcagcgcagc
 240
 gacaagtccc tcaaggggat gcgctggctg ctgctgaaga accgcgccag cctcaagccc
 300
 gaggtgccc ccatctgga tgcctgatc gccaggatgg ccactgtgcg caccgcgcgc
 360
 gcctgggtct acaaggagca gctgcgcgag atcctcgcgc gcaagcagat caacgtggca
 420
 cgcgacatgc tcaagcactg gtgc
 444

<210> 128
 <211> 148
 <212> PRT
 <213> Homo sapiens

Arg	Val	Ile	Ala	Val	Ala	Glu	Gly	Arg	Gly	Ala	Asp	Ser	Ile	Ala	Gln
1				5				10					15		
Leu	Thr	Thr	Glu	Leu	Gln	Ser	Arg	His	Cys	Pro	Ala	Glu	Gln	Ile	Thr
		20				25						30			
Ser	Val	Ser	Ile	Asp	Met	Ser	Pro	Ala	Phe	Ile	Arg	Gly	Cys	Ala	Glu
		35			40						45				
His	Leu	Pro	Asn	Ala	Arg	Val	Thr	Phe	Asp	Lys	Phe	His	Val	Ile	Gly
	50				55					60					
His	Ala	Asn	Ala	Ala	Val	Asp	Arg	Met	Arg	Arg	Ile	Glu	Gln	Arg	Ser
65				70				75						80	
Asp	Lys	Ser	Leu	Lys	Gly	Met	Arg	Trp	Ser	Leu	Leu	Lys	Asn	Arg	Ala
			85					90					95		
Ser	Leu	Lys	Pro	Glu	Ala	Ala	Ala	Asp	Leu	Asp	Ala	Leu	Ile	Ala	Arg

100 105 110
 Met Ala Thr Val Arg Thr Ala Arg Ala Trp Val Tyr Lys Glu Gln Leu
 115 120 125
 Arg Glu Ile Leu Ala Arg Lys Gln Ile Asn Val Ala Arg Asp Met Leu
 130 135 140
 Lys His Trp Cys
 145

<210> 129
 <211> 291
 <212> DNA
 <213> Homo sapiens

<400> 129
 gaggagggac gtaccgtccc cgttatagcc aagctcgaga agccgcaagc tatcgagaac
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 ttggacgaga ttattgacgt ctttgacgcc gtcattggtg cccgtggcga tatggccgct
 120
 gagggtccgc tcgaggaagt tccgctgac caaaagcaga tcatcgagaa ggctcgttta
 180
 caggctaagc ccgtcattgt ggccaccag atgcttgagt cgatgatcca cgctccccgt
 240
 ccgacccgcg ctgaggccgc cgacgtcgcg aacgccatcc ttgacggcgc g
 291

<210> 130
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 130
 Glu Glu Gly Arg Thr Val Pro Val Ile Ala Lys Leu Glu Lys Pro Gln
 1 5 10 15
 Ala Ile Glu Asn Leu Asp Glu Ile Ile Asp Val Phe Asp Ala Val Met
 20 25 30
 Val Ala Arg Gly Asp Met Ala Val Glu Cys Pro Leu Glu Glu Val Pro
 35 40 45
 Leu Ile Gln Lys Gln Ile Ile Glu Lys Ala Arg Leu Gln Ala Lys Pro
 50 55 60
 Val Ile Val Ala Thr Gln Met Leu Glu Ser Met Ile His Ala Pro Arg
 65 70 75 80
 Pro Thr Arg Ala Glu Ala Ala Asp Val Ala Asn Ala Ile Leu Asp Gly
 85 90 95
 Ala

<210> 131
 <211> 416
 <212> DNA
 <213> Homo sapiens

<400> 131
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attccaccgg tgctctacct ggaggccgca gccgtcgggg ttcgattctt cggcatctcc
 120
 cgcggtgtct tccgctacgc cgaacgtctg gtaggccacg acctggctct gcggatgcag
 180
 ggggcattgc ggatgcgggt ctacgaccgg ctgtcacgta ccnaccctgc tgggnnacgt
 240
 cgccgggggtg acctgctggt acgggttact gccgacgtcg acgcggtgtt ggacatggtc
 300
 gtgcgggtga tcgttccggc gtgcgcgtca agcctcgtca tcattggcac cacggtcctt
 360
 ctttgtccga gagaagggtg agttttctta gccggattcc aacacagcct gggggc
 416

<210> 132
 <211> 126
 <212> PRT
 <213> Homo sapiens

<400> 132
 Ser Gly Ala Ser Val Ala Leu Met Gly Val Ser Ala Trp Leu Leu Ser
 1 5 10 15
 Arg Ala Ala Glu Ile Pro Pro Val Leu Tyr Leu Glu Ala Ala Val
 20 25 30
 Gly Val Arg Phe Phe Gly Ile Ser Arg Gly Val Phe Arg Tyr Ala Glu
 35 40 45
 Arg Leu Val Gly His Asp Leu Ala Leu Arg Met Gln Gly Ala Leu Arg
 50 55 60
 Met Arg Val Tyr Asp Arg Leu Ser Arg Thr Xaa Pro Ala Gly Xaa Arg
 65 70 75 80
 Arg Arg Gly Asp Leu Leu Val Arg Val Thr Ala Asp Val Asp Ala Val
 85 90 95
 Leu Asp Met Val Val Arg Val Ile Val Pro Ala Cys Ala Ser Ser Leu
 100 105 110
 Val Ile Ile Gly Thr Thr Val Leu Leu Cys Pro Arg Glu Gly
 115 120 125

<210> 133
 <211> 327
 <212> DNA
 <213> Homo sapiens

<400> 133
 gccgttgcta tcgctgctgg tatgcgtgca gacgtcactg tttttgatat caatatcgct
 60
 gcgttgaaga gactcgccga catctaccag ggctcgtgttc acacagtagt atccaccgcg
 120
 gccgaaattg cgaaggcgct agaaaccgct gacgttgtga tcggttctgt ccttattccg
 180
 ggtagttcta ccccgaagct tggtactacc gatatgggtg ctcacatgca gcctgggtct
 240
 gttcttattg atattgctat agaccaagge ggctgcttcg aggattcgca ccccaccact
 300
 tacgatgacc ccactttcac tgtgcac
 327

<210> 134
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 134
 Ala Val Ala Ile Ala Ala Gly Met Arg Ala Asp Val Thr Val Phe Asp
 1 5 10 15
 Ile Asn Ile Ala Ala Leu Lys Arg Leu Ala Asp Ile Tyr Gln Gly Arg
 20 25 30
 Val His Thr Val Val Ser Thr Arg Ala Glu Ile Ala Lys Ala Leu Glu
 35 40 45
 Thr Ala Asp Val Val Ile Gly Ser Val Leu Ile Pro Gly Ser Ser Thr
 50 55 60
 Pro Lys Leu Val Thr Thr Asp Met Val Ala His Met Gln Pro Gly Ser
 65 70 75 80
 Val Leu Ile Asp Ile Ala Ile Asp Gln Gly Gly Cys Phe Glu Asp Ser
 85 90 95
 His Pro Thr Thr Tyr Asp Asp Pro Thr Phe Thr Val His
 100 105

<210> 135
 <211> 560
 <212> DNA
 <213> Homo sapiens

<400> 135
 taagatgtgg tcctgccctg ttcctgaagg ggctgcagct ctgatggaaa atacagggat
 60
 ttacactcag ggctacagcc acgggggggct gaggcccaag gctgcaatct cgggggaagg
 120
 ggaagtggc ttttcttggg ggattggaaa catcctcttg gaggcaaaga cttttcctgg
 180
 atcttacaga cttcccggga ttttttagatt agaattattgg gggcaaagga ggctgtcttg
 240
 ttttaaagca atgctacata gacacagtgg ggaagacctg gttcgacggc agataagcag
 300
 tgggtgatgg gcttgaggag gagagtcagg gcaaagtcta agactgagca gaaaggaatt
 360
 ccccatctc ccatggataa gtacgttcta gaacattctc tttgggtcta atactctgaa
 420
 atgacatctt gtcttcatgc tcgagagaga attacttcac tggctccact tggagtgcc
 480
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 540
 acttccaagt cccacgcgt
 560

<210> 136
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 136

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Met Trp Ser Cys Pro Val Pro Glu Gly Ala Ala Ala Leu Met Glu Asn
 1           5           10           15
Thr Gly Ile Tyr Thr Gln Gly Tyr Ser His Gly Gly Leu Arg Pro Lys
      20           25           30
Ala Ala Ile Ser Gly Glu Gly Glu Val Gly Phe Ser Trp Trp Ile Gly
      35           40           45
Asn Ile Leu Leu Glu Ala Lys Thr Phe Pro Gly Ser Tyr Arg Leu Pro
 50           55           60
Gly Ile Phe Arg Leu Glu Tyr Trp Gly Gln Arg Arg Leu Ser Cys Phe
65           70           75           80
Lys Ala Met Leu His Arg His Ser Gly Glu Asp Leu Val Arg Arg Gln
      85           90           95
Ile Ser Ser Gly
      100

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<210> 137

<211> 429

<212> DNA

<213> Homo sapiens

<400> 137

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accggttgga tggcctgcag gccaaagcgt tcctgcaaac tcagcaggcc ttcagcgcaa
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gaggcaaaca gctggtcgcg cacctgcttg aggtccaccg attgcgcatt gcccttgagc
120
aaggcgcgcc agttggtttt gtcggccact tggctgcgga acaggtcttc gacaaaaccg
180
gactgctggc gggtcgcaac gcgcatgatt ggcagcgctt ggctggcgcc ctggtcgagc
240
cagcgcgctg gcagttgggt ggcccgggtg ataccgacct tgatccccga cgaattggcc
300
aggtacacca catggtcggt catgcagaat gtttcgcccc agccgggatc acggcaagtg
360
ccggcgctgt aatggcaacg ttcggggctc atgatgcaca ggtcacactg ggccagcttg
420
gtcatgccc
429

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<210> 138

<211> 141

<212> PRT

<213> Homo sapiens

<400> 138

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Met Thr Lys Leu Ala Gln Cys Asp Leu Cys Ile Met Ser Pro Glu Arg
 1           5           10           15
Cys His Tyr Asp Ala Gly Thr Cys Arg Asp Pro Gly Trp Gly Glu Thr
      20           25           30
Phe Cys Met Thr Asp His Val Val Tyr Leu Ala Asn Ser Ser Gly Ile
      35           40           45
Lys Val Gly Ile Thr Arg Ala Thr Gln Leu Pro Thr Arg Trp Leu Asp
 50           55           60
Gln Gly Ala Ser Gln Ala Leu Pro Ile Met Arg Val Ala Thr Arg Gln

```

65		70		75		80									
Gln	Ser	Gly	Phe	Val	Glu	Asp	Leu	Phe	Arg	Ser	Gln	Val	Ala	Asp	Lys
			85						90					95	
Thr	Asn	Trp	Arg	Ala	Leu	Leu	Lys	Gly	Asp	Ala	Gln	Ser	Val	Asp	Leu
			100					105					110		
Lys	Gln	Val	Arg	Asp	Gln	Leu	Phe	Ala	Ser	Cys	Ala	Glu	Gly	Leu	Leu
		115				120						125			
Ser	Leu	Gln	Glu	Arg	Phe	Gly	Leu	Gln	Ala	Ile	Gln	Pro			
	130					135					140				

<210> 139
 <211> 341
 <212> DNA
 <213> Homo sapiens

<400> 139
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 ttgtgaacag cagaatcaag ccgctggtaa atcttcctgg gagcttcata ggcggggatg
 120
 ctacacgagc tggggagaca ctttgaaccc ggaattgtct gaataattct gtctcaaacc
 180
 tttgcagcct gtaacgactg agggttcgga tggaaaaaca catgctccag gatgggaccg
 240
 acggccactt caccgatctc ttcatagccc tggcgtttgt agaaatccag gtagcgcgaa
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 tcgccagcgt cgagcacgac gcctgatgag tgcgggtcat t
 341

<210> 140
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 140
Met Thr Arg Thr His Gln Ala Ser Cys Ser Thr Leu Ala Ile Arg Ala
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Thr Trp Ile Ser Thr Asn Ala Arg Ala Met Lys Arg Ser Val Lys Trp
20 25 30
Pro Ser Val Pro Ser Trp Ser Met Cys Phe Ser Ile Arg Thr Leu Ser
35 40 45
Arg Tyr Arg Leu Gln Arg Phe Glu Thr Glu Leu Phe Arg Gln Phe Arg
50 55 60
Val Gln Ser Val Ser Pro Ala Arg Val Ala Ser Pro Pro Met Lys Leu
65 70 75 80
Pro Gly Arg Phe Thr Ser Gly Leu Ile Leu Leu Phe Thr Ser Cys Gly
85 90 95
Ala Leu Ala Gln Ser Glu Leu Asp Val Arg Ile Lys Pro Ser Asn Asp
100 105 110
Ala

<210> 141
 <211> 324

<212> DNA

<213> Homo sapiens

<400> 141

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acctttactt actggtacat gaacaccatt tacattacag ctatcgtact caccctacgt
120
catgtgaaca gacacataac tgaaagggtt ataaaccaca gtctcacggt acgtatgacc
180
gtcaactgtg aacaccgcta agtaatagcc tgcgggggct tgcatagaact cctttgacca
240
tgcgtaataa atacgtccgt cattagtcac acctgatggg gcgaaacaaa aagaacggca
300
gcagttatca ccgcccatac gcgt
324

<210> 142

<211> 106

<212> PRT

<213> Homo sapiens

<400> 142

Met	Gly	Gly	Asp	Asn	Cys	Cys	Arg	Ser	Phe	Cys	Phe	Ala	Pro	Ser	Gly
1				5					10					15	
Val	Thr	Asn	Asp	Gly	Arg	Ile	Tyr	Tyr	Ala	Trp	Ser	Lys	Glu	Phe	Met
			20					25					30		
Gln	Ala	Pro	Ala	Gly	Tyr	Tyr	Leu	Ala	Val	Phe	Thr	Val	Asp	Gly	His
		35					40					45			
Thr	Tyr	Arg	Glu	Thr	Val	Val	Tyr	Lys	Pro	Phe	Ser	Tyr	Val	Ser	Val
	50					55					60				
His	Met	Thr	Trp	Gly	Glu	Tyr	Asp	Ser	Cys	Asn	Val	Asn	Gly	Val	His
65					70					75				80	
Val	Pro	Val	Ser	Lys	Gly	Cys	Gly	Cys	Ala	Pro	Asp	Ile	Cys	Cys	Thr
				85					90					95	
His	Leu	Pro	Glu	Ala	Ile	Gln	Glu	Glu	Phe						
			100					105							

<210> 143

<211> 1325

<212> DNA

<213> Homo sapiens

<400> 143

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gcaccccagg agaagaactt cctgtacaaa tgcataaggca ccaccctggg tgctgcttca
120
agtaaggagg tggtagaggaa gcaccttcaa gagctgctgg agacggccag ataccaggag
180
gaggcagaac gcgagggcct cgcctgctgc ttcgggatct gtgccatctc ccacctcgag
240
gacacgctgg cccagctgga ggacttcgtg aggtcagagg tcttcagaaa atccattggc
300

attctcaaca tttttaagga tcgaagtgag aacgaagtgg agaaggtgaa gaggctctg
 360
 atcctgtgct atgggcacgt ggcggcccgg gccccccggg agctggtgct ggccaaggta
 420
 gagtcagaca tcctccggaa catcntgcca gcacttcagc acnncaagga cccagccctg
 480
 aagctgtgcc ttgtccagag tgtgtgcatg gtcagccgag ccatctgcag cagcaccag
 540
 gctggctcct tccacttcac ccggaagca gaggctggtg cacagatgat ggagttcatc
 600
 agggcagagc ccccggaactc cttgaggaca cctattcgga agaaagccat gtcacctgc
 660
 acttacttgg tctccgtgga gccagcgctg gacgagcagg cccgggaggga tgtgatccat
 720
 ggctgcctgc acagcatcat ggccctgctg cctgagccca aggaggagga cggaggctgc
 780
 cagaagtccc tgtatctgga gacactgcac gcccttgagg atctgctgac gagcctcctg
 840
 cagcgggaaca tgacccccca aggcctgcag atcatgattg agcacctgag cccatggatc
 900
 aagtcccca gaggtcacgt agcggcgctg gccctaggcc tgagcgccct cctcgtgcgc
 960
 tacttcctgg agcacctgcg tgtcagtggc gcccaagtag ataccagggt tccatctgag
 1020
 cccaggatcc tgtgcaatgg cctggtgcc cttccacaac ctgggccttc tcacggcct
 1080
 cttctcccca cgggtgtgcgg acctgtggcc tgccaccgag caggaggccg tggactgtgt
 1140
 ctactccctg ctgtacctcc agctcggcta tgagggcttc tcccgggact accgcgatga
 1200
 cgtggcggag cggctcctca gcctcaagga cggcctcgtg caccctgacc ccgccattct
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 cttccacacc tgccacagtg taggccagat tattgccaag cgcctcccc cagcccttca
 1320
 cgcgt
 1325

<210> 144
 <211> 390
 <212> PRT
 <213> Homo sapiens

<400> 144
 Xaa Ala Trp Ile Cys Gln Leu Ser Leu Glu Leu Cys Arg Gln Leu Pro
 1 5 10 15
 Cys Tyr Asp Glu Ala Pro Gln Glu Lys Asn Phe Leu Tyr Lys Cys Ile
 20 25 30
 Gly Thr Thr Leu Gly Ala Ala Ser Ser Lys Glu Val Val Arg Lys His
 35 40 45
 Leu Gln Glu Leu Leu Glu Thr Ala Arg Tyr Gln Glu Glu Ala Glu Arg
 50 55 60
 Glu Gly Leu Ala Cys Cys Phe Gly Ile Cys Ala Ile Ser His Leu Glu
 65 70 75 80
 Asp Thr Leu Ala Gln Leu Glu Asp Phe Val Arg Ser Glu Val Phe Arg


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<210> 145
<211> 802
<212> DNA
<213> Homo sapiens
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494

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 360
 ggtcattgtg cgatcaagct gccgggggtct gtcagcgtgg tgaacccggt atgtactggg
 420
 gttcgggtgg ctctctggcc attctcggac tcattatcgg ggtcttgacg cagatctggc
 480
 tggagaagcg ctgggtggcac atgcttgcca tcgtcatccc ggctgttttc atcgtcgccg
 540
 gtatcttttt ctggctcgcc gtctaagaag gggcgtcaca gattccacaa acgacacagg
 600
 tattgatctc cgttttatcg gtccttagca gccgtgggtca acgtatcgct atcaagcgat
 660
 acaggactcg tcgttcgcat cgttgttggt ctgctgggaa acaatcccag cgatctactc
 720
 ggctaccgcc agacagttca ctcacaaccc ctcacgccgg cgcagacatc aaateccatt
 780
 ctcgatagac ggcccacacc ac
 802

<210> 146
 <211> 151
 <212> PRT
 <213> Homo sapiens

<400> 146
 Met Lys Val Tyr Ile Thr Leu Val Lys Ala Cys Thr Thr Ser Val Gly
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 Thr Ile Ser Pro Arg Arg Thr Arg His His Ala Pro Tyr Leu Asp Arg
 20 25 30
 Met Ser Asp Met Ser Met Pro Arg Arg Ala Ala Pro Glu Asp Asp Thr
 35 40 45
 Asp Leu Ala Asp Ala Ala Arg Ser Trp Arg Arg Tyr Leu Ile Leu Val
 50 55 60
 Ile Cys Gly Val Ile Val Ala Val Leu Gly Leu Gly Ile Phe Gly Tyr
 65 70 75 80
 Leu Ala Trp Trp Ser Leu Cys Asp Gln Ala Ala Gly Val Cys Gln Arg
 85 90 95
 Gly Glu Pro Val Met Tyr Trp Cys Ser Val Val Ser Leu Ala Ile Leu
 100 105 110
 Gly Leu Ile Ile Gly Val Leu Thr Gln Ile Trp Leu Glu Lys Arg Trp
 115 120 125
 Trp His Met Leu Ala Ile Val Ile Pro Ala Val Phe Ile Val Ala Gly
 130 135 140
 Ile Phe Phe Trp Leu Ala Val
 145 150

<210> 147
 <211> 368
 <212> DNA
 <213> Homo sapiens

<400> 147

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 ttacacagt gggcattagt agcccgcgat gttcatgaca ttcttgggtct acgaaaagtt
 120
 attggtcaga aagtaccttg tgttgccagt acgggggtcgg aaaaggtgct tcataaaaag
 180
 gattactggg atctagcaac acctatgcca attgcgtggg gtacaacgga ccgaacagtt
 240
 attgctgatg cacgacgtac aatccccacc acggagtggg atatccttgc aagactacgt
 300
 ccacgcctag aagaggttcg caagcaacgt aatgatgtat tgctcctcaa cgaggaggat
 360
 ccccccta
 368

<210> 148
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 148
 Met Thr Leu Leu Ala Leu Val Asp Leu Ser Lys Lys Pro Asp Glu Phe
 1 5 10 15
 Thr Gln Trp Ala Leu Val Ala Arg Asp Val His Asp Ile Pro Gly Leu
 20 25 30
 Arg Lys Val Ile Gly Gln Lys Val Pro Cys Val Ala Val Thr Gly Ser
 35 40 45
 Glu Lys Val Leu His Lys Lys Asp Tyr Trp Asp Leu Ala Thr Pro Met
 50 55 60
 Pro Ile Ala Trp Gly Thr Thr Asp Arg Thr Val Ile Ala Asp Ala Arg
 65 70 75 80
 Arg Thr Ile Pro Thr Thr Glu Trp Asp Ile Leu Ala Arg Leu Arg Pro
 85 90 95
 Arg Leu Glu Glu Val Arg Lys Gln Arg Asn Asp Val Leu Leu Leu Asn
 100 105 110
 Glu Glu Asp Pro Pro
 115

<210> 149
 <211> 407
 <212> DNA
 <213> Homo sapiens

<400> 149
 nngctagcat ggaccctagt cacacaggca gccatacccg aggtcaaagt gacccatttt
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 cctaatatgg ccgctcagat ccaatacttt gaagattcgt ccgtgggttat atggcacgat
 120
 gcggtggatg gtatcgtgta ccgaagtgcg gatgaaggca agtcgtgggc cccaattaag
 180
 gggcctgaac agggtcaggc gcaccttttc gtgctccatc cctacgacaa gactcaagcg
 240
 tatattctga cgcgcagcac tcagcattgg cgcacgtcga accgtggcga gacgtggcag
 300

tcattctcaa cgctcatcc gcctacgacc ttgaaagcta tgcctctgga ctttcatccg
360
acgcatcatg actggatcct tttcacgggc caggcttgca cggtaaa
407

<210> 150
<211> 135
<212> PRT
<213> Homo sapiens

<400> 150
Xaa Leu Ala Trp Thr Leu Val Thr Gln Ala Ala Ile Pro Glu Val Lys
1 5 10 15
Val Thr His Phe Pro Asn Met Ala Ala Gln Ile Gln Tyr Phe Glu Asp
20 25 30
Ser Ser Val Val Ile Trp His Asp Ala Val Asp Gly Ile Val Tyr Arg
35 40 45
Ser Ala Asp Glu Gly Lys Ser Trp Ala Pro Ile Lys Gly Pro Glu Gln
50 55 60
Gly Gln Ala His Leu Phe Val Leu His Pro Tyr Asp Lys Thr Gln Ala
65 70 75 80
Tyr Ile Leu Thr Arg Ser Thr Gln His Trp Arg Thr Ser Asn Arg Gly
85 90 95
Glu Thr Trp Gln Ser Phe Ser Thr Pro His Pro Pro Thr Thr Leu Lys
100 105 110
Ala Met Pro Leu Asp Phe His Pro Thr His His Asp Trp Ile Leu Phe
115 120 125
Thr Gly Gln Ala Cys Thr Val
130 135

<210> 151
<211> 448
<212> DNA
<213> Homo sapiens

<400> 151
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gcttttcgcg catccaggtc cccagcccca gctactgggtg cgccccgagc ccctaggtgc
120
cagagcgggtg gtcggccggg ctctgcccga gtctcggtc ctcctcctc cccaccagaa
180
ggaaaaactt gggcccttcg agaaccctgt ggaatgttct ttgtaatcaa ctgtacatcc
240
gcttcacagg cacggcctcg tgcaaaatcg cgggtttcgg ggccttggag caaattgcgc
300
ttgtcagcgg cgacgtcagg aggacaaggg gaggggttcg cggctgaaac tgcagcttcg
360
cagcacagag ccatttttagg ctgctcccca cctcgcgggg cccatgggaa gccggccccg
420
ggagggcgcg gctgcatgga tattcgac
448

<210> 152

<211> 149
 <212> PRT
 <213> Homo sapiens

<400> 152
 Thr Gly Val Arg Gly Tyr Cys Pro Glu Trp Ser Pro Ser Ala Ser Pro
 1 5 10 15
 Gly Thr Pro Ser Ala Phe Arg Ala Ser Arg Ser Pro Ala Pro Ala Thr
 20 25 30
 Gly Ala Pro Arg Ala Pro Arg Cys Gln Ser Gly Gly Arg Pro Gly Ser
 35 40 45
 Cys Pro Val Ser Ala Pro Pro Ser Ser Pro Pro Glu Gly Lys Thr Trp
 50 55 60
 Ala Leu Arg Glu Pro Cys Gly Met Phe Phe Val Ile Asn Cys Thr Ser
 65 70 75 80
 Ala Ser Thr Ala Arg Pro Arg Ala Lys Ser Arg Val Ser Gly Pro Trp
 85 90 95
 Ser Lys Leu Arg Leu Ser Ala Ala Thr Ser Gly Gly Gln Gly Glu Gly
 100 105 110
 Phe Ala Ala Glu Thr Ala Ala Ser Gln His Arg Ala Ile Leu Gly Cys
 115 120 125
 Ser Pro Pro Arg Gly Ala His Gly Lys Pro Ala Pro Gly Gly Arg Gly
 130 135 140
 Cys Met Asp Ile Arg
 145

<210> 153
 <211> 440
 <212> DNA
 <213> Homo sapiens

<400> 153
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 tgtccatggg tccatgtatg tgtgtgtata tgtgggggaa caggtgtgtg tccgagtgtg
 120
 tgcattgggtc cgtgtatatg cgtgtatatata tgcgggggata tgtatatgtg tgtgtgtatg
 180
 aacaggtgta agtgggggagc actcaggtgt gtctgtgtgt gtctgtgtac acgtgtgtaa
 240
 gtgggtgacc atgaaggggt gtgtgtgtcc gtgtgtaggt ttgcgtgcat gcacacatgc
 300
 atgtgtgtac tggggcatcc aagcccctgg tctccactcc attccaccct acgcctacct
 360
 ccttgatctc tgcgcccagc cttggctgtg ctcccctgct gtagtcacgt ggggtgtctgc
 420
 acgtgggtgt ctgcacgcgt
 440

<210> 154
 <211> 69
 <212> PRT
 <213> Homo sapiens

<400> 154

Gly Arg His Ala Gly Val Cys Pro Ser Val Cys Pro Trp Val His Val
 1 5 10 15
 Cys Val Cys Ile Cys Gly Gly Thr Gly Val Cys Pro Ser Val Cys Met
 20 25 30
 Gly Pro Cys Ile Cys Val Tyr Ile Cys Gly Asp Met Tyr Met Cys Val
 35 40 45
 Cys Met Asn Arg Cys Lys Trp Gly Ala Leu Arg Cys Val Cys Val Cys
 50 55 60
 Ser Cys Thr Arg Val
 65

<210> 155

<211> 344

<212> DNA

<213> Homo sapiens

<400> 155

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 gtgaacatgg ccgagttgat ggccgatgcc gcgaccggca cgaaaccgtc ctacctacag
 120
 cgatcttcct cctcgatcac ctcgtttgaa gtggacaggg aacaaagaca ctcagacaac
 180
 ggcgcgcagg aagtaaaaag ttcgctctcc gatcacggcc gtcgcgcgag tgcacaggga
 240
 gaactgggca cctcgcaagc tacgccaccg cgatccatgc ccccgcccgt atcttcggcc
 300
 tcctctacct ccccttacc gatcagcatt atatccgac taga
 344

<210> 156

<211> 92

<212> PRT

<213> Homo sapiens

<400> 156

Met Ala Glu Leu Met Ala Asp Ala Ala Thr Gly Thr Lys Pro Ser Tyr
 1 5 10 15
 Leu Gln Arg Ser Ser Ser Ile Thr Ser Phe Glu Val Asp Arg Glu
 20 25 30
 Gln Arg His Ser Asp Asn Ala Pro Gln Glu Val Lys Ser Ser Leu Ser
 35 40 45
 Asp His Gly Arg Arg Ala Ser Ala Gln Gly Glu Leu Gly Thr Ser Gln
 50 55 60
 Ala Thr Pro Pro Arg Ser Met Pro Pro Pro Val Ser Ser Ala Ser Ser
 65 70 75 80
 Thr Ser Pro Leu Pro Ile Ser Ile Ile Ser Asp Leu
 85 90

<210> 157

<211> 6816

<212> DNA

<213> Homo sapiens

<400> 157

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120
cttggcagca gacagtgaag tggaaatgga agaatggatc acaattctaa ataagatcct
180
ccagctcaac tttgaagctg caatgcaaga aaagcgaaat ggcgactctc acgaagatga
240
tgaacaaagc aaattggaag gttctgggtc cggttttagat agctacctgc cggaacttgc
300
caagagtga agagaagcag aaatcaaact gaaaagtga agcagagtca aactttttta
360
tttggacca gatgccaga agcttgactt ctcatcagct gagccagaag tgaagtcatt
420
tgaagagaag tttggaaaaa ggatccttgt caagtgaat gatttatctt tcaatttgca
480
atgctgtgtt gccgaaaatg aagaaggacc cactacaaat gttgaacctt tctttgttac
540
tctatccctg tttgacataa aatacaaccg gaagatttct gccgatttcc acgtagacct
600
gaaccatttc tcagtgaggc aaatgatcgc caccacgtcc ccggcgctga tgaatggcag
660
tgggccgaaa cccaatctgc cctcaggggc atccttcagc aagccgccat gcagtatccg
720
aagcagggaa tattttcagt cacttgctct catccagata tatttcttgt ggccagaatt
780
gaaaaagtcc ttcaggggag catcacacat tgcgctgagc catatatgaa aagttcagac
840
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cagtatagaa tgccatttgc ttgggcagca aggacattgt ttaaggatgc atctggaaat
960
cttgacaaaa atgccagatt ttctgccatc tacaggcaag acagcaataa gctatccaat
1020
gatgacatgc tcaagttact tgcagacttt cggaacctg agaagatggc taagctccca
1080
gtgatttttag gcaatctaga cattacaatt gataatgttt cctcagactt ccctaattat
1140
gttaattcat catacattcc caaaaacaa tttgaaacct gcagtaaaac tcccatcacg
1200
tttgaagtgg aggaatttgt gccctgcata ccaaaacaca ctacgcctta caccatctac
1260
accaatcacc tttacgttta tcctaagtac ttgaaatacg acagtcagaa gtcttttgcc
1320
aaggctagaa atattgcat ttgcattgaa ttcaaagatt cagatgagga agactctcag
1380
ccccttaagt gcatttatgg cagacctggt gggccagttt tcacaagaag cgcctttgct
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1500
actcagctgc atgaaaagca ccacctgttg ctacattct tccatgtcag ctgtgacaac
1560

tcaagtaaag gaagcacgaa gaagagggat gtcggtgaaa cccaagttgg ctactcctgg
1620
cttccccctcc tgaaagacgg aagggtggtg acaagcgagc agcacatccc ggtctcggcg
1680
aaccttcctt cgggctatct tggctaccag gagcttggga tgggcaggca ttatggtccg
1740
gaaattaaat gggtagatgg aggcaagcca ctgctgaaaa ttccactca tctggtttct
1800
acagtgtata ctcaggatca gcatttacat aattttttcc agtactgtca gaaaaccgaa
1860
tctggagccc aagccttagg aaacgaactt gtaaagtacc ttaagagtct gcatgcatg
1920
gaaggccacg tgatgatcgc cttcttgccc actatcctaa accagctgtt ccgagtcctc
1980
accagagcca cacaggaaga agtcgcggtt aacgtgactc gggtcattat tcatgtggtt
2040
gcccagtgcc atgaggaagg attggagagc cacttgaggt catatgttaa gtacgcgtat
2100
aaggctgagc catatgttgc ctctgaatac aagacagtgc atgaagaact gaccaaactc
2160
atgaccacga ttctcaagcc ttctgccgat ttcctcacca gcaacaaact actgaagtac
2220
tcatggtttt tctttgatgt actgatcaaa tctatggctc agcatttgat agagaactcc
2280
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2340
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<210> 158

<211> 1572

<212> PRT

<213> Homo sapiens

<400> 158

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			20					25					30		
Asp	Phe	Arg	Lys	Pro	Glu	Lys	Met	Ala	Lys	Leu	Pro	Val	Ile	Leu	Gly
		35					40					45			
Asn	Leu	Asp	Ile	Thr	Ile	Asp	Asn	Val	Ser	Ser	Asp	Phe	Pro	Asn	Tyr
	50					55					60				
Val	Asn	Ser	Ser	Tyr	Ile	Pro	Thr	Lys	Gln	Phe	Glu	Thr	Cys	Ser	Lys
65					70				75					80	
Thr	Pro	Ile	Thr	Phe	Glu	Val	Glu	Glu	Phe	Val	Pro	Cys	Ile	Pro	Lys
				85					90					95	
His	Thr	Gln	Pro	Tyr	Thr	Ile	Tyr	Thr	Asn	His	Leu	Tyr	Val	Tyr	Pro
			100					105					110		
Lys	Tyr	Leu	Lys	Tyr	Asp	Ser	Gln	Lys	Ser	Phe	Ala	Lys	Ala	Arg	Asn
		115					120					125			
Ile	Ala	Ile	Cys	Ile	Glu	Phe	Lys	Asp	Ser	Asp	Glu	Glu	Asp	Ser	Gln
	130					135					140				
Pro	Leu	Lys	Cys	Ile	Tyr	Gly	Arg	Pro	Gly	Gly	Pro	Val	Phe	Thr	Arg
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Ser	Ala	Phe	Ala	Ala	Val	Leu	His	His	His	Gln	Asn	Pro	Glu	Phe	Tyr
				165					170					175	
Asp	Glu	Ile	Lys	Ile	Glu	Leu	Pro	Thr	Gln	Leu	His	Glu	Lys	His	His
			180					185					190		
Leu	Leu	Leu	Thr	Phe	Phe	His	Val	Ser	Cys	Asp	Asn	Ser	Ser	Lys	Gly
		195					200					205			
Ser	Thr	Lys	Lys	Arg	Asp	Val	Val	Glu	Thr	Gln	Val	Gly	Tyr	Ser	Trp
	210					215					220				
Leu	Pro	Leu	Leu	Lys	Asp	Gly	Arg	Val	Val	Thr	Ser	Glu	Gln	His	Ile
225					230					235				240	
Pro	Val	Ser	Ala	Asn	Leu	Pro	Ser	Gly	Tyr	Leu	Gly	Tyr	Gln	Glu	Leu
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Gly	Met	Gly	Arg	His	Tyr	Gly	Pro	Glu	Ile	Lys	Trp	Val	Asp	Gly	Gly

505

690	695	700
Ser Thr Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser		
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Leu Ile Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu		720
	725	730
Lys Ser Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn		735
	740	745
Ser Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu		750
	755	760
Leu Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu		765
	770	775
Phe Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe		780
785	790	795
Thr Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg		800
	805	810
Tyr Ile Ala Arg Thr Gly Met Met His Ala Arg Leu Gln Gln Leu Gly		815
	820	825
Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His Ser Asp		830
	835	840
Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu		845
	850	855
Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe		860
865	870	875
Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys		880
	885	890
Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Thr		895
	900	905
Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe		910
	915	920
Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala Leu Cys		925
	930	935
Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr		940
945	950	955
Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr		960
	965	970
Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser		975
	980	985
Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe		990
	995	1000
Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu		1005
	1010	1015
Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg		1020
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Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn		1040
	1045	1050
Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr		1055
	1060	1065
Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg		1070
	1075	1080
Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val		1085
	1090	1095
His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Val		1100
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Gln Trp Glu Pro Pro Leu Leu Pro His Ser His Ser Ala Cys Leu Arg		1120

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1565

<210> 159
<211> 540
<212> DNA
<213> Homo sapiens

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<210> 160
<211> 110
<212> PRT
<213> Homo sapiens

<400> 160
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35 40 45
Trp Lys Ser Ser Gln Ser Met Arg Ser Met Glu Thr His Gly Ser Gly
50 55 60
Gly Gln Pro Gln Pro Lys Arg Thr Pro Ser Pro Ala Leu Cys Pro Arg
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Pro Gly His Gln Phe Ser Ser Met Thr Lys Lys Gly Ala Phe
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<210> 161
<211> 351
<212> DNA
<213> Homo sapiens

<400> 161

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<210> 162

<211> 117

<212> PRT

<213> Homo sapiens

<400> 162

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Phe	Ala	Gly	Arg	Arg	Ala	Trp	Leu	Ala	Ala	Thr	Met	Lys	Gly	Asp	Asp
			20					25					30		
Ser	Ser	Lys	Ile	Thr	His	Lys	Ile	Ala	Arg	Ala	Lys	Arg	Glu	Gly	Arg
		35					40					45			
Val	Trp	Trp	Ser	Phe	Glu	Tyr	Phe	Pro	Pro	Arg	Thr	Pro	Gln	Gly	Met
	50					55					60				
Gln	Asn	Leu	Tyr	Asp	Arg	Ile	Glu	Arg	Met	Ser	Gln	Leu	Gly	Pro	Glu
65					70				75					80	
Phe	Val	Asp	Ile	Thr	Trp	Asn	Ala	Gly	Gly	Arg	Thr	Ser	Asp	Met	Thr
			85					90					95		
Thr	Gln	Leu	Val	Lys	Thr	Val	His	Ala	Tyr	Phe	Gly	Val	Glu	Thr	Cys
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Met	His	Leu	Thr	Cys											
			115												

<210> 163

<211> 360

<212> DNA

<213> Homo sapiens

<400> 163

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 120
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 180
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 gccggtgtgc cggccggcgt gctcaacgtg gtgcacggcg gcaaggatgt ggtggatgcg
 300

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<210> 164

<211> 120

<212> PRT

<213> Homo sapiens

<400> 164

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Ala	Gly	Gly	Val	Asp	Thr	Tyr	Thr	Leu	Arg	Gln	Pro	Ile	Gly	Val	Cys
			20					25					30		
Ala	Gly	Ile	Thr	Pro	Phe	Asn	Phe	Pro	Ala	Met	Ile	Pro	Leu	Trp	Met
		35					40					45			
Phe	Pro	Met	Ala	Ile	Ala	Cys	Gly	Asn	Thr	Phe	Val	Leu	Lys	Pro	Ser
	50					55				60					
Glu	Gln	Asp	Pro	Leu	Ser	Thr	Met	Leu	Leu	Val	Glu	Leu	Ala	Leu	Glu
65				70					75					80	
Ala	Gly	Val	Pro	Ala	Gly	Val	Leu	Asn	Val	Val	His	Gly	Gly	Lys	Asp
			85					90					95		
Val	Val	Asp	Ala	Leu	Cys	Thr	His	Lys	Asp	Ile	Lys	Ala	Val	Ser	Phe
		100						105					110		
Val	Gly	Ser	Thr	Ala	Val	Gly	Thr								
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<210> 165

<211> 728

<212> DNA

<213> Homo sapiens

<400> 165

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720

ctacgcgt

728

<210> 166

<211> 242

<212> PRT

<213> Homo sapiens

<400> 166

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			20					25					30		
Arg	Ala	Arg	Gly	Asn	Ser	Phe	Thr	Lys	Phe	Gly	Asn	Arg	Asn	Val	Phe
		35					40				45				
Met	Lys	Asp	Asn	Ser	Ser	Ser	Ser	Ser	Thr	Asp	Ser	Arg	Ser	Arg	Ser
	50					55					60				
Ser	Ser	Arg	Ser	Pro	Thr	Arg	His	Phe	Arg	Arg	Ser	Asp	Ser	His	Ser
65					70				75					80	
Asp	Ser	Asp	Ser	Ser	Tyr	Ser	Gly	Asn	Glu	Cys	His	Pro	Val	Gly	Arg
				85				90						95	
Arg	Asn	Pro	Pro	Pro	Lys	Gly	Arg	Gly	Gly	Arg	Gly	Ala	His	Met	Asp
			100					105					110		
Arg	Gly	Arg	Gly	Arg	Ala	Gln	Arg	Gly	Lys	Arg	His	Asp	Leu	Ala	Pro
		115					120					125			
Thr	Lys	Arg	Ser	Arg	Lys	Lys	Met	Ala	Ala	Leu	Glu	Cys	Glu	Asp	Pro
		130				135						140			
Glu	Arg	Glu	Leu	Lys	Lys	Gln	Lys	Arg	Ala	Ala	Arg	Phe	Gln	His	Gly
145					150				155						160
His	Ser	Arg	Arg	Leu	Arg	Leu	Glu	Pro	Leu	Val	Leu	Gln	Met	Ser	Ser
				165				170						175	
Leu	Glu	Ser	Ser	Gly	Ala	Asp	Pro	Asp	Trp	Gln	Glu	Leu	Gln	Ile	Val
			180					185					190		
Gly	Thr	Cys	Pro	Asp	Ile	Thr	Lys	His	Tyr	Leu	Arg	Leu	Thr	Cys	Ala
		195					200					205			
Pro	Asp	Pro	Ser	Thr	Val	Arg	Pro	Val	Ala	Phe	Pro	Val	Ala	Gly	Phe
	210					215					220				
Glu	Lys	Val	Ala	Val	His	Gly	Gln	Val	Pro	Leu	Glu	Arg	Glu	Ala	Gly
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Leu	Arg														

<210> 167

<211> 510

<212> DNA

<213> Homo sapiens

<400> 167

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120

tgggtgagggg caggtggctc ccgccaggcg cctgctggcc tgaccgcact ccgtccacag
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 300
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Ala	Thr	Ala	Gly	Pro	Arg	Ala	Gly	Ala	Gln	Asp	Ala	Leu	Pro	Arg	Ser

521

545					550					555				560
Asp	Lys	Tyr	Ser	Asn	Lys	Asp	Cys	Pro	Asp	Ser	Ala	Glu	Glu	Tyr
				565					570					575
Arg	Ala	Thr	Arg	Tyr	Asn	Tyr	Thr	Ser	Glu	Glu	Lys	Phe	Ala	Leu
			580					585					590	
Glu	Val	Ile	Ala	Met	Ile	Lys	Gly	Leu	Gln	Val	Leu	Met	Gly	Arg
		595					600				605			
Glu	Ser	Val	Phe	Asn	His	Ala	Ile	Arg	His	Thr	Val	Tyr	Ala	Ala
	610					615					620			
Gln	Asp	Phe	Ser	Gln	Val	Thr	Leu	Arg	Glu	Pro	Leu	Arg	Gln	Ala
625					630				635					640
Lys	Lys	Lys	Lys	Asn	Val	Ile	Gln	Ser	Val	Leu	Gln	Ala	Ile	Arg
				645				650					655	
Thr	Val	Cys	Asp	Trp	Glu	Thr	Gly	His	Glu	Pro	Phe	Asn	Asp	Pro
		660					665					670		
Leu	Arg	Gly	Glu	Lys	Asp	Pro	Lys	Ser	Gly	Phe	Asp	Ile	Lys	Val
	675					680					685			
Arg	Arg	Ala	Val	Gly	Pro	Ser	Ser	Thr	Gln	Leu	Tyr	Met	Val	Arg
	690				695						700			
Met	Leu	Glu	Ser	Leu	Ile	Ala	Asp	Lys	Ser	Gly	Ser	Lys	Lys	Thr
705				710					715					720
Arg	Ser	Ser	Leu	Glu	Gly	Pro	Thr	Ile	Leu	Asp	Ile	Glu	Lys	Phe
			725					730					735	
Arg	Glu	Ser	Phe	Phe	Tyr	Thr	His	Leu	Ile	Asn	Phe	Ser	Glu	Thr
		740					745					750		
Gln	Gln	Cys	Cys	Asp	Leu	Ser	Gln	Leu	Trp	Phe	Arg	Glu	Phe	Phe
	755					760					765			
Glu	Leu	Thr	Met	Gly	Arg	Arg	Ile	Gln	Phe	Pro	Ile	Glu	Met	Ser
	770					775					780			
Pro	Trp	Ile	Leu	Thr	Asp	His	Ile	Leu	Glu	Thr	Lys	Glu	Ala	Ser
785				790						795				800
Met	Glu	Tyr	Val	Leu	Tyr	Ser	Leu	Asp	Leu	Tyr	Asn	Asp	Ser	Ala
			805					810					815	
Tyr	Ala	Leu	Thr	Arg	Phe	Asn	Lys	Gln	Phe	Leu	Tyr	Asp	Glu	Ile
		820					825					830		
Ala	Glu	Val	Asn	Leu	Cys	Phe	Asp	Gln	Phe	Val	Tyr	Lys	Leu	Ala
	835					840					845			
Gln	Ile	Phe	Ala	Tyr	Tyr	Lys	Val	Met	Ala	Gly	Ser	Leu	Leu	Leu
	850					855				860				
Lys	Arg	Leu	Arg	Ser	Glu	Cys	Lys	Asn	Gln	Gly	Ala	Thr	Ile	His
865				870					875					880
Pro	Pro	Ser	Asn	Arg	Tyr	Glu	Thr	Leu	Leu	Lys	Gln	Arg	His	Val
			885					890					895	
Leu	Leu	Gly	Arg	Ser	Ile	Asp	Leu	Asn	Arg	Leu	Ile	Thr	Gln	Arg
		900					905					910		
Ser	Ala	Ala	Met	Tyr	Lys	Ser	Leu	Glu	Leu	Ala	Ile	Gly	Arg	Phe
	915					920					925			
Ser	Glu	Asp	Leu	Thr	Ser	Ile	Val	Glu	Leu	Asp	Gly	Leu	Leu	Glu
	930				935					940				
Asn	Arg	Met	Thr	His	Lys	Leu	Leu	Ser	Arg	Tyr	Leu	Thr	Leu	Asp
945				950					955					960
Phe	Asp	Ala	Met	Phe	Arg	Glu	Ala	Asn	His	Asn	Val	Ser	Ala	Pro
			965					970					975	
Gly	Arg	Ile	Thr	Leu	His	Val	Phe	Trp	Glu	Leu	Asn	Tyr	Asp	Phe

523

<210> 177
 <211> 417
 <212> DNA
 <213> Homo sapiens

<400> 177
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 gcagttcgtg gcgcgcatag tttctggcat gcttcgcgca tcctggagac cgatcccgcc
 120
 gctgccgtga aaccgcctaa aaatgtgaag cgattgccca aagccgtgtc cgtggagcaa
 180
 atgcaaaagc tccttgccat acccagtctt aagactccta ccggcctgcg taatcgagcg
 240
 atacttgagt tcttatatgc taccggcgcg cgctgagcg agatgctggc aacagacctg
 300
 gacgatatac acctgggcga aaaaccccgcg gatgaaaacg gggaatctat tgcacttccc
 360
 gggatatgtgc gcctttttgg aaagggaggt aaagagcggt tagtcccttt gggatcc
 417

<210> 178
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 178
 Thr Arg Asp Val Thr Leu Pro Leu Pro Leu Gly Pro Asn Ser Ile Ala
 1 5 10 15
 Arg Thr Met Ala Ala Val Arg Gly Ala His Ser Phe Trp His Ala Ser
 20 25 30
 Arg Ile Leu Glu Thr Asp Pro Ala Ala Val Lys Pro Pro Lys Asn
 35 40 45
 Val Lys Arg Leu Pro Lys Ala Val Ser Val Glu Gln Met Gln Lys Leu
 50 55 60
 Leu Ala Ile Pro Ser Leu Lys Thr Pro Thr Gly Leu Arg Asn Arg Ala
 65 70 75 80
 Ile Leu Glu Phe Leu Tyr Ala Thr Gly Ala Arg Val Ser Glu Met Leu
 85 90 95
 Ala Thr Asp Leu Asp Asp Ile His Leu Gly Glu Lys Pro Arg Asp Glu
 100 105 110
 Asn Gly Glu Ser Ile Ala Leu Pro Gly Tyr Val Arg Leu Phe Gly Lys
 115 120 125
 Gly Gly Lys Glu Arg Leu Val Pro Leu Gly Ser
 130 135

<210> 179
 <211> 362
 <212> DNA
 <213> Homo sapiens

<400> 179
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 60

aggtgattgc ccgtgggttg atggtggaag atccccgcatc cccaagaatc cgggaattcg
 120
 ccattggggcc gggcagccccg aatccaaaat gtcggggcac gccagtgagg agtatggtaa
 180
 ggggcccggca ccgatgttgg nggcagcata cggatggaag tgctgggcga gcgcctgggt
 240
 ttgccggcag agcaactggg gcagctcaag gcgggcgggg tgatcgagca gttggattga
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 gcaatggcgg ccgcgaagcc cgccatttac cttgatgact gtttagcgcg cggattcttt
 360
 aa
 362

<210> 180
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 180
 Met Ala Gly Phe Ala Ala Ala Ile Ala Gln Ser Asn Cys Ser Ile Thr
 1 5 10 15
 Pro Pro Ala Leu Ser Cys Pro Ser Cys Ser Ala Gly Lys Pro Arg Arg
 20 25 30
 Ser Pro Ser Thr Ser Ile Arg Met Leu Pro Pro Thr Ser Val Pro Ala
 35 40 45
 Pro Tyr His Thr Pro Thr Gly Arg Ala Pro Thr Phe Trp Ile Arg Ala
 50 55 60
 Ala Arg Pro Asn Gly Glu Phe Pro Asp Ser Trp Gly Cys Gly Ile Phe
 65 70 75 80
 His His Gln Pro Thr Gly Asn His Leu Arg Leu Phe Gln Gly Leu Arg
 85 90 95
 Asp Val Ile Asp Arg Pro His Arg His Leu Arg Arg
 100 105

<210> 181
 <211> 297
 <212> DNA
 <213> Homo sapiens

<400> 181
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 60
 ccgattcact tgctcggtaca ggccaatacg gtgaattggg ccagcgtcga gttctggcaa
 120
 cagcaaggta tctgccgggt aatcctgtcg cgggaattgt cactggaaga aatcggcgaa
 180
 atccgccaac aggtgccggc catggagctg gaagtgtttg tgcacggtgc cctgtacatg
 240
 gcctattccg ggcgctgttt gttgtccggc tatatgaaca agcgcgatgc caaccaa
 297

<210> 182
 <211> 99
 <212> PRT

<213> Homo sapiens

<400> 182

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Ala Leu Ile Met Ser Asp Pro Gly Leu Ile Met Leu Val Arg Arg His
 1             5             10             15
Phe Pro Cys Met Pro Ile His Leu Ser Val Gln Ala Asn Thr Val Asn
      20             25             30
Trp Ala Ser Val Glu Phe Trp Gln Gln Gln Gly Ile Cys Arg Val Ile
      35             40             45
Leu Ser Arg Glu Leu Ser Leu Glu Glu Ile Gly Glu Ile Arg Gln Gln
      50             55             60
Val Pro Ala Met Glu Leu Glu Val Phe Val His Gly Ala Leu Tyr Met
65             70             75             80
Ala Tyr Ser Gly Arg Cys Leu Leu Ser Gly Tyr Met Asn Lys Arg Asp
      85             90             95
Ala Asn Gln

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<210> 183

<211> 351

<212> DNA

<213> Homo sapiens

<400> 183

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cgggacgtca ccatgaagcc gaccggctcg ggggatgtgg cgaacaaggt catcacccat
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attccgttta acatcgtctc ccaggcgact catccattcc ttcgtacctt ggacgatgtc
120
aagcgcattc ctttggcgac cgacgggctc ggccaccagg tcctgctcaa gggctaccag
180
gccgagggcc acgactacgc acaccccgac tacggcggca acgtctccca ccgtgccggc
240
gggatgaagg atctcgagaa gctcaccgag tcgggcaggc agtggaacac cgatttcggc
300
attcacgtca acctggtgga gtcctatcct gaggcgaatc acttcggcga c
351

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<210> 184

<211> 117

<212> PRT

<213> Homo sapiens

<400> 184

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Arg Asp Val Thr Met Lys Pro Thr Gly Ser Gly Asp Val Ala Asn Lys
 1             5             10             15
Val Ile Thr His Ile Pro Phe Asn Ile Val Ser Gln Ala Thr His Pro
      20             25             30
Phe Leu Arg Thr Leu Asp Asp Val Lys Arg Ile Ser Leu Ala Thr Asp
      35             40             45
Gly Leu Gly His Gln Val Leu Leu Lys Gly Tyr Gln Ala Glu Gly His
      50             55             60
Asp Tyr Ala His Pro Asp Tyr Gly Gly Asn Val Ser His Arg Ala Gly
65             70             75             80
Gly Met Lys Asp Leu Glu Lys Leu Thr Glu Ser Gly Arg Gln Trp Asn

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	85		90		95
Thr Asp Phe Gly Ile His Val Asn Leu Val Glu Ser Tyr Pro Glu Ala					
	100		105		110
Asn His Phe Gly Asp					
	115				

<210> 185
 <211> 396
 <212> DNA
 <213> Homo sapiens

<400> 185
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 gctgttggtg gcattgtggt ttatgcaggc catgaaacca aagcaatgct gaacaacagt
 120
 gggccacggt ataagcgcag caaattagaa agaagagcaa acacagatgt cctctggtgt
 180
 gtcattgcttc tggtcataat gtgcttaact ggcgtagtag gtcattggaat ctggctgagc
 240
 aggtatgaaa agatgcattt tttcaatggt cccgagcctg atggacatat catatcacca
 300
 ctgttggcag gattttatat gttttggacc gtgatcattt tgttacaggt cttgattcct
 360
 atttctctct atgtttccat cgaaattgtg aagctt
 396

<210> 186
 <211> 132
 <212> PRT
 <213> Homo sapiens

<400> 186
 Arg Val Gly Leu Ser Lys Glu Asn Leu Leu Leu Arg Gly Cys Thr Ile
 1 5 10 15
 Arg Asn Thr Glu Ala Val Val Gly Ile Val Val Tyr Ala Gly His Glu
 20 25 30
 Thr Lys Ala Met Leu Asn Asn Ser Gly Pro Arg Tyr Lys Arg Ser Lys
 35 40 45
 Leu Glu Arg Arg Ala Asn Thr Asp Val Leu Trp Cys Val Met Leu Leu
 50 55 60
 Val Ile Met Cys Leu Thr Gly Ala Val Gly His Gly Ile Trp Leu Ser
 65 70 75 80
 Arg Tyr Glu Lys Met His Phe Phe Asn Val Pro Glu Pro Asp Gly His
 85 90 95
 Ile Ile Ser Pro Leu Leu Ala Gly Phe Tyr Met Phe Trp Thr Val Ile
 100 105 110
 Ile Leu Leu Gln Val Leu Ile Pro Ile Ser Leu Tyr Val Ser Ile Glu
 115 120 125
 Ile Val Lys Leu
 130

<210> 187
 <211> 423

<212> DNA

<213> Homo sapiens

<400> 187

cgagtgtca ccgcgtcagc cgtcatgcgt cccactgagg ctgttgtctc tcggtcggca
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gaacctcgac gagttcagcg gatcctggac cagcgcgagt gggctggcgt cttegttgtc
120
gatgagcatc gtcgtttgct tggcacggtc ggcgatcaag aggtcatcga ggctgctcgc
180
cgcgagatc gcagtattgc tgacgcggtg gaaactaacg gcatcctcac ggcgcgagacc
240
gacactccgt tgtccgagct cttegtctccg accagcaacg ccagggtgcc gttggccggt
300
gtcgacgagg acttccacct catgggtgtc atctctcggg tgaccctgct cgacgcgatg
360
tcacgagctc gcgacgaggc aggagagggg tctgtcatgt ccttggagaa caccggaaag
420
ctt
423

<210> 188

<211> 141

<212> PRT

<213> Homo sapiens

<400> 188

Arg	Val	Leu	Thr	Ala	Ser	Ala	Val	Met	Arg	Pro	Thr	Glu	Ala	Val	Val
1				5				10					15		
Ser	Arg	Ser	Ala	Glu	Pro	Arg	Arg	Val	Gln	Arg	Ile	Leu	Asp	Gln	Arg
		20					25					30			
Glu	Trp	Ala	Gly	Val	Phe	Val	Val	Asp	Glu	His	Arg	Arg	Leu	Leu	Gly
	35					40					45				
Thr	Val	Gly	Asp	Gln	Glu	Val	Ile	Glu	Ala	Ala	Arg	Arg	Gly	Asp	Arg
	50				55				60						
Ser	Ile	Ala	Asp	Ala	Val	Glu	Thr	Asn	Gly	Ile	Leu	Thr	Ala	Arg	Thr
65				70				75					80		
Asp	Thr	Pro	Leu	Ser	Glu	Leu	Phe	Ala	Pro	Thr	Ser	Asn	Ala	Arg	Val
			85				90						95		
Pro	Leu	Ala	Val	Val	Asp	Glu	Asp	Phe	His	Leu	Met	Gly	Val	Ile	Ser
		100					105					110			
Arg	Val	Thr	Leu	Leu	Asp	Ala	Met	Ser	Arg	Ala	Arg	Asp	Glu	Ala	Gly
	115					120						125			
Glu	Gly	Ser	Val	Met	Ser	Leu	Glu	Asn	Thr	Gly	Lys	Leu			
	130					135					140				

<210> 189

<211> 429

<212> DNA

<213> Homo sapiens

<400> 189

ngatggttta ccaacatatg cacgggttcga gcggcaatag ctctcgggg gctggcagtg
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aaatgtttga agatgccggc gtttccggcc tcaacttgtt tcgatgccgt ggttccaccg
 120
 atttcgccga tgcggctcat cgcacgggta agaagtttcg tccagataac ccaggacaga
 180
 gcaaggtata tcaggctcag aaccaggaaa agcaggggctt taccccagtg ccccatatag
 240
 accgcgctag ctacggcaaa aggcgcgccc agtgggggtcc aggacagcac tttcatggct
 300
 gaagggagcg catcccnagc ttcgcctagc cccagagcta acccagcgac cagtggacca
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 420
 ctgatttcn
 429

<210> 190
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 190
 Met Met Gly Ala Gly Pro Leu Val Ala Gly Leu Ala Leu Gly Leu Gly
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 Glu Ala Xaa Asp Ala Leu Pro Ser Ala Met Lys Val Leu Ser Trp Thr
 20 25 30
 Pro Leu Gly Ala Pro Phe Ala Val Ala Ser Ala Val Tyr Met Gly His
 35 40 45
 Trp Gly Lys Ala Leu Leu Phe Leu Val Leu Ser Leu Ile Tyr Leu Ala
 50 55 60
 Leu Ser Trp Val Ile Trp Thr Lys Leu Leu Asn Arg Ala Met Ser Arg
 65 70 75 80
 Ile Gly Glu Ile Gly Gly Thr Thr Ala Ser Lys Gln Val Glu Ala Gly
 85 90 95
 Asn Ala Gly Ile Phe Lys His Phe Thr Ala Ser Pro Arg Gly Ala Ile
 100 105 110
 Ala Ala Arg Thr Val His Met Leu Val Asn His
 115 120

<210> 191
 <211> 4845
 <212> DNA
 <213> Homo sapiens

<400> 191
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 cctccggctt ctgcctccgg ccaggagttc tggcccggac aatcggcggc cgatattctg
 120
 tcgggggagg cttcccgcag acggtatctt ctgtatgacg tcaaccccc ggaaggcttc
 180
 aacctgcgca gggatgtcta tatccgaatc gcctctctcc tgaagactct gctgaagacg
 240
 gaggagtggg tgcttgctct gcctccatgg ggccgcctct atcactggca gagtccctgac
 300

atccaccagg tccggattcc ctggtctgag ttttttgatc ttccaagtct caataaaaac
360
atccccgtca tcgagtatga gcagttcatc gcagaatctg gtgggccctt tattgaccag
420
gtttacgtcc tgcaaagtta cgcagagggg tggaaagaag ggacctggga agagaagggtg
480
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540
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660
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720
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1920

gcgtgcgtct ctgtgggtta gtctgtctct ctctgcccc aggaatgctg agcgccctga
1980
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2340
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2400
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3180
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 4260
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 4320
 gaaggtgcag cagtgcctca ggggtcctca gggtcaggga gccccctca ccctcttggc
 4380
 ccgttaccct ttgtgacttt ccaccatggt gtcgtgtgac cctcagtcag gttggtggg
 4440
 gctgagtcct cactgagcag ccactttcca catctgctag aggaacagt acatggacac
 4500
 ctgtgacaga gagaggacag ttagtgagga gggacagaca gctcttcctt tcggagcctg
 4560
 gctagtctag gacatcacct tgctgtgtct tctcaagctt ttaaaattga ccctgaacgt
 4620 cctatggtgt tactcaaagc tgtgcagggt aaatgatgac atatttatc 4680
 tttttccatt tgttctagaa acagtgcctt tttcatcagt tgcattttcc aggtgagag
 4740
 ctgtataaaa cattttggac tgtgaccatg taccttcctt ttaagaaaa ataaactgct
 4800
 ttatggaagt tggtaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa
 4845

<210> 192

<211> 428

<212> PRT

<213> Homo sapiens

<400> 192

Pro Pro Gly Ala Met Ala Thr Leu Ser Phe Val Phe Leu Leu Leu Gly
 1 5 10 15
 Ala Val Ser Trp Pro Pro Ala Ser Ala Ser Gly Gln Glu Phe Trp Pro
 20 25 30
 Gly Gln Ser Ala Ala Asp Ile Leu Ser Gly Ala Ala Ser Arg Arg Arg

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<210> 193
<211> 350
<212> DNA
<213> Homo sapiens
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<400> 193

gccggcgagc tggactgcg catcatggcc gagcccttcc ccgacaccgg cctggccacg
60
gcgcagctgt acgacgagcc cttcgtcgtc gcgctgcggg cgtcgacccc gctggccgac
120
cgtgccagca tcagccccga ggaggtcaag ggcgagacca tggtgatgtt gggcacgggc
180
ccctgggtttc cccgggccccg cgggtgggggt ttggcccga tttggcgct ttctccagcg
240
ccgttaaggg catacgccgc agtttcgagg gtcgtcgct ggagaccatc aagcacatcg
300
tggtttcggg catggcggtga cgggtgggtgcc gcagctgtcc gtgccgcgcg
350

<210> 194

<211> 116

<212> PRT

<213> Homo sapiens

<400> 194

Ala	Gly	Glu	Leu	Asp	Cys	Ala	Ile	Met	Ala	Glu	Pro	Phe	Pro	Asp	Thr
1				5				10						15	
Gly	Leu	Ala	Thr	Ala	Gln	Leu	Tyr	Asp	Glu	Pro	Phe	Val	Val	Ala	Leu
			20					25						30	
Arg	Ala	Ser	His	Pro	Leu	Ala	Asp	Arg	Ala	Ser	Ile	Ser	Pro	Glu	Glu
		35					40					45			
Val	Lys	Gly	Glu	Thr	Met	Leu	Met	Leu	Gly	Thr	Gly	Pro	Trp	Phe	Pro
	50					55					60				
Arg	Ala	Arg	Gly	Gly	Gly	Leu	Ala	Arg	Ile	Trp	Arg	Val	Ser	Pro	Ala
65					70					75				80	
Pro	Leu	Arg	Ala	Tyr	Ala	Ala	Val	Ser	Arg	Ala	Arg	Arg	Trp	Arg	Pro
				85					90					95	
Ser	Ser	Thr	Ser	Trp	Leu	Arg	Ala	Trp	Arg	Asp	Gly	Gly	Ala	Ala	Ala
			100					105					110		
Val	Arg	Ala	Ala												
			115												

<210> 195

<211> 495

<212> DNA

<213> Homo sapiens

<400> 195

acgcgtgaac gcgacggctt ggcgatcgga ggcgtcggcc ccgtcggtga gtgggcccgtt
60
gaaatgggttc gcttcgacga aagcgagact ctcgaccgcc ttgcatcggg cgtccttgaa
120
ccagaacttg gcgacgattt ggccgccgtc ctgctcgatt ctcacgggt tgctgtcatc
180
agcgagggat cgaactggct tgcctcgcta cccgtgatcg taggtcgcaa cacggaacag
240
tttcgcagca taccagacct tgcccgcgac cggatcgaca aactgcacca gttgagccat
300

cgcgaaatag cacgaaatcg cgagctcctg cgtgcccgcg ctgcgtcggg gcaggtgcgg
 360
 cactgccacg gcgacgcaca cctcggcaac atcgatcatga ttgacggcaa gccggtcctg
 420
 ttcgacgcga tcgaatttga tctgatatac gcgacaacgg atgtgctgta cgatttcgcg
 480
 ttccctctga tggat
 495

<210> 196
 <211> 165
 <212> PRT
 <213> Homo sapiens

<400> 196
 Thr Arg Glu Arg Asp Gly Leu Ala Ile Gly Gly Val Gly Pro Val Val
 1 5 10 15
 Glu Trp Ala Val Glu Met Val Arg Phe Asp Glu Ser Glu Thr Leu Asp
 20 25 30
 Arg Leu Ala Ser Gly Val Leu Glu Pro Glu Leu Gly Asp Asp Leu Ala
 35 40 45
 Ala Val Leu Leu Asp Ser His Arg Val Ala Val Ile Ser Glu Gly Ser
 50 55 60
 Asn Trp Leu Ala Ser Leu Pro Val Ile Val Gly Arg Asn Thr Glu Gln
 65 70 75 80
 Phe Arg Ser Ile Pro Asp Leu Ala Arg Asp Arg Ile Asp Lys Leu His
 85 90 95
 Gln Leu Ser His Arg Glu Ile Ala Arg Asn Arg Glu Leu Leu Arg Ala
 100 105 110
 Arg Ala Ala Ser Gly Gln Val Arg His Cys His Gly Asp Ala His Leu
 115 120 125
 Gly Asn Ile Val Met Ile Asp Gly Lys Pro Val Leu Phe Asp Ala Ile
 130 135 140
 Glu Phe Asp Pro Asp Ile Ala Thr Thr Asp Val Leu Tyr Asp Phe Ala
 145 150 155 160
 Phe Pro Leu Met Asp
 165

<210> 197
 <211> 402
 <212> DNA
 <213> Homo sapiens

<400> 197
 caagcaatgc ttgacgcagt tggtgaatac ttaccagcac cgactgatata tccagcaatc
 60
 aaaggtatca atccagatga aactgaaggc gaacgtcacg caagcgatga tgagccattc
 120
 tcttcattag cattcaaaat tgcaactgac ccattcgtag gtaacttaac cttcttccgt
 180
 gtgtactcag gtgtaattaa ctctggtgat acagtattaa actctgtacg tcaaaaacgt
 240
 gaacgttttg gtcgtatcgt acagatgcac gctaataaac gtgaagaaat taaagaagtt
 300

cgtgcgggcg atatcgctgc agcaatcggc ttaaaagatg taactacggg tgaaccatta
360

tgtgctgtcg atgcaccaat cattcttgag cgtatggaat tc
402

<210> 198

<211> 134

<212> PRT

<213> Homo sapiens

<400> 198

Gln	Ala	Met	Leu	Asp	Ala	Val	Val	Glu	Tyr	Leu	Pro	Ala	Pro	Thr	Asp
1				5				10						15	
Ile	Pro	Ala	Ile	Lys	Gly	Ile	Asn	Pro	Asp	Glu	Thr	Glu	Gly	Glu	Arg
			20					25					30		
His	Ala	Ser	Asp	Asp	Glu	Pro	Phe	Ser	Ser	Leu	Ala	Phe	Lys	Ile	Ala
		35					40					45			
Thr	Asp	Pro	Phe	Val	Gly	Asn	Leu	Thr	Phe	Phe	Arg	Val	Tyr	Ser	Gly
	50					55					60				
Val	Ile	Asn	Ser	Gly	Asp	Thr	Val	Leu	Asn	Ser	Val	Arg	Gln	Lys	Arg
65				70					75					80	
Glu	Arg	Phe	Gly	Arg	Ile	Val	Gln	Met	His	Ala	Asn	Lys	Arg	Glu	Glu
			85						90				95		
Ile	Lys	Glu	Val	Arg	Ala	Gly	Asp	Ile	Ala	Ala	Ala	Ile	Gly	Leu	Lys
			100					105					110		
Asp	Val	Thr	Thr	Gly	Glu	Pro	Leu	Cys	Ala	Val	Asp	Ala	Pro	Ile	Ile
		115					120					125			
Leu	Glu	Arg	Met	Glu	Phe										
															130

<210> 199

<211> 507

<212> DNA

<213> Homo sapiens

<400> 199

acgcgtgaag tcgtgcatag atcgggtgtga catagagaag cctccgaccc aagctgcgta
60
tatacgacaa agaccaagcg accctggacg ttctagacag aactctgcta cgaggcctga
120
caatagtga atccccgaga acccagctat ggaagggttt ccagatgctc gaaggcctgt
180
cataccagag gttagggttaa actgtatgga gactttcgag gtgaaagttg actcgccggt
240
aaagcctgct cctaaagagg atttagatct gatagatcta tcctcagatt caacctcggg
300
gcctgaaaaa cactctatac tctcaacctc cgacagcgac tctcttgat ttgagcctct
360
tccctctctc agaatagtcg agagtgcga agaagaggag acgatgaacc aaggcgatga
420
cgccccctcc ggtaaaaatg ctgcctcttc tccctccatc cccagccatc cctccgtcct
480
cagcctgagc acagctccgc ttgtaca
507

<210> 200
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 200
 Met Glu Gly Glu Glu Ala Ala Phe Leu Pro Glu Gly Pro Ser Ser Pro
 1 5 10 15
 Trp Phe Ile Val Ser Ser Ser Ser Ser Leu Ser Thr Ile Leu Arg Glu
 20 25 30
 Gly Arg Gly Ser Asn Thr Arg Glu Ser Leu Ser Glu Val Glu Ser Ile
 35 40 45
 Glu Cys Phe Ser Gly Pro Glu Val Glu Ser Glu Asp Arg Ser Ile Arg
 50 55 60
 Ser Lys Ser Ser Leu Gly Ala Gly Phe Thr Gly Glu Ser Thr Phe Thr
 65 70 75 80
 Ser Lys Val Ser Ile Gln Phe Asn Leu Thr Ser Gly Met Thr Gly Leu
 85 90 95
 Arg Ala Ser Gly Asn Pro Ser Ile Ala Gly Phe Ser Gly Ile Ser Leu
 100 105 110
 Leu Ser Gly Leu Val Ala Glu Phe Cys Leu Glu Arg Pro Gly Ser Leu
 115 120 125
 Gly Leu Cys Ala Ile Tyr Ala Ala Trp Val Gly Gly Phe Ser Met Ser
 130 135 140
 His Arg Ser Met His Asp Phe Thr Arg
 145 150

<210> 201
 <211> 527
 <212> DNA
 <213> Homo sapiens

<400> 201
 gatgtggcta ttatccctgt ttcccaggtg agaaacaggg tcagtgatag agctgggatg
 60
 tgtgcctgca ggctcaccag ccagtcacct cctcaccaag gatgatgttc tccgtggtga
 120
 gctggtcctt ggtctcctgg aactcgtggc gcacctgggc cagctgcgcc tcgaaggcat
 180
 ccttctccat ctctttggct agctgcaagt tctggagctg ctcgttgagg tctgtgatct
 240
 catccacctg ctggttgagc gtgcgcttga ggaaggccac aatctccttc ttgttattgg
 300
 ccagctgctc aaactcctgg cggaacatct tctcctgcac agccagctca tcccacttcc
 360
 gctggtagcg ggctagccgg tcctccaggt ctcgatctg gatgtggtag aactccttca
 420
 tctccttggc cagaggcggc tccacggcca ccaccggctc cttcttgccc cttttcttct
 480
 tgaattcaag ctcttgctt gccttgetca cactcttttt gggaggc
 527

<210> 202

<211> 70
 <212> PRT
 <213> Homo sapiens

<400> 202
 Gly Arg Pro Gln Ser Pro Ser Cys Tyr Trp Pro Ala Ala Gln Thr Pro
 1 5 10 15
 Gly Gly Thr Ser Ser Pro Ala Gln Pro Ala His Pro Thr Ser Ala Gly
 20 25 30
 Thr Gly Leu Ala Gly Pro Pro Gly Leu Gly Ser Gly Cys Gly Arg Thr
 35 40 45
 Pro Ser Ser Pro Trp Pro Glu Ala Ala Pro Arg Pro Pro Pro Ala Pro
 50 55 60
 Ser Cys Pro Leu Ser Ser
 65 70

<210> 203
 <211> 304
 <212> DNA
 <213> Homo sapiens

<400> 203
 ngtgcaccgg tggatcatgga caacgccgcc tacgtggtct acacctcggg atccaccggc
 60
 cgacccaagg gagttgtcgt caccacacacc ggactcgaca gcttcgcact cgaccagcag
 120
 cgtcgattcc acgcagatca ccaactctcga accctgcact tcgccacccc cagcttcgac
 180
 ggagccgtct tcgagtacct gcaggcattc ggtgtcggag ccaccatggt gatcgteccg
 240
 accgacatct acggcggcgc cgaactggca agtctcatcc gccgcgaaca cgtcactcac
 300
 gcgt
 304

<210> 204
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 204
 Xaa Ala Pro Val Val Met Asp Asn Ala Ala Tyr Val Val Tyr Thr Ser
 1 5 10 15
 Gly Ser Thr Gly Arg Pro Lys Gly Val Val Val Thr His Thr Gly Leu
 20 25 30
 Asp Ser Phe Ala Leu Asp Gln Gln Arg Arg Phe His Ala Asp His His
 35 40 45
 Ser Arg Thr Leu His Phe Ala Thr Pro Ser Phe Asp Gly Ala Val Phe
 50 55 60
 Glu Tyr Leu Gln Ala Phe Gly Val Gly Ala Thr Met Val Ile Val Pro
 65 70 75 80
 Thr Asp Ile Tyr Gly Gly Ala Glu Leu Ala Ser Leu Ile Arg Arg Glu
 85 90 95
 His Val Thr His Ala

100

<210> 205
 <211> 356
 <212> DNA
 <213> Homo sapiens

<400> 205
 nngaattcag caatgataac tggctcaatt gaaggtaaga caacaattga gggaattaat
 60
 gcacaattaa atacagtgtt aactttatctt tcaccacaat caaaagataa agattttaatc
 120
 atgccagatc aacaagaaga aatagatatt ctgattgcaa ccgactgtat ttcagaagga
 180
 cagaacttac aagattgtga ttacttaata aactatgaca ttcattggaa tccagttcgt
 240
 atcattcaaa gatttggacg gattgatcga attgggtcga agaataaatg tgtacaatta
 300
 gttaactttt ggccagatat tacattagat gaatatattg atctaaaggg acgcgt
 356

<210> 206
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 206
 Xaa Asn Ser Ala Met Ile Thr Gly Ser Ile Glu Gly Lys Thr Thr Ile
 1 5 10 15
 Glu Gly Ile Asn Ala Gln Leu Asn Thr Val Leu Thr Leu Phe Ser Pro
 20 25 30
 Gln Ser Lys Asp Lys Asp Leu Ile Met Pro Asp Gln Gln Glu Glu Ile
 35 40 45
 Asp Ile Leu Ile Ala Thr Asp Cys Ile Ser Glu Gly Gln Asn Leu Gln
 50 55 60
 Asp Cys Asp Tyr Leu Ile Asn Tyr Asp Ile His Trp Asn Pro Val Arg
 65 70 75 80
 Ile Ile Gln Arg Phe Gly Arg Ile Asp Arg Ile Gly Ser Lys Asn Lys
 85 90 95
 Cys Val Gln Leu Val Asn Phe Trp Pro Asp Ile Thr Leu Asp Glu Tyr
 100 105 110
 Ile Asp Leu Lys Gly Arg
 115

<210> 207
 <211> 324
 <212> DNA
 <213> Homo sapiens

<400> 207
 acgcgtgcac tgtgtgtatg catggtaacg tacacgtgtg cactgtgtgt ggtgtgcatg
 60
 catggtgtgt gcacgtgtng cactgtgtgt ggatgcatgg taatgtgcac gtgtgcactg
 120

tgtgtggtgt gtatgcatgg tgtgtgcacg tgtgcactgt gtgtgtgtgt atgcatgtgt
 180
 gtgcacatgt gcactgtgtg gtgtgtatgc atggtgtgtg cacgtgtgca ctgtgtatgc
 240
 atgngtgtgt gcatgtgtgc actgtgtatg catagtgtgc acgtgtgcac tgtgtggtgt
 300
 gtatgcatgg taatgtgcac gtgt
 324

<210> 208
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 208
 Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys
 1 5 10 15
 Val Val Cys Met His Gly Val Cys Thr Cys Xaa Thr Val Cys Gly Cys
 20 25 30
 Met Val Met Cys Thr Cys Ala Leu Cys Val Val Cys Met His Gly Val
 35 40 45
 Cys Thr Cys Ala Leu Cys Val Cys Val Cys Met Cys Val His Met Cys
 50 55 60
 Thr Val Trp Cys Val Cys Met Val Cys Ala Arg Val His Cys Val Cys
 65 70 75 80
 Met Xaa Val Cys Met Cys Ala Leu Cys Met His Ser Val His Val Cys
 85 90 95
 Thr Val Trp Cys Val Cys Met Val Met Cys Thr Cys
 100 105

<210> 209
 <211> 168
 <212> DNA
 <213> Homo sapiens

<400> 209
 nntccagag gttatgaggt tggaagcccg gtttttttca ggtgcagaaa aggctaccat
 60
 attcaagggt ccacgactcg cacctgcctt gccaatTTaa catggagtgg gatacagacc
 120
 gaatgtatac ctcatgcctg cagacagcca gaaaccccg caccgcg
 168

<210> 210
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 210
 Xaa Ser Arg Gly Tyr Glu Val Gly Ser Pro Val Phe Phe Arg Cys Arg
 1 5 10 15
 Lys Gly Tyr His Ile Gln Gly Ser Thr Thr Arg Thr Cys Leu Ala Asn
 20 25 30
 Leu Thr Trp Ser Gly Ile Gln Thr Glu Cys Ile Pro His Ala Cys Arg

35 40 45
 Gln Pro Glu Thr Pro Ala His Ala
 50 55

<210> 211
 <211> 354
 <212> DNA
 <213> Homo sapiens

<400> 211
 tacatgggct ttgacacagt ggtggctgaa gctgcactaa ggggtgtttgg aggcaatgtc
 60
 cagctggcag ctcagaccct tgcacacccat ggaggaagcc tcccacccga cctgcagttc
 120
 tcaggagagg actcctcccc cacaccgtcc acatccccc atgactctgc agggacctct
 180
 agtgcctcga cagatgaaga catggagacg gaggtgtca acgaaatcct ggaggacatt
 240
 ccggagcacg aggaggacta cctggactcc acgctggagg atgaagaagt cattattgct
 300
 gaatacttgt cctgcgttga aagtataagt tctgccngca aagaacaact gatc
 354

<210> 212
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 212
 Tyr Met Gly Phe Asp Thr Val Val Ala Glu Ala Ala Leu Arg Val Phe
 1 5 10 15
 Gly Gly Asn Val Gln Leu Ala Ala Gln Thr Leu Ala His His Gly Gly
 20 25 30
 Ser Leu Pro Pro Asp Leu Gln Phe Ser Gly Glu Asp Ser Ser Pro Thr
 35 40 45
 Pro Ser Thr Ser Pro Ser Asp Ser Ala Gly Thr Ser Ser Ala Ser Thr
 50 55 60
 Asp Glu Asp Met Glu Thr Glu Ala Val Asn Glu Ile Leu Glu Asp Ile
 65 70 75 80
 Pro Glu His Glu Glu Asp Tyr Leu Asp Ser Thr Leu Glu Asp Glu Glu
 85 90 95
 Val Ile Ile Ala Glu Tyr Leu Ser Cys Val Glu Ser Ile Ser Ser Ala
 100 105 110
 Xaa Lys Glu Gln Leu Ile
 115

<210> 213
 <211> 669
 <212> DNA
 <213> Homo sapiens

<400> 213
 attgcccaat ctcagagtgt ccaggaaagc ctggagagcc tggtgcagtc tattggggaa
 60

gttgaacaaa acctggaagg gaaacaggtg tcatcactct catcaggagt catccaggaa
 120
 gccttagcca caaatatgaa attgaagcag gacattgctc ggcaaaagag cagcttggag
 180
 gccacccgtg agatggtgac ccgattcatg gagacagcag acagtactac agcagcagtg
 240
 ctgcagggca aactggcaga ggtgagccag cggttcgaac agctctgtct acagcagcaa
 300
 gaaaaggaga gctccctaaa gaagcttcta ccccaggcag agatgtttga acacctctct
 360
 ggtaagctgc agcagttcat ggaaaacaaa agtcggatgc tggcctctgg aaatcagcca
 420
 gatcaagata ttacacattt cttccaacag atccaggagc tcaatttgga aatggaagac
 480
 caacaggaga acctagatac tcttgagcac ctggtcactg aactgagctc ttgtggcttt
 540
 gcgctggact tgtgccagca tcaggacagg gtacagaatc taagaaaaga cttcacagag
 600
 ctacagaaga cagttaaaga gagagagaaa gatgcatcat cttgccagga acagttggat
 660
 gaattccgg
 669

<210> 214

<211> 223

<212> PRT

<213> Homo sapiens

<400> 214

Ile	Ala	Gln	Ser	Gln	Ser	Val	Gln	Glu	Ser	Leu	Glu	Ser	Leu	Leu	Gln
1				5					10					15	
Ser	Ile	Gly	Glu	Val	Glu	Gln	Asn	Leu	Glu	Gly	Lys	Gln	Val	Ser	Ser
			20					25					30		
Leu	Ser	Ser	Gly	Val	Ile	Gln	Glu	Ala	Leu	Ala	Thr	Asn	Met	Lys	Leu
		35					40					45			
Lys	Gln	Asp	Ile	Ala	Arg	Gln	Lys	Ser	Ser	Leu	Glu	Ala	Thr	Arg	Glu
	50					55					60				
Met	Val	Thr	Arg	Phe	Met	Glu	Thr	Ala	Asp	Ser	Thr	Thr	Ala	Ala	Val
65					70				75					80	
Leu	Gln	Gly	Lys	Leu	Ala	Glu	Val	Ser	Gln	Arg	Phe	Glu	Gln	Leu	Cys
			85						90					95	
Leu	Gln	Gln	Gln	Glu	Lys	Glu	Ser	Ser	Leu	Lys	Lys	Leu	Leu	Pro	Gln
			100					105						110	
Ala	Glu	Met	Phe	Glu	His	Leu	Ser	Gly	Lys	Leu	Gln	Gln	Phe	Met	Glu
		115						120					125		
Asn	Lys	Ser	Arg	Met	Leu	Ala	Ser	Gly	Asn	Gln	Pro	Asp	Gln	Asp	Ile
		130				135						140			
Thr	His	Phe	Phe	Gln	Gln	Ile	Gln	Glu	Leu	Asn	Leu	Glu	Met	Glu	Asp
145				150					155					160	
Gln	Gln	Glu	Asn	Leu	Asp	Thr	Leu	Glu	His	Leu	Val	Thr	Glu	Leu	Ser
			165					170						175	
Ser	Cys	Gly	Phe	Ala	Leu	Asp	Leu	Cys	Gln	His	Gln	Asp	Arg	Val	Gln
		180						185					190		
Asn	Leu	Arg	Lys	Asp	Phe	Thr	Glu	Leu	Gln	Lys	Thr	Val	Lys	Glu	Arg

	195		200		205									
Glu	Lys	Asp	Ala	Ser	Ser	Cys	Gln	Glu	Gln	Leu	Asp	Glu	Phe	Arg
	210					215					220			

<210> 215
 <211> 814
 <212> DNA
 <213> Homo sapiens

<400> 215
 aaatttcgta cccgctccgg cacagtacga gcccttgacg atgtgagcct ggctattaag
 60
 agaggttcca tctcagccgt tatcgggcac tccggagccg gcaaateccac cctgggttcgc
 120
 ctcacaaacg gattagagac tcccacgcgt ggccgcgtct tggtagacgg caccgacgtc
 180
 tcgcagctct cggacaaagc gatgcgcccg ctacgcgcag acatcgggat gatcttccaa
 240
 cagttcaacc tattcggctc aaggaccatc tacgacaacg ttgcctatcc actcaagctg
 300
 gctcattgga agaaagcaga cgagaagaag cgcgtcaccg aattgctgag cttcgtcggg
 360
 ttgacgagca aagcctggga ccatccagac cagctctcgg gcggacagaa acagcgggtt
 420
 ggtattgccc gagcgctagc aactaaacca tcgattttgt tggctgacga gtccacctcg
 480
 gcgctggatc cagaaacgac agctgatgtc ctatccctgc tcaagcgggt caatgcggaa
 540
 ctagggggtga cggtcgtcgt catcaccac gagatggagg tcgtccgctc gattgccag
 600
 caggtctcgg tactagcagc tggccatctc gtcgagtctg gaagcgcggc ccaggtcttc
 660
 gctcatccac agtcagagac caccacgcgt ttcttgggca cgattatcgg ccagcaccg
 720
 agtggggagg aacaggcacg gttgcagtcg gaaaaccag atgcacgact cgtcgacgtc
 780
 agttcgggtg ccagtcactc gttcgggtgac gcgt
 814

<210> 216
 <211> 271
 <212> PRT
 <213> Homo sapiens

<400> 216
 Lys Phe Arg Thr Arg Ser Gly Thr Val Arg Ala Leu Asp Asp Val Ser
 1 5 10 15
 Leu Ala Ile Lys Arg Gly Ser Ile Ser Ala Val Ile Gly His Ser Gly
 20 25 30
 Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Glu Thr Pro
 35 40 45
 Thr Arg Gly Arg Val Leu Val Asp Gly Thr Asp Val Ser Gln Leu Ser
 50 55 60
 Asp Lys Ala Met Arg Pro Leu Arg Ala Asp Ile Gly Met Ile Phe Gln


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65          70          75          80
Gln Phe Asn Leu Phe Gly Ser Arg Thr Ile Tyr Asp Asn Val Ala Tyr
          85          90          95
Pro Leu Lys Leu Ala His Trp Lys Lys Ala Asp Glu Lys Lys Arg Val
          100          105          110
Thr Glu Leu Leu Ser Phe Val Gly Leu Thr Ser Lys Ala Trp Asp His
          115          120          125
Pro Asp Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala Arg
          130          135          140
Ala Leu Ala Thr Lys Pro Ser Ile Leu Leu Ala Asp Glu Ser Thr Ser
145          150          155          160
Ala Leu Asp Pro Glu Thr Thr Ala Asp Val Leu Ser Leu Leu Lys Arg
          165          170          175
Val Asn Ala Glu Leu Gly Val Thr Val Val Val Ile Thr His Glu Met
          180          185          190
Glu Val Val Arg Ser Ile Ala Gln Gln Val Ser Val Leu Ala Ala Gly
          195          200          205
His Leu Val Glu Ser Gly Ser Ala Arg Gln Val Phe Ala His Pro Gln
          210          215          220
Ser Glu Thr Thr Gln Arg Phe Leu Ala Thr Ile Ile Gly Gln His Pro
225          230          235          240
Ser Gly Glu Glu Gln Ala Arg Leu Gln Ser Glu Asn Pro Asp Ala Arg
          245          250          255
Leu Val Asp Val Ser Ser Val Ala Ser His Ser Phe Gly Asp Ala
          260          265          270

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<210> 217

<211> 500

<212> DNA

<213> Homo sapiens

<400> 217

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nnacgcgtcg cgatgaaaga ggcgctgaaa ggtgccatcc agattccaac agtgactttt
60
agctctgaga agtccaatac tacagccctg gctgagttcg gaaaatacat tcataaagtc
120
tttcctacag tggtcagcac cagctttatc cagcatgaag tcgtggaaga gtatagccac
180
ctgttcacta tccaaggctc ggaccccage ttgcagccct acctgctgat ggctcacttt
240
gatgtggtgc ctgcccctga agaaggctgg gaggtgcccc cattctctgg gttggagcgt
300
gatggcgtca tctatggttg gggcacactg gacgacaaga actctgtgat ggcattactg
360
caggccttgg agctcctgct gatcaggaag tacatcccc gaagatcttt cttcatttct
420
ctgggccatg atgaggagtc atcagggaca ggggctcaga ggatctcagc cctgctacag
480
tcaaggggcg tccagctagc
500

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<210> 218

<211> 166

<212> PRT

<213> Homo sapiens

<400> 218

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Xaa Arg Val Ala Met Lys Glu Ala Leu Lys Gly Ala Ile Gln Ile Pro
 1           5           10           15
Thr Val Thr Phe Ser Ser Glu Lys Ser Asn Thr Thr Ala Leu Ala Glu
      20           25           30
Phe Gly Lys Tyr Ile His Lys Val Phe Pro Thr Val Val Ser Thr Ser
      35           40           45
Phe Ile Gln His Glu Val Val Glu Glu Tyr Ser His Leu Phe Thr Ile
      50           55           60
Gln Gly Ser Asp Pro Ser Leu Gln Pro Tyr Leu Leu Met Ala His Phe
65           70           75           80
Asp Val Val Pro Ala Pro Glu Glu Gly Trp Glu Val Pro Pro Phe Ser
      85           90           95
Gly Leu Glu Arg Asp Gly Val Ile Tyr Gly Trp Gly Thr Leu Asp Asp
      100          105          110
Lys Asn Ser Val Met Ala Leu Leu Gln Ala Leu Glu Leu Leu Leu Ile
      115          120          125
Arg Lys Tyr Ile Pro Arg Arg Ser Phe Phe Ile Ser Leu Gly His Asp
      130          135          140
Glu Glu Ser Ser Gly Thr Gly Ala Gln Arg Ile Ser Ala Leu Leu Gln
145          150          155          160
Ser Arg Gly Val Gln Leu
      165

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<210> 219

<211> 361

<212> DNA

<213> Homo sapiens

<400> 219

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acgcgttgaa acgggtatat tggggatgac gccgctgtgc aatatgcgca aggccataca
60
caaggtccgc acgctcccat gtccctcggt ttcgacagtt cttttgcgcc gcattatggc
120
gaagccgctcg agattgcgcc tgatatcaag cgcattcacgg tcaacaaccc cagccccttc
180
acttttttcg gcaccaacag ttatctgatc ggccgcgata cgctggcatt gatcgatccc
240
ggtcgcgttg acgaggccca tcacgcggcg ctgctgcgtg ccattgccgg ccggccggtc
300
agccatatct ttgtcagcca cacacaccgg gaccactcgc cagtcgcgac ggttttgaaa
360
g
361

```

<210> 220

<211> 102

<212> PRT

<213> Homo sapiens

<400> 220

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Met Ala Asp Arg Pro Ala Gly Asn Gly Thr Gln Gln Arg Arg Val Met

```

```

      1           5           10           15
Gly Leu Val Lys Arg Thr Gly Ile Asp Gln Cys Gln Arg Ile Ala Ala
      20           25           30
Asp Gln Ile Thr Val Gly Ala Glu Lys Ser Glu Gly Ala Gly Val Val
      35           40           45
Asp Arg Asp Ala Leu Asp Ile Arg Arg Asn Leu Asp Gly Phe Ala Ile
      50           55           60
Met Arg Arg Lys Arg Thr Val Glu Asn Glu Gly His Gly Ser Val Arg
      65           70           75           80
Thr Leu Cys Met Ala Leu Arg Ile Leu His Ser Gly Val Ile Pro Asn
      85           90           95
Ile Pro Val Ser Thr Arg
      100

```

<210> 221
 <211> 401
 <212> DNA
 <213> Homo sapiens

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<400> 221
agatctctgt gtcgtcggct gcaaagagga tgagcccaga tgcatatcag gggctccctc
60
ccacatccca cctgctcggg cagcccacgg cagccccaca ctgctgcagc acacctcgct
120
gcagctctgg ttctctctca gaaatatccc tgccaccctg ctaagccttg gccaacactg
180
caccctgtcc caatgcggct ccagtgacca cacccccagg gcataccctc ctacagagca
240
ttcccaaaaa aggctagagt agacaccagc ctgctccgta gggggcctcc accccattct
300
ccaaggcctc caccagggga cgcttggtga accagcatcc aggctggcc cacctccctg
360
ctcagagtcc atgttctgtg acaagggtgg caactgggat t
401

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<210> 222
 <211> 124
 <212> PRT
 <213> Homo sapiens

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<400> 222
Met Asp Ser Glu Gln Gly Gly Gly Pro Gly Leu Asp Ala Gly Ser Pro
      1           5           10           15
Gly Val Pro Gly Trp Arg Pro Trp Arg Met Gly Trp Arg Pro Pro Thr
      20           25           30
Glu Gln Ala Gly Val Tyr Ser Ser Leu Phe Trp Glu Cys Ser Val Gly
      35           40           45
Gly Tyr Ala Leu Gly Val Trp Ser Leu Glu Pro His Trp Asp Arg Val
      50           55           60
Gln Cys Trp Pro Arg Leu Ser Arg Val Ala Gly Ile Phe Leu Arg Arg
      65           70           75           80
Asn Gln Ser Cys Ser Glu Val Cys Cys Ser Ser Val Gly Leu Pro Trp
      85           90           95
Ala Ala Arg Ala Gly Gly Met Trp Glu Gly Ala Pro Asp Met His Leu

```

100 105 110
 Gly Ser Ser Ser Leu Gln Pro Thr Thr Gln Arg Ser
 115 120

<210> 223
 <211> 331
 <212> DNA
 <213> Homo sapiens

<400> 223
 tcatgaaatc tgtgggcagt gacccaggag ggtatgggca ggcccaacca gggtggtgtg
 60
 cccttgaagc cccacagacc tgccagggca gcagggcagt tgggagccgg agaacctgag
 120
 aaccaagcca ggctgcatgc aggaggctgg cacgtgaacg ctgcaggtgt tgccggcagc
 180
 cgtggtgcct ggcagatagt gtccgacccc cnaggacctt cttgctgggc agcccagtcc
 240
 aaaagctgtt cccgcttaag ccacccccac cgccttggcc acacctggca catgggtgaa
 300
 gcaagggcat ttcccggggc ttctgttcc c
 331

<210> 224
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 224
 Met Pro Leu Leu His Pro Cys Ala Arg Cys Gly Gln Gly Gly Gly Gly
 1 5 10 15
 Gly Leu Ser Gly Asn Ser Phe Trp Thr Gly Leu Pro Ser Lys Lys Val
 20 25 30
 Leu Gly Gly Arg Thr Leu Ser Ala Arg His His Gly Cys Arg Gln His
 35 40 45
 Leu Gln Arg Ser Arg Ala Ser Leu Leu His Ala Ala Trp Leu Gly Ser
 50 55 60
 Gln Val Leu Arg Leu Pro Thr Ala Leu Leu Pro Trp Gln Val Cys Gly
 65 70 75 80
 Ala Ser Arg Ala His Gln Pro Gly Trp Ala Cys Pro Tyr Pro Pro Gly
 85 90 95
 Ser Leu Pro Thr Asp Phe Met
 100

<210> 225
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 225
 tgatcacggg cgtgagccac cagcccagca tcccttgctt ttcattcgca cctccacctc
 60
 cagaatgacc ctcatccctt cctgcacaga cggtgacagc agtaactcct acaaacacca
 120

ccagactgat cttcaagagc agaggaactc ccaatcacga ttccaccccc gccgggctct
 180
 caaatcctcc agggctgcct gctatggggg agggaggcac actttgcttg gctctcaagg
 240
 cctcagccag ccgggtccaa accaactccc agcctggcct caccatccca ccgccaacc
 300
 ttgctcaca ctggcccctc ttcttgaac atgggcctn
 339

<210> 226
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 226
 Met Thr Leu Ile Pro Ser Cys Thr Asp Gly Asp Ser Ser Asn Ser Tyr
 1 5 10 15
 Lys His His Gln Thr Asp Leu Gln Glu Gln Arg Asn Ser Gln Ser Arg
 20 25 30
 Phe His Pro Arg Arg Ala Leu Lys Ser Ser Arg Ala Ala Cys Tyr Gly
 35 40 45
 Gly Gly Arg His Thr Leu Leu Gly Ser Gln Gly Leu Ser Gln Pro Gly
 50 55 60
 Pro Asn Gln Leu Pro Ala Trp Pro His His Pro Thr Ala Lys Pro Leu
 65 70 75 80
 Leu Thr Leu Ala Pro Leu Pro Gly Thr Trp Ala
 85 90

<210> 227
 <211> 353
 <212> DNA
 <213> Homo sapiens

<400> 227
 gtcgaccct tcgattgtgg cgaactccat ggctgctgcg ggctgcgta ggctctcgag
 60
 tagctcgacg tcgggttcgc gagggctcgc agcgtggcca tgctgcttct tggatgggtc
 120
 gggcaactcc tcgggggatt cgagcagttc ttggcgcacc tgctctggcg tcatcccgga
 180
 ggccaggccg acaagtgctg cctcctgccca cccgctgagc gacgctgccca tgttgagtac
 240
 ggcgtcttca ctggtcaggg cgagcgcggt atcgaccagg ttggcgtcca ggccgagaga
 300
 cagcatgtct gctcagtcgc ggtgatgact ggagtggcgg tctcctgcac ggg
 353

<210> 228
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 228
 Met Leu Ser Leu Gly Leu Asp Ala Asn Leu Val Asp Thr Ala Leu Ala

1	5	10	15
Leu Thr Ser Glu Asp Ala Val Leu Asn Met Ala Ala Ser Leu Ser Gly			
20	25	30	
Trp Gln Glu Ala Ala Leu Val Gly Leu Ala Ser Gly Met Thr Pro Glu			
35	40	45	
Gln Val Arg Gln Glu Leu Leu Glu Ser Pro Glu Glu Leu Pro Glu Pro			
50	55	60	
Ser Lys Lys Gln His Gly His Ala Ala Ser Pro Arg Glu Pro Asp Val			
65	70	75	80
Glu Leu Leu Glu Ser Leu Arg Arg Pro Ala Ala Ala Met Glu Phe Ala			
85	90	95	
Thr Ile Glu Gly Val Asp			
100			

<210> 229

<211> 743

<212> DNA

<213> Homo sapiens

<400> 229

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nnggctaggg acacggcctc ctcctcaaca ggcagtgcct gtgcaggctc aggggcatca
60
tcaaagataa cacagggctg gtcaggggct gctggctgct cctgccccag gactggctcc
120
aggatgggca aggctgcctc cctggtagcc agggggagag gggaaggag caccaggag
180
tgggccagca ggtgtggcat cggccaggag gagatggagg ccagcagcag ccaagaccag
240
agtaaagtgt ctgccccagg ggtgtcaca gcccaggacc gggtagttgg aaagccagcc
300
cagcttggca ctcagcggag ccaggaggca gatgttcagg actgggagtt cagaaagagg
360
gattcccagg gcacttactc cagccgggat gcagaactcc aggaccagga attcggaaag
420
agagattcac tgggtaccta cagtagtcga gatgtaagcc ttggggactg ggaatttggg
480
aagagagatt ctctgggtgc ttatgccagc caagatgcca acgagcaggg ccaagatttg
540
gggaagaggg accaccatgg taggtacagc agccaggatg ccgatgagca ggactgggag
600
tttcagaaga gagatgtgtc actcggcacc tatggcagcc gggctgcgga gccacaggaa
660
caggagtttg ggaagagcgc ttggataagg gactacagca gtggtggcag ctccaggacc
720
cttgacgccc aggacagaag ctt
743

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<210> 230

<211> 247

<212> PRT

<213> Homo sapiens

<400> 230

Xaa Ala Arg Asp Thr Ala Ser Ser Ser Thr Gly Ser Ala Cys Ala Gly

1	5	10	15
Ser Gly Ala Ser Ser Lys Ile Thr Gln Gly Trp Ser Gly Ala Ala Gly			
20	25	30	
Cys Ser Cys Pro Arg Thr Gly Ser Arg Met Gly Lys Ala Ala Ser Leu			
35	40	45	
Val Ala Arg Gly Arg Gly Glu Gly Ser Thr Arg Glu Trp Ala Ser Arg			
50	55	60	
Cys Gly Ile Gly Gln Glu Glu Met Glu Ala Ser Ser Ser Gln Asp Gln			
65	70	75	80
Ser Lys Val Ser Ala Pro Gly Val Leu Thr Ala Gln Asp Arg Val Val			
85	90	95	
Gly Lys Pro Ala Gln Leu Gly Thr Gln Arg Ser Gln Glu Ala Asp Val			
100	105	110	
Gln Asp Trp Glu Phe Arg Lys Arg Asp Ser Gln Gly Thr Tyr Ser Ser			
115	120	125	
Arg Asp Ala Glu Leu Gln Asp Gln Glu Phe Gly Lys Arg Asp Ser Leu			
130	135	140	
Gly Thr Tyr Ser Ser Arg Asp Val Ser Leu Gly Asp Trp Glu Phe Gly			
145	150	155	160
Lys Arg Asp Ser Leu Gly Ala Tyr Ala Ser Gln Asp Ala Asn Glu Gln			
165	170	175	
Gly Gln Asp Leu Gly Lys Arg Asp His His Gly Arg Tyr Ser Ser Gln			
180	185	190	
Asp Ala Asp Glu Gln Asp Trp Glu Phe Gln Lys Arg Asp Val Ser Leu			
195	200	205	
Gly Thr Tyr Gly Ser Arg Ala Ala Glu Pro Gln Glu Gln Glu Phe Gly			
210	215	220	
Lys Ser Ala Trp Ile Arg Asp Tyr Ser Ser Gly Gly Ser Ser Arg Thr			
225	230	235	240
Leu Asp Ala Gln Asp Arg Ser			
245			

<210> 231

<211> 431

<212> DNA

<213> Homo sapiens

<400> 231

acgcgttggc caccgagagg ctggcgaggg tgtgcagcac ggcgcagtgt ggcaggggtcc
60cagggtgcag cctgcgcagc agctcctcca tcaccttgct gatgaactgt cttcccacgg
120ccaccaggac gccactcgcc gcctgctgcc agtcccagac caggtccttc gtcttggtca
180tctcgctgga ggccaggagg atgatggtgc tggctgtgtc cttgtccagc tcaactggcgc
240gactgctcag gacctctcc atggccctca ggaccgctgc tcggtatggg tgtgccagct
300tgtcatgctg ccgcagatac tctcgcagg cacggagcgt ctccaccctg ctggacgcca
360tcaccgataa ggaccccctg gtgcaggagc aggtctgcag tgccctgtgc tccctcgggg
420

aggtgcggcc g

431

<210> 232
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 232
 Met Ala Ser Ser Arg Val Glu Thr Leu Arg Ala Cys Glu Glu Tyr Leu
 1 5 10 15
 Arg Gln His Asp Lys Leu Ala His Pro Tyr Arg Ala Ala Val Leu Arg
 20 25 30
 Ala Met Glu Arg Val Leu Ser Ser Arg Ala Ser Glu Leu Asp Lys Asp
 35 40 45
 Thr Ala Ser Thr Ile Ile Leu Leu Ala Ser Ser Glu Met Thr Lys Thr
 50 55 60
 Lys Asp Leu Val Trp Asp Trp Gln Gln Ala Ala Ser Gly Val Leu Val
 65 70 75 80
 Ala Val Gly Arg Gln Phe Ile Ser Lys Val Met Glu Glu Leu Leu Arg
 85 90 95
 Arg Leu His Pro Gly Thr Leu Pro His Cys Ala Val Leu His Thr Leu
 100 105 110
 Ala Ser Leu Ser Val Ala Asn Ala
 115 120

<210> 233
 <211> 606
 <212> DNA
 <213> Homo sapiens

<400> 233
 acgcgttcag ggatgccaga aatctaactg ggtaataaaa agctgggaga acattccaga
 60
 aaggtgggca cccttagcat tcccaaaaag caccagccct cctcatcctt cccagcttct
 120
 gtgctggaat gcacccccat cggaaaggct cgaaaactca ggacacatta ggatcacctg
 180
 gaaagcattt gtcaaaacgc atctccctgc gggtcagggt ccaagttaaa atcaaacttc
 240
 aggtgatgct gactcagggt gctccagaaa cacctgggga agcagcactt tggaggctgc
 300
 ctctcacatc caccacacag caagtgggca gggagctagg taaatctcct tcccagttga
 360
 gaaggggctc ggagcaggca cagagaagag atacccttag aatgcaagtt gttcagctgc
 420
 gaaagtccag cctgcaggct tcctgggcaa gctagtgggc tgaagtatgc cacagcaaca
 480
 ggcttctaga gccggctgcc cagctcctac tctgcctctg ccactcactg actgtgtggt
 540
 cttgagcagg tcacctgtct gacttggtga gagctgacag gcatcacctg ttagaggctt
 600
 acgcgt
 606

<210> 234

<211> 108
 <212> PRT
 <213> Homo sapiens

<400> 234
 Met His Pro His Arg Lys Gly Ser Lys Thr Gln Asp Thr Leu Gly Ser
 1 5 10 15
 Pro Gly Lys His Leu Ser Lys Arg Ile Ser Leu Arg Val Arg Val Gln
 20 25 30
 Val Lys Ile Lys Leu Gln Val Met Leu Thr Gln Val Ala Pro Glu Thr
 35 40 45
 Pro Gly Glu Ala Ala Leu Trp Arg Leu Pro Leu Thr Ser Thr Pro Gln
 50 55 60
 Gln Val Gly Arg Glu Leu Gly Lys Ser Pro Ser Gln Leu Arg Arg Gly
 65 70 75 80
 Ser Glu Gln Ala Gln Arg Arg Asp Thr Leu Arg Met Gln Val Val Gln
 85 90 95
 Leu Arg Lys Ser Ser Leu Gln Ala Ser Trp Ala Ser
 100 105

<210> 235
 <211> 328
 <212> DNA
 <213> Homo sapiens

<400> 235
 cgaccgttga ctattctcta caaaccacaa agacaatgat tgatttaact gaatttagaa
 60
 atagcaaaca cttaaaacag cagcagtaca gagctgaaaa ccagattctt ttgaaagaga
 120
 ttgaaagtct agaggaagaa cgacttgatc tgaaaaaaaa aattcgccaa atggctcaag
 180
 aaagaggaaa aagaaggga acttcaggat taaccactgg ggacctgaac ctaactgaaa
 240
 acatttctca aggagataga ataagtgaaa gaaaattgga tttattgagc ctcaaaaata
 300
 tgagtgaagc acaatcaaag aatgaatt
 328

<210> 236
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 236
 Met Ile Asp Leu Thr Glu Phe Arg Asn Ser Lys His Leu Lys Gln Gln
 1 5 10 15
 Gln Tyr Arg Ala Glu Asn Gln Ile Leu Leu Lys Glu Ile Glu Ser Leu
 20 25 30
 Glu Glu Glu Arg Leu Asp Leu Lys Lys Lys Ile Arg Gln Met Ala Gln
 35 40 45
 Glu Arg Gly Lys Arg Arg Ala Thr Ser Gly Leu Thr Thr Gly Asp Leu
 50 55 60
 Asn Leu Thr Glu Asn Ile Ser Gln Gly Asp Arg Ile Ser Glu Arg Lys

65					70					75					80
Leu	Asp	Leu	Leu	Ser	Leu	Lys	Asn	Met	Ser	Glu	Ala	Gln	Ser	Lys	Asn
				85					90					95	
Glu															

<210> 237

<211> 2059

<212> DNA

<213> Homo sapiens

<400> 237

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ggccataagg gcacgacgca ttcctagccg atgcaccaac acgggcatga agcctgccga
60
gagcacgaag ccggcgtcca tagctacggc ccatacggtc atgtctgccca tggctccggt
120
gatgtcagac tgcacatgaa atcgggttacg gtaccccagg atcatcgcta ccgagtacac
180
cccgaacagc acccgctggg cgccgatcag cgtgaggagg tgccccacca gtggcacttt
240
tcttagatag cggaacccat ccaccacatc ccagtcacc gttctcatcg tccgggaacg
300
atccaccagt ggcggcccaa gctcccagc tgaaaactgc agcccctagg cgaccgagac
360
tgcaagagg gctgcggaga tgcagaaaat gatcgtgtcg gcgtggtgca caggaatatg
420
gcgtccggca atcatgcgca ctgctgcagc aacaaccgca ccgatcatga gccctagcgg
480
ccaatcgttg gcatgattga cgatgccgtc aggtagtcgc gcttgctgat ggtgtattcc
540
aaccagcga ccaaggcggg gagcaaaaac cggttcaggc tcatcgcgat gagcaacca
600
atgagcaagg ccagggtggga gggcttatcg cgcgcaccac ccagaccaa gatccccagc
660
ccgacccagg tgacggcacg cattcatctg cgtattgtcc cgactacacc gtgagggcgc
720
tctctgatct gcagctcatc aagggttacg gactgcagta cctcaatgca ctctggcta
780
cccagagcca gaacctgcc aagtcccctg agaacaccga cctgcagggt attccaggca
840
gccagaccag gtccttggt gagaagacca ccacagcggc agctttccca gtagcccttt
900
ccctctttgg cacagttgga acctccagtt gataaatgac tgtggactag cgcgcgtttt
960
ttgttttcag agcacacgta aggggtccagc cacagcaggc ccggcgtccc ggtggaaggc
1020
agccctgggc ggaacccagg cgtttaacgg ctactaggc agccccagat ctggggaagc
1080
agatgagcac gtggggagct ggagtgagct gagcagaagt tttgtgccg cctgccccca
1140
tcccctccag gccacgtttt agatggccct tgtagttgcg ggtcctgggt gtcctcagaa
1200
ctagacatca atgcctggat ccttcagccg gccctgccct cctttaggag acaggagtca
1260

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ccagggcaca gccctccagg cccgcctcag gaaggaatga aaggaatgcc atcatctcta
 1320
 gttcccaggg cccagccttc cccttctccc ccggggcagg gacagtgcgg catattcaga
 1380
 ttcagacctc tttgggctga gccaccttgt gagtgcagtt actgcctttg tgtggccgtg
 1440
 acctctattt gtttgctttt aatttgccaa cctatcgctg ctggcagcac tttttgagca
 1500
 agccgagagc acccattttg gctggggatt cagatcgatg gccttgacca tgttgctcct
 1560
 tctggcttcc ctgatgggtg catgtttcag cgcatgcgcc ccagcctttc ccatgtgcca
 1620
 aaccagaagc tccactgccc gtaggctgtc cctgtagccc tgctccctcc ctggagggtg
 1680
 ctcttctgat tctgagagct ggcctagtgg tgctgagggc ccctttctgc ttctctgccc
 1740
 acctgctgag ttgccactcg cagtgttggtc agttcccgtg ttctgagaag aggtcatgcc
 1800
 tgggaggaag ggatcgatc gctgcatcga atcctctctc cgccgtgtgg cccccaggag
 1860
 agtagctgcc tgttgcacct gctccacacc tccccacagc ctccctgcag gtgctgtgtg
 1920
 gccgtgatgt gcagagagca gtgaggagg gttcatgaac caggtggatc ctctttaaaa
 1980
 aaaaaaaaaag tttttgttat atctctaaaa tcccatagct aggaacagaa aaaaaggaaa
 2040
 agacttgaaa tgttctaga
 2059

<210> 238

<211> 129

<212> PRT

<213> Homo sapiens

<400> 238

Ala	Glu	Gln	Lys	Phe	Cys	Ala	Arg	Leu	Pro	Pro	Ser	Pro	Pro	Gly	His
1				5					10					15	
Val	Leu	Asp	Gly	Pro	Cys	Ser	Cys	Gly	Ser	Trp	Val	Ser	Ser	Glu	Leu
			20					25						30	
Asp	Ile	Asn	Ala	Trp	Ile	Leu	Gln	Pro	Ala	Leu	Pro	Ser	Phe	Arg	Arg
			35				40					45			
Gln	Glu	Ser	Pro	Gly	His	Ser	Pro	Pro	Gly	Pro	Pro	Gln	Glu	Gly	Met
			50			55					60				
Lys	Gly	Met	Pro	Ser	Ser	Leu	Val	Pro	Arg	Ala	Gln	Pro	Ser	Pro	Ser
65					70				75					80	
Pro	Pro	Gly	Gln	Gly	Gln	Cys	Gly	Ile	Phe	Arg	Phe	Arg	Pro	Leu	Trp
			85				90							95	
Ala	Glu	Pro	Pro	Cys	Glu	Cys	Ser	Tyr	Cys	Leu	Cys	Val	Ala	Val	Thr
			100				105						110		
Ser	Ile	Cys	Leu	Leu	Leu	Ile	Cys	Gln	Pro	Ile	Ala	Ala	Gly	Ser	Thr
			115				120						125		
Phe															

<210> 239
<211> 388
<212> DNA
<213> Homo sapiens

<400> 239
ntctagatca ctctgtagcg catgggttaa tgctgacaca atagaaaagt gcgaggacat
60
cctcgaatta atgagatggg ggactggatg agtcaagttc tcgtcgttgc ggcggctgtc
120
ggtcagctgc ccctcctcca cttctgcttc tcggcggttac cccataccgt attggccgcg
180
tggtcacctt tgaatgcagc catgtcgtcg tctccgtatc gaaatgatgt gccatcgaag
240
atgccgacct cagcatcggc atctgcagtg atgagtgcgt atcgcgccac acgaaacgcc
300
cagcgcaacc gtgtcctcgc acgatacgaa gtgcttgggt atctcagctc tgggtacctat
360
ggtcgtgtat ataaagcaaa ggaacttn
388

<210> 240
<211> 104
<212> PRT
<213> Homo sapiens

<400> 240
Met Val Asp Trp Met Ser Gln Val Leu Val Val Ala Ala Ala Val Gly
1 5 10 15
Gln Leu Pro Leu Leu His Phe Cys Phe Ser Ala Leu Pro His Thr Val
20 25 30
Leu Ala Ala Cys Ser Pro Leu Asn Ala Ala Met Ser Ser Ser Pro Tyr
35 40 45
Arg Asn Asp Val Pro Ser Lys Met Pro Thr Ser Ala Ser Ala Ser Ala
50 55 60
Val Met Ser Ala Tyr Arg Ala Thr Arg Asn Ala Gln Arg Asn Arg Val
65 70 75 80
Leu Ala Arg Tyr Glu Val Leu Gly Tyr Leu Ser Ser Gly Thr Tyr Gly
85 90 95
Arg Val Tyr Lys Ala Lys Glu Leu
100

<210> 241
<211> 330
<212> DNA
<213> Homo sapiens

<400> 241
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60
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<210> 242
 <211> 100
 <212> PRT
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<400> 242
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Gly Lys Ile Phe Val Val Asn Ser Arg Trp Met Pro Arg Asp Ala Ser
      35              40              45
Ile Arg Ser Glu Cys Arg Leu Pro Pro Thr Val Asn Phe Cys Phe Cys
    50              55              60
Asn Thr Leu His Ser Thr Phe Pro Arg Trp Val Trp Leu Pro Ser Ser
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 <213> Homo sapiens

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 Val Asp Arg Val Phe Val Asp His Pro Leu Phe Leu Glu Arg Val Trp
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 Gly Lys Thr Glu Glu Lys Ile Tyr Gly Pro Asp Ala Gly Thr Asp Tyr
 65 70 75 80
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<210> 250

<211> 927

<212> PRT

<213> Homo sapiens

<400> 250

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Phe	Val	Gln	Arg	Asn	Pro	Gly	Gly	Ser	Pro	Arg	Thr	Ala	Cys	His	Leu
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Asn	Pro	Ser	Pro	Asp	Gly	Glu	Ala	Tyr	Thr	Leu	Ala	Ser	Arg	Pro	Pro
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Val	Arg	Leu	Asn	Asp	Val	Met	Leu	Arg	Leu	Val	Thr	Glu	Leu	Arg	Trp
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Gln	Lys	Phe	Val	Met	Phe	Tyr	Asp	Ser	Glu	Tyr	Asp	Ile	Arg	Gly	Leu
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Lys	Gly	His	Ile	Thr	Gly	Leu	Thr	Gly	Val	Met	Glu	Phe	Arg	Glu	Asp		
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Ala Gln Ala Asp Gly Lys Ser Leu Lys Leu His Ser Phe Ala Gly Val		735
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Phe Cys Ile Leu Ala Ile Gly Leu Leu Leu Ala Cys Leu Val Ala Ala		750
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Leu Glu Leu Trp Trp Asn Ser Asn Arg Cys His Gln Glu Thr Pro Lys		765
	770	775
Glu Asp Lys Glu Val Asn Leu Glu Gln Val His Arg Arg Met Asn Ser		780
785	790	795
Leu Met Asp Glu Asp Ile Ala His Lys Gln Ile Ser Pro Ala Ser Ile		800
	805	810
Glu Leu Ser Ala Leu Glu Met Gly Gly Leu Ala Pro Thr Gln Thr Leu		815
	820	825
Glu Pro Thr Arg Glu Tyr Gln Asn Thr Gln Leu Ser Val Ser Thr Phe		830
	835	840
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Ser Met Gln Cys Lys His Arg Ser Pro Asn Gly Gly Leu Phe Arg Gln		880
	885	890
Ser Pro Val Lys Thr Pro Ile Pro Met Ser Phe Gln Pro Val Pro Gly		895
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<211> 291

<212> DNA

<213> Homo sapiens

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<210> 252

<211> 97

<212> PRT

<213> Homo sapiens

<400> 252

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 <211> 327
 <212> DNA
 <213> Homo sapiens

<400> 253
 gtgcacggat gggagcgcctc gcgcgcgtgc tgggtgccttc acagcccggc gagcggcgtg
 60
 cgctcacggt cctgtaccga ccgatctcgc aaccttccgc agaccgatcc accaaccgcg
 120
 cccacatgtc ggcagtgatg gcgggcacct tgcgggagaa ggccgggaag gtcgagcgag
 180
 ccaatgaccg tcgcacggtc ggcacgctcc acgagcggga cgagaagctc gcggcaggac
 240
 gctcactcgt cgcggtgtcc tccgcggtct ccatcaccgt ccctgcgaca tggaacgccc
 300
 acgacttcgg acggcgactc gacgcgt
 327

<210> 254
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 254
Met Gly Ala Leu Ala Arg Val Leu Val Pro Ser Gln Pro Gly Glu Arg
1 5 10 15
Arg Ala Leu Thr Val Leu Tyr Arg Pro Ile Ser Gln Pro Ser Ala Asp
20 25 30
Arg Ser Thr Asn Arg Ala His Met Ser Ala Val Met Ala Gly Thr Leu
35 40 45
Arg Glu Lys Ala Gly Lys Val Glu Arg Ala Asn Asp Arg Arg Thr Val
50 55 60
Gly Thr Leu His Glu Arg Asp Glu Lys Leu Ala Ala Gly Arg Ser Leu
65 70 75 80
Val Ala Val Ser Ser Ala Val Ser Ile Thr Val Pro Ala Thr Trp Asn
85 90 95
Ala His Asp Phe Gly Arg Arg Leu Asp Ala
100 105

<210> 255
 <211> 372
 <212> DNA
 <213> Homo sapiens

<400> 255
 ctagaaatgg ctggctacga atacatggaa gctgaaaata gccacaagc ccacgaaatt
 60
 atcgtggacc atagacctga cttaatctta tgtgattgga tgatgccagg agggagtggc
 120
 atcgagctaa ctcgtcgctt aaagaaagac agcacgacag cagaaatccc tggtatttta
 180
 ctaacggcca aaagtgaaga agacaataaa attcaaggct tagaagtcgg tgcagatgac
 240
 tacatcacta aacctttctc tcctcgtgaa ctagtagcac gcctcaaggc ggtattacgc
 300
 cgagcgactc cacaaggtat tgatgatcct attgaaattg atggtttaac gcttgatccc
 360
 attagccaac gc
 372

<210> 256
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 256
 Leu Glu Met Ala Gly Tyr Glu Tyr Met Glu Ala Glu Asn Ser Gln Gln
 1 5 10 15
 Ala His Glu Ile Ile Val Asp His Arg Pro Asp Leu Ile Leu Cys Asp
 20 25 30
 Trp Met Met Pro Gly Gly Ser Gly Ile Glu Leu Thr Arg Arg Leu Lys
 35 40 45
 Lys Asp Ser Thr Thr Ala Glu Ile Pro Val Ile Leu Leu Thr Ala Lys
 50 55 60
 Ser Glu Glu Asp Asn Lys Ile Gln Gly Leu Glu Val Gly Ala Asp Asp
 65 70 75 80
 Tyr Ile Thr Lys Pro Phe Ser Pro Arg Glu Leu Val Ala Arg Leu Lys
 85 90 95
 Ala Val Leu Arg Arg Ala Thr Pro Gln Gly Ile Asp Asp Pro Ile Glu
 100 105 110
 Ile Asp Gly Leu Thr Leu Asp Pro Ile Ser Gln Arg
 115 120

<210> 257
 <211> 639
 <212> DNA
 <213> Homo sapiens

<400> 257
 nnacgcgtag cggtcgaggt tgcggacacc atgcccgaa cgggcctgct cgccatcgag
 60
 gcacccatgg gacacggcaa gaccgaggcc gccctcatgt gcgcacaggt gctcgccgaa
 120

cggttcgggc tcggcggcat cttcttcggt ctaccgacga tggccacgtc caatcccatg
 180
 ttcggtcgag ttcgggaatg gctggacgct gtgccagcca aggaccgctc aagcatttcc
 240
 ctggctcact cgaaagctgg actcaacgag gagtaccagc agtcatgcc gtggaacgcc
 300
 accatggccg tctacgacga aggtgccggc acgcagcgtg aagcttcggc gatcgtccat
 360
 gagtggttct tgggccgcaa gcgcgcgac ctggccgacc acgtcgtcgg gaccatcgac
 420
 caggcactgt tcaccggtct caaagccaag catgtggtgt tacgccacct cggctctggcg
 480
 agcaaggctc tcattcattga tgaggccac gccgccgacg tctatatgcy cgaatacctc
 540
 aaggtcgtcc tcgaatggct cggcgcctac cgcacgccag tcctcctcat gtccgcgacg
 600
 ctgccaccgg cccaacgtca tgaactcgcg ctagecgtac
 639

<210> 258

<211> 213

<212> PRT

<213> Homo sapiens

<400> 258

Xaa	Arg	Val	Ala	Val	Glu	Val	Ala	Asp	Thr	Met	Pro	Glu	Pro	Gly	Leu
1				5					10					15	
Leu	Ala	Ile	Glu	Ala	Pro	Met	Gly	His	Gly	Lys	Thr	Glu	Ala	Ala	Leu
			20					25					30		
Met	Cys	Ala	Gln	Val	Leu	Ala	Glu	Arg	Phe	Gly	Leu	Gly	Gly	Ile	Phe
		35					40					45			
Phe	Gly	Leu	Pro	Thr	Met	Ala	Thr	Ser	Asn	Pro	Met	Phe	Gly	Arg	Val
	50					55					60				
Arg	Glu	Trp	Leu	Asp	Ala	Val	Pro	Ala	Lys	Asp	Pro	Ser	Ser	Ile	Ser
65				70					75					80	
Leu	Ala	His	Ser	Lys	Ala	Gly	Leu	Asn	Glu	Glu	Tyr	Gln	Gln	Leu	Met
			85					90						95	
Pro	Trp	Asn	Ala	Thr	Met	Ala	Val	Tyr	Asp	Glu	Gly	Ala	Gly	Thr	Gln
		100						105					110		
Arg	Glu	Ala	Ser	Ala	Ile	Val	His	Glu	Trp	Phe	Leu	Gly	Arg	Lys	Arg
		115					120					125			
Ala	Ile	Leu	Ala	Asp	His	Val	Val	Gly	Thr	Ile	Asp	Gln	Ala	Leu	Phe
	130					135					140				
Thr	Gly	Leu	Lys	Ala	Lys	His	Val	Val	Leu	Arg	His	Leu	Gly	Leu	Ala
145				150					155					160	
Ser	Lys	Val	Val	Ile	Ile	Asp	Glu	Val	His	Ala	Ala	Asp	Val	Tyr	Met
			165					170						175	
Arg	Glu	Tyr	Leu	Lys	Val	Val	Leu	Glu	Trp	Leu	Gly	Ala	Tyr	Arg	Thr
		180					185					190			
Pro	Val	Ile	Leu	Met	Ser	Ala	Thr	Leu	Pro	Pro	Ala	Gln	Arg	His	Glu
		195					200					205			
Leu	Ala	Leu	Ala	Tyr											
		210													

<210> 259
 <211> 252
 <212> DNA
 <213> Homo sapiens

<400> 259
 acgcgtgcac tgtgtgtatg catggtaacg tacacgtgtg cactgtgtgt ggtgtgcatg
 60
 ncatgggtgtg tgcacgtgtg cnactgtgtg tgcacgtgtg tgcacgtgtg tgcacgtgtg
 120
 tgtnggtgtg tatgcatgng tgtgtgcacg tgtgcactgn agtgtggggg gtatgcatgg
 180
 tgtgtgcaca tgagcactgt gtggtgtgtg tgcacgtgtg ggtgcacgtg tgcactgtgt
 240
 atgcaatggg gt
 252

<210> 260
 <211> 84
 <212> PRT
 <213> Homo sapiens

<400> 260
 Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys
 1 5 10 15
 Val Val Cys Met Xaa Trp Cys Val His Val Cys Xaa Cys Val Cys Met
 20 25 30
 Val Met Cys Thr Cys Ala Xaa Val Cys Xaa Cys Val Cys Met Xaa Val
 35 40 45
 Cys Thr Cys Ala Leu Xaa Cys Gly Val Tyr Ala Trp Cys Val His Met
 50 55 60
 Ser Thr Val Trp Cys Val Cys Met Val Xaa Cys Thr Cys Ala Leu Cys
 65 70 75 80
 Met Gln Trp Cys

<210> 261
 <211> 1202
 <212> DNA
 <213> Homo sapiens

<400> 261
 gctagcccg gtcggttcgt cgtcgatttg ctggcggcag tcccctcgat cgtcttcggt
 60
 ctgtggggcg gcatcgcttt cggatcgctg ggaatcatca acggttacgc gggggcctta
 120
 ttcaaagcgc tcggctggat tccgatcttt tccgaagatc cgtcgtgggc ctccggtact
 180
 ggcacggtct accttgccag tctcgtcctg gccatcatga tcctgccaat tatcactgct
 240
 gtttagcccg acgtcatgcc ccgaacgcc catgatcaag tcgaggccgc gctcgccttc
 300
 ggatcgacgc gctgggaggt catcaagctt gcagtgttcc cccactcgcg gtccggcatc
 360

atttccggat ccatgttggg tctaggacgc gccctcggcg agaccctggc tgtcaccctc
 420
 atcctgcaga cgatgagccc catggcgctc aaacagaacc tcaacctgtc gatcttcgtc
 480
 ggtggtgaga cattcgcgtc gaagattgcc ggtaacttct ccgaggccat tagcgatccc
 540
 acctcgctgg gtgccctcgt ggcgtcggcc ctggccctgt tcgtcattac cttcgtggtc
 600
 aacgcgactg cccggttgat tgcggcgaag ggggttaagc gatgagcgcc accaccctg
 660
 accacatcac ccacatggc gacaacacgc ccggacagct agatctctcc cgcccgtctg
 720
 gtaaacggac tatcaagagc ggctgcgcct caacattcat gatcgtggcc accgtactgg
 780
 ctgttatccc actggcctgg ctgctcttcg cggccgtccg gcgcggcatc ggatcactat
 840
 tccacgcgtc gtggtggacc cactcgatgg atccctcctt cgacttggcc gagcagggcg
 900
 ccatccacgc tatcgtcgga acccttgaaa ttggccttat tacatcgatt atctcggtac
 960
 cgatcgctct gatgaccgcy atcttcctag tcgagtacgc ccgcggaact aagatcgcca
 1020
 aggtcattag cttcgccgtc gacgtgctaa ccggtgtacc ttcaatcgtc gcggccctct
 1080
 tcgtcttcgc cgtagtcgtt accaccttcg gtggcaccca atccgcgtgg gcctcctcgt
 1140
 tggccctcat gatcctcatg gttccgacgg tgctgcgac aaccgaggaa atgctcaagc
 1200
 tt
 1202

<210> 262

<211> 214

<212> PRT

<213> Homo sapiens

<400> 262

Ala	Ser	Pro	Val	Ala	Phe	Val	Val	Asp	Leu	Leu	Ala	Ala	Val	Pro	Ser
1				5				10						15	
Ile	Val	Phe	Gly	Leu	Trp	Gly	Gly	Ile	Val	Phe	Gly	Ser	Ser	Gly	Ile
			20					25						30	
Ile	Asn	Gly	Tyr	Ala	Gly	Ala	Leu	Phe	Lys	Ala	Leu	Gly	Trp	Ile	Pro
			35				40						45		
Ile	Phe	Ser	Glu	Asp	Pro	Ser	Trp	Ser	Ser	Ala	Thr	Gly	Thr	Val	Tyr
			50				55						60		
Leu	Ala	Ser	Leu	Val	Leu	Ala	Ile	Met	Ile	Leu	Pro	Ile	Ile	Thr	Ala
65					70					75					80
Val	Ser	Arg	Asp	Val	Met	Pro	Arg	Thr	Pro	His	Asp	Gln	Val	Glu	Ala
				85					90					95	
Ala	Leu	Ala	Leu	Gly	Ser	Thr	Arg	Trp	Glu	Val	Ile	Lys	Leu	Ala	Val
			100					105					110		
Phe	Pro	His	Ser	Arg	Ser	Gly	Ile	Ile	Ser	Gly	Ser	Met	Leu	Gly	Leu
			115				120					125			
Gly	Arg	Ala	Leu	Gly	Glu	Thr	Leu	Ala	Val	Thr	Leu	Ile	Leu	Gln	Thr

```

      130              135              140
Met Ser Pro Met Ala Leu Lys Gln Asn Leu Asn Leu Ser Ile Phe Val
145              150              155              160
Gly Gly Glu Thr Phe Ala Ser Lys Ile Ala Gly Asn Phe Ser Glu Ala
      165              170              175
Ile Ser Asp Pro Thr Ser Leu Gly Ala Leu Val Ala Ser Ala Leu Ala
      180              185              190
Leu Phe Val Ile Thr Phe Val Val Asn Ala Thr Ala Arg Leu Ile Ala
      195              200              205
Ala Lys Gly Val Lys Arg
      210

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<210> 263
 <211> 424
 <212> DNA
 <213> Homo sapiens

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<400> 263
acgcgtgagt gctctgcgct ggaaacaacg gtgatagagc ccatccgccg tgaactttcc
60
gacgtggtgc tcgtgaacaa gctcgaaaag tatgtacgcg aacgtacctc ggaagacgtt
120
gcgcacatgg aagaggatgc ggaccagacg ggcaacgaca tcctcacgac gatcctgctg
180
tcgaactggg atccactatt ggatatgacg acgcaggatc atgtgctggc catgcaaag
240
gcttatatgg cctcgccatt ccgtgccaat ttggacctgg cataccatc ttcgacgcca
300
caggcccagt cccagccggc gatgccgccg tgggagacag ggacctcagc cagtagcatg
360
gcggatgctc gtgaatttgc gctgctgaag ctgtacctgc gtagcttgct gcagaagcac
420
gann
424

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<210> 264
 <211> 99
 <212> PRT
 <213> Homo sapiens

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<400> 264
Met Glu Glu Asp Ala Asp Gln Thr Gly Asn Asp Ile Leu Thr Thr Ile
1      5      10      15
Leu Leu Ser Asn Trp Asp Pro Leu Leu Asp Met Thr Thr Gln Asp His
      20      25      30
Val Leu Ala Met Gln Lys Ala Tyr Met Ala Ser Pro Phe Arg Ala Asn
      35      40      45
Leu Asp Leu Ala Tyr Pro Ser Ser Thr Pro Gln Ala Gln Ser Gln Pro
      50      55      60
Ala Met Pro Pro Trp Glu Thr Gly Thr Ser Ala Ser Ser Met Ala Asp
65      70      75      80
Ala Arg Glu Phe Ala Leu Leu Lys Leu Tyr Leu Arg Ser Leu Leu Gln
      85      90      95
Lys His Xaa

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<210> 265
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 265
 ncgtacggcc ctggcgctccg catggacgag ggataccatt ccggcatgac ggtgccgggt
 60
 gccttcgact ccctcatcgg caagctcatc atcactgggtg atagccgtga gcaagccctg
 120
 gctcgagctg cccgcgccct cgacgaaatc gtcacgacg gcatgccgac ggtcattccc
 180
 tttcaccagg cgggtggttca cgacccggct ttcactgccg ccgacggctg ctcgggcgtc
 240
 tttaccgact ggatcgaaac cgagttcgac aacaagatcg agccatacac cgggtctctg
 300
 ggcgagtctg ccaattccga gcctcctcgt gaggtcgtcg tcgaggtcaa cggtaaacgc
 360

<210> 266
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 266
 Xaa Tyr Gly Pro Gly Val Arg Met Asp Glu Gly Tyr His Ser Gly Met
 1 5 10 15
 Thr Val Pro Gly Ala Phe Asp Ser Leu Ile Gly Lys Leu Ile Ile Thr
 20 25 30
 Gly Asp Ser Arg Glu Gln Ala Leu Ala Arg Ala Arg Ala Leu Asp
 35 40 45
 Glu Ile Val Ile Asp Gly Met Pro Thr Val Ile Pro Phe His Gln Ala
 50 55 60
 Val Val His Asp Pro Ala Phe Thr Ala Ala Asp Gly Cys Phe Gly Val
 65 70 75 80
 Phe Thr Asp Trp Ile Glu Thr Glu Phe Asp Asn Lys Ile Glu Pro Tyr
 85 90 95
 Thr Gly Ser Leu Gly Glu Ser Ala Asn Ser Glu Pro Pro Arg Glu Val
 100 105 110
 Val Val Glu Val Asn Gly Lys Arg
 115 120

<210> 267
 <211> 471
 <212> DNA
 <213> Homo sapiens

<400> 267
 natcctcaac gtgtgttcag ttccacgcga aagatcatgt tcgtcatcgg atcgatgccg
 60
 ttaacgcatc ctagtcaatc caccgatggc gaccctggca aaaaatacga ggtgacttgg
 120

ctagatctcg ggcaccttca ccctagtcgg cggggactcg tcactatcac cacaactgtc
 180
 gatgatgacg tcatcacctc ttcccaggta aatgtcggca acctccaccg cggggatgaa
 240
 aaacttttcg aagctcgcga ttaccgccag attccgatgc ttgcatcacg tcatggctgg
 300
 acagctccat tcattggtga gaccggcgca gcccatgcc a tcgaggatgc gatgggcatt
 360
 accatcccaa ctgcgctggc atggatacga acctgctcg ctgagttcag cagaatcacc
 420
 tcacacttca catttttgtc atgggtaggc catcactgtg atgatgccgg c
 471

<210> 268

<211> 157

<212> PRT

<213> Homo sapiens

<400> 268

Xaa	Pro	Gln	Arg	Val	Phe	Ser	Ser	Thr	Arg	Lys	Ile	Met	Phe	Val	Ile
1				5					10					15	
Gly	Ser	Met	Pro	Leu	Thr	His	Pro	Ser	Gln	Ser	Thr	Asp	Gly	Asp	Pro
			20					25					30		
Gly	Lys	Lys	Tyr	Glu	Val	Thr	Trp	Leu	Asp	Leu	Gly	His	Leu	His	Pro
		35					40					45			
Ser	Arg	Pro	Gly	Leu	Val	Thr	Ile	Thr	Thr	Thr	Val	Asp	Asp	Asp	Val
	50					55					60				
Ile	Thr	Ser	Ser	Gln	Val	Asn	Val	Gly	Asn	Leu	His	Arg	Gly	Asp	Glu
65				70					75					80	
Lys	Leu	Phe	Glu	Ala	Arg	Asp	Tyr	Arg	Gln	Ile	Pro	Met	Leu	Ala	Ser
			85					90					95		
Arg	His	Gly	Trp	Thr	Ala	Pro	Phe	Ile	Gly	Glu	Thr	Gly	Ala	Ala	His
			100					105					110		
Ala	Ile	Glu	Asp	Ala	Met	Gly	Ile	Thr	Ile	Pro	Thr	Arg	Val	Ala	Trp
		115					120					125			
Ile	Arg	Thr	Leu	Leu	Ala	Glu	Phe	Ser	Arg	Ile	Thr	Ser	His	Phe	Thr
	130					135					140				
Phe	Leu	Ser	Trp	Val	Gly	His	His	Cys	Asp	Asp	Ala	Gly			
145				150						155					

<210> 269

<211> 387

<212> DNA

<213> Homo sapiens

<400> 269

acgcgtgtcg tgtttccaga aaaaaccaat aaattagagt ttatggtaga agtgattgct
 60
 gatatgacgg taatcaatcc atttgatttc tttgtggaaa gctacgcaga agactaccca
 120
 tttgcttatg acaaagctct taaaaaagag ttagaacctt atttacaggt ttctgaacct
 180
 tgttcggttac tcgacaaatg gctgtctggt gttgatcgtg aaaaaacacc gatcaatgat
 240

tttctagtcg caataaacag tcgccttgcc ggtgatattg gctatgggtat tcgcttagaa
 300
 ccgggcggttc agtcacctga agaaacgctc acattaatga aaggctcttg tcgcgatacc
 360
 tcgggggttat tgggttcaaact actacgc
 387

<210> 270
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 270
 Thr Arg Val Val Phe Pro Glu Lys Thr Asn Lys Leu Glu Phe Met Val
 1 5 10 15
 Glu Val Ile Ala Asp Met Thr Val Ile Asn Pro Phe Asp Phe Phe Val
 20 25 30
 Glu Ser Tyr Ala Glu Asp Tyr Pro Phe Ala Tyr Asp Lys Ala Leu Lys
 35 40 45
 Lys Glu Leu Glu Pro Tyr Leu Gln Val Ser Glu Pro Cys Ser Leu Leu
 50 55 60
 Asp Lys Trp Leu Ser Gly Val Asp Arg Glu Lys Thr Pro Ile Asn Asp
 65 70 75 80
 Phe Leu Val Ala Ile Asn Ser Arg Leu Ala Gly Asp Ile Gly Tyr Gly
 85 90 95
 Ile Arg Leu Glu Pro Gly Val Gln Ser Pro Glu Glu Thr Leu Thr Leu
 100 105 110
 Met Lys Gly Ser Cys Arg Asp Thr Ser Gly Leu Leu Val Gln Ile Leu
 115 120 125
 Arg

<210> 271
 <211> 443
 <212> DNA
 <213> Homo sapiens

<400> 271
 gccggcacca acggaaagtc ctctaccgcg cgcattgggtcg attcgctttt gcgtgccttc
 60
 caccgcccag tgggttttgg aaccagccca cacctgcagc gcgttactga gcgcatcggc
 120
 attgatggcc agccattca cccgcgcgat tatgtacgca tctggcacga gattaagcca
 180
 tttgtggaaa tggtcgatgc cgaatcggac gtgcctatgt ctaagtccga ggtcttcgtg
 240
 ggcctgtcct atgctgcgtt tgccgacgcc cccggggacg tcgctgtcgt cgaagtcggc
 300
 cttggcggac gttgggacgc taccaatgtg gtcaacgcgg atgtctctgt cattaccccg
 360
 gtgggcatgg accacacgga ttacctgggg gagacgatca ctgaaatcgc aggcgagaaa
 420
 gctggcatta ttaagccacg cgt
 443

<210> 272
 <211> 147
 <212> PRT
 <213> Homo sapiens

<400> 272
 Ala Gly Thr Asn Gly Lys Ser Ser Thr Ala Arg Met Val Asp Ser Leu
 1 5 10 15
 Leu Arg Ala Phe His Arg Arg Val Gly Leu Val Thr Ser Pro His Leu
 20 25 30
 Gln Arg Val Thr Glu Arg Ile Gly Ile Asp Gly Gln Pro Ile His Pro
 35 40 45
 Arg Asp Tyr Val Arg Ile Trp His Glu Ile Lys Pro Phe Val Glu Met
 50 55 60
 Val Asp Ala Glu Ser Asp Val Pro Met Ser Lys Phe Glu Val Phe Val
 65 70 75 80
 Gly Leu Ser Tyr Ala Ala Phe Ala Asp Ala Pro Gly Asp Val Ala Val
 85 90 95
 Val Glu Val Gly Leu Gly Gly Arg Trp Asp Ala Thr Asn Val Val Asn
 100 105 110
 Ala Asp Val Ser Val Ile Thr Pro Val Gly Met Asp His Thr Asp Tyr
 115 120 125
 Leu Gly Glu Thr Ile Thr Glu Ile Ala Gly Glu Lys Ala Gly Ile Ile
 130 135 140
 Lys Pro Arg
 145

<210> 273
 <211> 864
 <212> DNA
 <213> Homo sapiens

<400> 273
 caaagtaaga ctgcttcaaa ttttgtgttc tgctctgcag ctcgctcccc cctgctgtcg
 60
 aagagaagcc aaagcccccc cccccacct caaaggctcg gaagtctggc atccctactt
 120
 ccgagcctgg atcccagtaa ggatcttgcc ctccctgcaa caccgagtgc cttagacagc
 180
 tgctgctga gaactggcct ccagccggtg tcctcattcc atggggctcc ctgctgactg
 240
 catttcctga tctgggatga tgtttaccag cccaaaacca gtcattgttct tccaaaagct
 300
 tctctttgat agaattttga ggccatgcca cctcccttcc agtccacatg gaattccaga
 360
 atcagtcaca gcctctgatt ttttccaaga agagattgcc ttcaccattg ttaaattgtca
 420
 gcctgtacgg cagagacatg gtggtctgca caagcctgga caagttcttc catattgatg
 480
 gtgggagcaa cccctgtaat ctactccttg gaaggatttt ttgctttgct tatgaaaagc
 540
 tgtgcttgag acttaggtac ttttctcacg tggacacact gatcccatcc catattgcat
 600

ctttgaagag atggatatca agtacacttt ggtagctgaa ataatcatat ctttctgatg
 660
 tctattgtat ctcctttgag gaaaagaaca cacattttta atggagattg gctgctttca
 720
 ggtatgtgtg tctatcattg aaagagcatg gactcaaaca tcagccctga gttcttgagt
 780
 ccaccaact cccatcttct tgtggcacag gaaagctgcc ctctccctct cccaccacac
 840
 tcctgactaa tgcccttcac gcgt
 864

<210> 274
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 274
 Met Trp Thr Gly Arg Glu Val Ala Trp Pro Gln Asn Ser Ile Lys Glu
 1 5 10 15
 Lys Leu Leu Glu His Asp Trp Phe Trp Ala Gly Lys His His Pro
 20 25 30
 Arg Ser Gly Asn Ala Val Ser Arg Glu Pro His Gly Met Arg Thr Pro
 35 40 45
 Ala Gly Gly Gln Phe Ser Gly Ser Ser Cys Leu Arg His Ser Val Leu
 50 55 60
 Gln Gly Gly Gln Asp Pro Tyr Trp Asp Pro Gly Ser Glu Val Gly Met
 65 70 75 80
 Pro Asp Phe Arg Ala Phe Glu Val Gly Gly Gly Phe Gly Phe Ser
 85 90 95
 Ser Thr Ala Gly Gly Ser Glu Leu Gln Ser Arg Thr Gln Asn Leu Lys
 100 105 110
 Gln Ser Tyr Phe
 115

<210> 275
 <211> 911
 <212> DNA
 <213> Homo sapiens

<400> 275
 naaatttaaa ggaacctccc ttctataacg gagagtattt attgcagctt tcctttctgt
 60
 ttattttcag gaatgaaagg aattaccag ccttctgctt ttatacctac agctgaaagt
 120
 aattcctttc agcctcaggt gaagactttg ccctctccaa ttgatgctaa acagcagttg
 180
 caacggaaaa tccagaagaa gcagcaagaa cagaaactac aatccccttt gccaggagaa
 240
 tctgcagcaa aaaagtcaga aagtgtaca agcaatggag tgactaatct tcctaattgga
 300
 aatccttcaa tcctttctcc tcaacctatt ggtatcggtg tggcagctgt ccctagtcct
 360
 attccggtcc agcggactag gcaattggta acttcaccga gtccaatgag ttcttctnga
 420

cggcaaagtt cttccctca atgtacaggt ggtcactcag cacatgcagt ctgtgaaaca
 480
 ggcaccaaag actccccaga acgttccagc agtcctgggtg ggaatcggtc tgcccggcac
 540
 cgttaccctc agatcttacc caaaccagcg aacaccagtg cactcaccat tcgctctcca
 600
 actactgtcc tctttactag tagtcccatc aaaactgctg ttgtaccgcg ttcacacatg
 660
 agttctctaa atgtggtgaa aatgacaaca atatccctca caccagcaa cagtaacacc
 720
 cctcttaaac attctgcctc agtcagcagt gctacaggaa caacagaaga atcaaggagt
 780
 gttccacaga tcaagaatgg ttctgtcgtg tcgcttcagt ctctggggtc caggagcagc
 840
 agtgcggggg gaacatctgc tgtggaagtc aaagtggaac ccgaaacatc atcagatgag
 900
 catcctgtac a
 911

<210> 276

<211> 279

<212> PRT

<213> Homo sapiens

<400> 276

Met	Lys	Gly	Ile	Thr	Gln	Pro	Ser	Ala	Phe	Ile	Pro	Thr	Ala	Glu	Ser
1				5					10					15	
Asn	Ser	Phe	Gln	Pro	Gln	Val	Lys	Thr	Leu	Pro	Ser	Pro	Ile	Asp	Ala
			20					25					30		
Lys	Gln	Gln	Leu	Gln	Arg	Lys	Ile	Gln	Lys	Lys	Gln	Gln	Glu	Gln	Lys
		35					40					45			
Leu	Gln	Ser	Pro	Leu	Pro	Gly	Glu	Ser	Ala	Ala	Lys	Lys	Ser	Glu	Ser
	50					55					60				
Ala	Thr	Ser	Asn	Gly	Val	Thr	Asn	Leu	Pro	Asn	Gly	Asn	Pro	Ser	Ile
65				70					75					80	
Leu	Ser	Pro	Gln	Pro	Ile	Gly	Ile	Val	Val	Ala	Ala	Val	Pro	Ser	Pro
			85					90						95	
Ile	Pro	Val	Gln	Arg	Thr	Arg	Gln	Leu	Val	Thr	Ser	Pro	Ser	Pro	Met
			100					105					110		
Ser	Ser	Ser	Xaa	Arg	Gln	Ser	Ser	Ser	Pro	Gln	Cys	Thr	Gly	Gly	His
		115				120						125			
Ser	Ala	His	Ala	Val	Cys	Glu	Thr	Gly	Thr	Lys	Asp	Ser	Pro	Glu	Arg
	130					135					140				
Ser	Ser	Ser	Pro	Gly	Gly	Asn	Arg	Ser	Ala	Arg	His	Arg	Tyr	Pro	Gln
145				150					155					160	
Ile	Leu	Pro	Lys	Pro	Ala	Asn	Thr	Ser	Ala	Leu	Thr	Ile	Arg	Ser	Pro
			165						170					175	
Thr	Thr	Val	Leu	Phe	Thr	Ser	Ser	Pro	Ile	Lys	Thr	Ala	Val	Val	Pro
		180						185					190		
Ala	Ser	His	Met	Ser	Ser	Leu	Asn	Val	Val	Lys	Met	Thr	Thr	Ile	Ser
	195					200						205			
Leu	Thr	Pro	Ser	Asn	Ser	Asn	Thr	Pro	Leu	Lys	His	Ser	Ala	Ser	Val
	210					215					220				
Ser	Ser	Ala	Thr	Gly	Thr	Thr	Glu	Glu	Ser	Arg	Ser	Val	Pro	Gln	Ile

225		230		235		240									
Lys	Asn	Gly	Ser	Val	Val	Ser	Leu	Gln	Ser	Pro	Gly	Ser	Arg	Ser	Ser
				245				250						255	
Ser	Ala	Gly	Gly	Thr	Ser	Ala	Val	Glu	Val	Lys	Val	Glu	Pro	Glu	Thr
				260				265						270	
Ser	Ser	Asp	Glu	His	Pro	Val									
				275											

<210> 277
 <211> 652
 <212> DNA
 <213> Homo sapiens

<400> 277
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 atgaaccttg ttggtgggct gcgtcaggca atggccacca ctggttactc ggagggtcaaa
 120
 gagttccagc gcatcgagct gacgattcgc taaccgttcc accacgcaga atggtgttcc
 180
 ggtgagcggg tggatagcta gccttcggcc atgagtgaag tgcccgatga attggtcgtg
 240
 ttgcgtggcg cgattgacaa catggacgcc gccctcatcc atctgcttgc cgaaagggtc
 300
 cggattactc gcgaggtagg ccgcctcaag gcggagtgcg gtttacctcc ggccgacccc
 360
 gcccgtaggg ctgagcagat cgcgcgggtg cggcagttag cggtcgagtc gaacctcgac
 420
 cccgaattcg cgcagaaggt catcacgttc atcgtggccg aggtggtgcg tcaccacgaa
 480
 gctattgctg acgattcttg cgacgactct ggagtggcgg atacggggga ggcggatgtc
 540
 cctgggtcgg gcagctgagt tacagatcag gcgatgacgt cgccctggtg caccttcgac
 600
 gggattccga cgacgactgt gccgggggcg acatccttga cgaccaacgc gt
 652

<210> 278
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 278
 Met Ser Glu Val Pro Asp Glu Leu Val Val Leu Arg Gly Ala Ile Asp
 1 5 10 15
 Asn Met Asp Ala Ala Leu Ile His Leu Leu Ala Glu Arg Phe Arg Ile
 20 25 30
 Thr Arg Glu Val Gly Arg Leu Lys Ala Glu Cys Gly Leu Pro Pro Ala
 35 40 45
 Asp Pro Ala Arg Glu Ala Glu Gln Ile Ala Arg Leu Arg Gln Leu Ala
 50 55 60
 Val Glu Ser Asn Leu Asp Pro Glu Phe Ala Gln Lys Val Ile Thr Phe
 65 70 75 80
 Ile Val Ala Glu Val Val Arg His His Glu Ala Ile Ala Asp Asp Ser

	85		90		95
Gly Asp Asp Ser Gly Val Ala Asp Thr Gly Glu Ala Asp Val Pro Gly					
	100		105		110
Ser Gly Ser					
	115				

<210> 279
 <211> 348
 <212> DNA
 <213> Homo sapiens

<400> 279
 cgggaggtca cacaagcatt caaacatag cagatggtaa atgttatgtt atgtgtatatt
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 taccacaatc cttaaaaaga aaagaaagaa aggcatatgg aacccttagt taccttcat
 120
 ccagcttcaa aattgtcagt gcatgggtcaa tcttgtctta tctgcccctc acccaccctt
 180
 ttccagaaag aagaccaga ggattccaca tctgcctgga aaccacgacc agtctcgact
 240
 ggaagttgtt gttaatgttg catgtattca taaaacctct aggcatttct agtgtccctc
 300
 agaatttttc caaattcagg caaacacaga aattacttcc aaaaattt
 348

<210> 280
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 280
 Met Cys Ile Leu Pro Gln Ser Leu Lys Arg Lys Glu Arg Lys Ala Tyr
 1 5 10 15
 Gly Thr Pro Ser Tyr Leu Ser Ser Ser Phe Lys Ile Val Ser Ala Trp
 20 25 30
 Ser Ile Leu Ser Tyr Leu Pro Leu Thr His Pro Phe Pro Glu Arg Arg
 35 40 45
 Pro Arg Gly Phe His Ile Cys Leu Glu Thr Thr Thr Ser Leu Asp Trp
 50 55 60
 Lys Leu Leu Leu Met Leu His Val Phe Ile Lys Pro Leu Gly Ile Ser
 65 70 75 80
 Ser Val Pro Gln Asn Phe Ser Lys Phe Arg Gln Thr Gln Lys Leu Leu
 85 90 95
 Pro Lys Ile

<210> 281
 <211> 384
 <212> DNA
 <213> Homo sapiens

<400> 281
 agatctgcgc agatcgataa tggattaaag actcttgacg ctggagtcac cgagatgaac
 60

aacaagggtgt tgggggcaac gaaggctgtc ggtgattcca ccactaccgt caaccagggtg
120
aattctgcgt taggaantgc cgactcagcg gcagagaaga cgtcgagcgc cgttactcag
180
acgcgcgtgg gtgcccaggc gattaccggc gctgctcaaa atgtcatggc tgattcccaa
240
gctgtcaact cagccatggt tccgcttatt aataacgtga caaagaatct tcctaccttg
300
caaaaacagg ccaggaatct cgtgtcagtg aacggtagcc tgcagaaccc caacgggtgat
360
tctgtcatta agattcaaca gacc
384

<210> 282
<211> 110
<212> PRT
<213> Homo sapiens

<400> 282
Met Asn Asn Lys Val Leu Gly Ala Thr Lys Ala Val Gly Asp Ser Thr
1 5 10 15
Thr Thr Val Asn Gln Val Asn Ser Ala Leu Gly Xaa Ala Asp Ser Ala
20 25 30
Ala Glu Lys Thr Ser Ser Ala Val Thr Gln Thr Arg Val Gly Ala Gln
35 40 45
Ala Ile Thr Gly Ala Ala Gln Asn Val Met Ala Asp Ser Gln Ala Val
50 55 60
Asn Ser Ala Met Val Pro Leu Ile Asn Asn Val Thr Lys Asn Leu Pro
65 70 75 80
Thr Leu Gln Lys Gln Ala Arg Asn Leu Val Ser Val Asn Gly Thr Leu
85 90 95
Gln Asn Pro Asn Gly Asp Ser Val Ile Lys Ile Gln Gln Thr
100 105 110

<210> 283
<211> 426
<212> DNA
<213> Homo sapiens

<400> 283
cgcgtagacc aatgtgagac ggccgtcacc aagggtcatgc gcgacaagtc gggttggttagc
60
ggaccggata ttgtgcgtcg cgagctgcgc catgtcgtga cgagcggcac gattgtcgat
120
ggaagcgtac tggctgacga attgagcagc tactgcatga gtatcaagga gcacgtccgc
180
tctgatggcc tatccgagtt tggcatctgc accctcgacg ccgccaccgc cgagttccga
240
tacatgacat tcgtcgacga tgccgtgctg tcacaactcg agacattgct gcgttctcta
300
cgcatcaagg aagtcttgca tgaaaaaggg gtcattgtgc cttccacgct gcgcttgatc
360
cgcaacgcgg tgcccaccac ctgccaatt accatgtcca agcctgatac cgaattgtcg
420

gagaga
426

<210> 284
<211> 142
<212> PRT
<213> Homo sapiens

<400> 284
Arg Val Asp Gln Cys Glu Thr Ala Val Thr Lys Gly Met Arg Asp Lys
1 5 10 15
Ser Val Gly Ser Gly Pro Asp Ile Val Arg Arg Glu Leu Arg His Val
20 25 30
Val Thr Ser Gly Thr Ile Val Asp Gly Ser Val Leu Ala Asp Glu Leu
35 40 45
Ser Ser Tyr Cys Met Ser Ile Lys Glu His Val Arg Ser Asp Gly Leu
50 55 60
Ser Glu Phe Gly Ile Cys Thr Leu Asp Ala Ala Thr Ala Glu Phe Arg
65 70 75 80
Tyr Met Thr Phe Val Asp Asp Ala Val Leu Ser Gln Leu Glu Thr Leu
85 90 95
Leu Arg Ser Leu Arg Ile Lys Glu Val Leu His Glu Lys Gly Val Met
100 105 110
Leu Pro Ser Thr Leu Arg Leu Ile Arg Asn Ala Val Pro Thr Thr Cys
115 120 125
Gln Ile Thr Met Leu Lys Pro Asp Thr Glu Leu Ser Glu Arg
130 135 140

<210> 285
<211> 345
<212> DNA
<213> Homo sapiens

<400> 285
acgcgtgcag tcccttaccg acatgctggc agatgagctc gacggcagcc gcttcaccgg
60
cgattttctca gaaatctaca aacgtcagaa ctcgatcttc ggcgatgtaa ggaataactt
120
ttacaaaaaa ggataccgca tcatcaacgt agcgaatggg gtattgcgca agatttcact
180
ggtaagcgca ggcaatgcag acaatgtgaa aggtcaggcc ctgttcttcc gcggtgtggc
240
gcatttcgaa ctcggtgcgtt tgtttgcaca accctggggt tatacttcgg acaattcaca
300
ctacggcatc ccgctccgca atgaaatcgt aattggttct attcn
345

<210> 286
<211> 107
<212> PRT
<213> Homo sapiens

<400> 286
Met Leu Ala Asp Glu Leu Asp Gly Ser Arg Phe Thr Gly Asp Phe Ser

1	5	10	15
Glu Ile Tyr Lys Arg Gln Asn Ser Ile Phe Gly Asp Val Arg Asn Asn			
	20	25	30
Phe Tyr Lys Lys Gly Tyr Arg Ile Ile Asn Val Ala Asn Gly Val Leu			
	35	40	45
Arg Lys Ile Ser Leu Val Ser Ala Gly Asn Ala Asp Asn Val Lys Gly			
	50	55	60
Gln Ala Leu Phe Phe Arg Gly Val Ala His Phe Glu Leu Val Arg Leu			
65	70	75	80
Phe Ala Gln Pro Trp Gly Tyr Thr Ser Asp Asn Ser His Tyr Gly Ile			
	85	90	95
Pro Leu Arg Asn Glu Ile Val Ile Gly Ser Ile			
	100	105	

<210> 287

<211> 1379

<212> DNA

<213> Homo sapiens

<400> 287

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tcagttgagg gattcgggac aatagcagtg ctgatggtaa tggtggcgat ttcctgttt
120
gttttgcagg tcacggccag gggctttggg cgcgtgttac agtttgccta cactgccaag
180
ctgttactca gcagagaaaa catccgcgag gtcatccgct gtgctgagtt cctgcgcatg
240
cacaacctgg aggactcctg cttcagcttc ctgcagaccc agctcctgaa cagtgaggat
300
ggcctgtttg tgtgccggaa ggatgctgcg tgccagcgcc cacacgagga ctgcgagaac
360
tctgcaggag aggaggagga tgaagaggag gagacgatgg attcagagac ggccaagatg
420
gcttgcccca gggaccagat gcttccagag cccatcagct ttgaggccgc cgccatcccc
480
gtagcagaga aggaagaagc cctgctgccc gagcctgacg tgcccacaga caccaaggag
540
agctcagaaa aggacgcgtt aacgcagtac cccagatata agaaatacca gcttgcattg
600
accaagaatg tctataatgc atcatcacac agtacctcag gttttgcaag cacattccgg
660
gaagataact ctagcaacag cctcaagccg gggcttgcca gggggcagat taaaagttag
720
ccgcccagtg aagagaatga ggaagagagc atcacgctct gcctgtctgg agatgagcct
780
gacgccaagg acagagcggg ggatgtcgag atggaccgga aacagcccag ccctgcccct
840
acccccacgg ccccagctgg ggccgcctgc ctggagagat ccaggagcgt ggcctcgccc
900
tcttgcttaa ggtctctgtt cagcataacg aaaagtgtgg agctgtctgg cctgcccagt
960
acatctcagc agcactttgc caggagtcca gctgcccctt ttgacaaggg gatcactcag
1020

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ggtgacctta aaactgacta cacccttttc acaggaatt atggacagcc ccacgtgggc
 1080
 cagaaggagg tgtccaactt caccatgggg tcgcccctca gggggcctgg gttggaggct
 1140
 ctctgtaaac aggagggaga gctggaccgg aggagcgtga tcttctctc cagcgcttgt
 1200
 gaccaagtga gcacctcggt gcattcttat tctgggggtga gcagtttgga caaagacctc
 1260
 tctgagccgg tgccaaaggg tctgtgggtg ggagccggcc agtccctccc cagctcgag
 1320
 gcctactccc acggtgggct gatggccgac cacttgccag gaaggatgcg gcccaacac
 1379

<210> 288

<211> 428

<212> PRT

<213> Homo sapiens

<400> 288

Met	Val	Met	Leu	Ala	Ile	Ser	Leu	Phe	Val	Leu	Gln	Val	Thr	Ala	Arg
1				5					10					15	
Gly	Phe	Gly	Pro	Leu	Leu	Gln	Phe	Ala	Tyr	Thr	Ala	Lys	Leu	Leu	Leu
			20					25					30		
Ser	Arg	Glu	Asn	Ile	Arg	Glu	Val	Ile	Arg	Cys	Ala	Glu	Phe	Leu	Arg
		35					40					45			
Met	His	Asn	Leu	Glu	Asp	Ser	Cys	Phe	Ser	Phe	Leu	Gln	Thr	Gln	Leu
	50					55					60				
Leu	Asn	Ser	Glu	Asp	Gly	Leu	Phe	Val	Cys	Arg	Lys	Asp	Ala	Ala	Cys
65					70					75					80
Gln	Arg	Pro	His	Glu	Asp	Cys	Glu	Asn	Ser	Ala	Gly	Glu	Glu	Glu	Asp
			85						90					95	
Glu	Glu	Glu	Glu	Thr	Met	Asp	Ser	Glu	Thr	Ala	Lys	Met	Ala	Cys	Pro
			100					105					110		
Arg	Asp	Gln	Met	Leu	Pro	Glu	Pro	Ile	Ser	Phe	Glu	Ala	Ala	Ala	Ile
		115					120					125			
Pro	Val	Ala	Glu	Lys	Glu	Glu	Ala	Leu	Leu	Pro	Glu	Pro	Asp	Val	Pro
		130				135					140				
Thr	Asp	Thr	Lys	Glu	Ser	Ser	Glu	Lys	Asp	Ala	Leu	Thr	Gln	Tyr	Pro
145					150					155					160
Arg	Tyr	Lys	Lys	Tyr	Gln	Leu	Ala	Cys	Thr	Lys	Asn	Val	Tyr	Asn	Ala
			165						170					175	
Ser	Ser	His	Ser	Thr	Ser	Gly	Phe	Ala	Ser	Thr	Phe	Arg	Glu	Asp	Asn
		180					185						190		
Ser	Ser	Asn	Ser	Leu	Lys	Pro	Gly	Leu	Ala	Arg	Gly	Gln	Ile	Lys	Ser
		195					200					205			
Glu	Pro	Pro	Ser	Glu	Glu	Asn	Glu	Glu	Glu	Ser	Ile	Thr	Leu	Cys	Leu
	210					215						220			
Ser	Gly	Asp	Glu	Pro	Asp	Ala	Lys	Asp	Arg	Ala	Gly	Asp	Val	Glu	Met
225					230					235					240
Asp	Arg	Lys	Gln	Pro	Ser	Pro	Ala	Pro	Thr	Pro	Thr	Ala	Pro	Ala	Gly
			245						250					255	
Ala	Ala	Cys	Leu	Glu	Arg	Ser	Arg	Ser	Val	Ala	Ser	Pro	Ser	Cys	Leu
		260					265						270		
Arg	Ser	Leu	Phe	Ser	Ile	Thr	Lys	Ser	Val	Glu	Leu	Ser	Gly	Leu	Pro

275	280	285
Ser Thr Ser Gln Gln His Phe Ala Arg Ser Pro Ala Cys Pro Phe Asp		
290	295	300
Lys Gly Ile Thr Gln Gly Asp Leu Lys Thr Asp Tyr Thr Pro Phe Thr		
305	310	315
Gly Asn Tyr Gly Gln Pro His Val Gly Gln Lys Glu Val Ser Asn Phe		
325	330	335
Thr Met Gly Ser Pro Leu Arg Gly Pro Gly Leu Glu Ala Leu Cys Lys		
340	345	350
Gln Glu Gly Glu Leu Asp Arg Arg Ser Val Ile Phe Ser Ser Ser Ala		
355	360	365
Cys Asp Gln Val Ser Thr Ser Val His Ser Tyr Ser Gly Val Ser Ser		
370	375	380
Leu Asp Lys Asp Leu Ser Glu Pro Val Pro Lys Gly Leu Trp Val Gly		
385	390	395
Ala Gly Gln Ser Leu Pro Ser Ser Gln Ala Tyr Ser His Gly Gly Leu		
405	410	415
Met Ala Asp His Leu Pro Gly Arg Met Arg Pro Asn		
420	425	

<210> 289

<211> 822

<212> DNA

<213> Homo sapiens

<400> 289

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ngcattaccg ggctgaagac ggggtgctcat gacctcaacg atataggcta ttgctagaac
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cacgccggcc cacgccgcgc aaagcgcaga cacggcacca ggaggggtca catggctgat
120
agcaagtcca aggcgaagga cgagcgcact gccgatgaga tcaggcggga tattgcagcg
180
acccgtgctt gcctggcagc cggggtggag aacctcgtgg aggaggtgca tccggcaacc
240
ctcaagcgtg aagcatctga tcgtgcccggt gattttgtgc aggggtgagtt tgatcaggtc
300
aagagccagg tcaaagatga gaaatgggtg cgcgctgcagc ggatcgcgat ggccgcagga
360
gtgctcgctg ccggcgctcg cagcattatt gtgctgcgcg cgatagtcgg tcgcgcaacg
420
ggcgctaccg ctcgctcgcaa gcttgagaag ctgcagcttt ctcaggcgaa gcgggttcga
480
aaagatgcca agcagcgtag taaggaagat gaaaaggcag ccaagaaaaa tgccaagctc
540
ggcaagaaga acgctaagaa gtacggcaag ctcgataccg atgactcgtc ggtaagcaac
600
cttgccgaga aaatgctcaa acaggccgcc gtgctgcgtg cacaggcggc tgccggggcg
660
tgagaacagt gccgcctagc aaacagcggg cacagcgcaa aacaggtttg gctccgaccc
720
atggtggacc ggagccaaac tgtgttaccg catcatttga taccgccagc agccaggcct
780
gcgacaatgc gacgctggaa taccagcacc atgatgacta gt
822

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<210> 290
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 290
 Met Ala Asp Ser Lys Ser Lys Ala Lys Asp Glu Arg Thr Ala Asp Glu
 1 5 10 15
 Ile Arg Arg Asp Ile Ala Ala Thr Arg Ala Cys Leu Ala Ala Gly Val
 20 25 30
 Glu Asn Leu Val Glu Glu Val His Pro Ala Thr Leu Lys Arg Glu Ala
 35 40 45
 Ser Asp Arg Ala Arg Asp Phe Val Gln Gly Glu Phe Asp Gln Val Lys
 50 55 60
 Ser Gln Val Lys Asp Glu Lys Trp Trp Arg Val Gln Arg Ile Ala Met
 65 70 75 80
 Ala Ala Gly Val Leu Ala Ala Gly Val Val Ser Ile Ile Val Leu Arg
 85 90 95
 Ala Ile Val Gly Arg Ala Thr Gly Ala Thr Ala Arg Arg Lys Leu Glu
 100 105 110
 Lys Leu Gln Leu Ser Gln Ala Lys Arg Val Arg Lys Asp Ala Lys Gln
 115 120 125
 Arg Ser Lys Glu Asp Glu Lys Ala Ala Lys Lys Asn Ala Lys Leu Gly
 130 135 140
 Lys Lys Asn Ala Lys Lys Tyr Gly Lys Leu Asp Thr Asp Asp Ser Ser
 145 150 155 160
 Val Ser Asn Leu Ala Glu Lys Met Leu Lys Gln Ala Ala Val Leu Arg
 165 170 175
 Ala Gln Ala Ala Ala Gly Ala
 180

<210> 291
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 291
 ctccacgccg acaagactta cgacgggCGT cgctgccggg ctgagtgccg ggcccGctcc
 60
 atcaccccc gcacGctcg ccgCGgCGtg gagaccagcg agcGcttggg ccggtatcgc
 120
 tgggtcGtcg agcgcacctt cgctggGtc aaccGctttc ggCGcctcgc catccGctac
 180
 gagCGgCGtg ctgacatcca cgaagccttc gtgacCctcg gctgcGccct catctGcctc
 240
 aaccagatca gacggttttg ttaggtGctg taaagggaga atggctgcag ctgggctatc
 300
 tgctccctcg tcaaccagaa acaggctgct catcctcact caacaacgcg t
 351

<210> 292
 <211> 87
 <212> PRT

<213> Homo sapiens

<400> 292

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Leu His Ala Asp Lys Thr Tyr Asp Gly Arg Arg Cys Arg Ala Glu Cys
 1           5           10           15
Arg Ala Arg Ser Ile Thr Pro Arg Ile Ala Arg Arg Gly Val Glu Thr
          20           25           30
Ser Glu Arg Leu Gly Arg Tyr Arg Trp Val Val Glu Arg Thr Phe Ala
          35           40           45
Trp Leu Asn Arg Phe Arg Arg Leu Ala Ile Arg Tyr Glu Arg Arg Ala
          50           55           60
Asp Ile His Glu Ala Phe Val Ile Leu Gly Cys Ala Leu Ile Cys Leu
65           70           75           80
Asn Gln Ile Arg Arg Phe Cys
          85

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<210> 293

<211> 716

<212> DNA

<213> Homo sapiens

<400> 293

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nncttcacca caccggccat caacgcacct cctcgtgata acttgacctt ctgccgaacc
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ggttaatcag tttagtggcg aggcattgaca cgttgacgag tcagctgtgg tacatgtgcg
120
gaacactcac aatgccacgg cggcatgttg ctgtcgggtca cgacccttat ggtgatcgtc
180
gtgagaaccc gaacggcaga tgcgattctg gcggcactgg atctgaacag gtttaagggt
240
gcgaagactt tcgatgttcc agtgtgcgtc atagctgggtg ccgggacagg taaaactcgt
300
gctgtcactc atcgcattgc ctacgggtgca gcgacaggca agcttgatcc gcgtcgtacc
360
ctcgcgggtca cttttacgac taaggcagct ggcacgatga gaggtcgact cgccgatctg
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540
gtggcgggaga cgacccatcg cattgggtctg ggcaatgaca aggcgctgct gcgcgacttg
600
tccgcccgaga tctcgtgggc gaaggtctca aatgtgccga ctgatcaata cgcacccctg
660
gctagggcgg aaggtcgggt ggtggcggga gtttcggcaa ctgacgtagg acgcgt
716

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<210> 294

<211> 190

<212> PRT

<213> Homo sapiens

<400> 294

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Met Leu Leu Ser Val Thr Thr Leu Met Val Ile Ala Val Arg Thr Arg

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      1           5           10           15
Thr Ala Asp Ala Ile Leu Ala Ala Leu Asp Leu Asn Arg Phe Lys Val
      20           25           30
Ala Lys Thr Phe Asp Val Pro Val Cys Val Ile Ala Gly Ala Gly Thr
      35           40           45
Gly Lys Thr Arg Ala Val Thr His Arg Ile Ala Tyr Gly Ala Ala Thr
      50           55           60
Gly Lys Leu Asp Pro Arg Arg Thr Leu Ala Val Thr Phe Thr Thr Lys
      65           70           75           80
Ala Ala Gly Thr Met Arg Gly Arg Leu Ala Asp Leu Gly Val Val Gly
      85           90           95
Val Gln Ala Arg Thr Ile His Ser Ala Ala Leu Arg Gln Ile Lys Phe
      100          105          110
Phe Trp Pro Arg Ala Tyr Asn Cys Glu Leu Pro Pro Val Ser Asp Ser
      115          120          125
Arg Phe Ser Met Val Ala Glu Thr Thr His Arg Ile Gly Leu Gly Asn
      130          135          140
Asp Lys Ala Leu Leu Arg Asp Leu Ser Ala Glu Ile Ser Trp Ala Lys
      145          150          155          160
Val Ser Asn Val Pro Thr Asp Gln Tyr Ala Ser Leu Ala Arg Ala Glu
      165          170          175
Gly Arg Val Val Ala Gly Val Ser Ala Thr Asp Val Gly Arg
      180          185          190

```

<210> 295
 <211> 417
 <212> DNA
 <213> Homo sapiens

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<400> 295
ttcatatcag gcagtacccg agtccatgcg atcaacaacg tcagcgtatc tttcacccat
60
tctggagtgc accttctcat gggagaaagc ggatcaggaa aaagcaccct catcaatctc
120
ctagctggtc tggatacccc agattcgggg tccgtctacg cagaaggcgt caccgtatct
180
gatcagagcg aggcgagcag agcccaattt cgattacgcc acatcgccgt catcttccag
240
gacgacaacc tcatcgctga gttgaccaat accgagaata ttgcgctacc cctgtgggcg
300
cagggcacat cgaagtccga tgccactgaa atcgcccacg aagccatgcg aaaactagga
360
atcgagtcac tgggcagacg ctaccccggc gaggtctcgg gtggccaacg gcaacgc
417

```

<210> 296
 <211> 139
 <212> PRT
 <213> Homo sapiens

```

<400> 296
Phe Ile Ser Gly Ser Thr Arg Val His Ala Ile Asn Asn Val Ser Val
1           5           10           15
Ser Phe Thr His Ser Gly Val His Leu Leu Met Gly Glu Ser Gly Ser

```

```

      20      25      30
Gly Lys Ser Thr Leu Ile Asn Leu Leu Ala Gly Leu Asp Thr Pro Asp
      35      40      45
Ser Gly Ser Val Tyr Ala Glu Gly Val Thr Val Ser Asp Gln Ser Glu
      50      55      60
Ala Ser Arg Ala Gln Phe Arg Leu Arg His Ile Ala Val Ile Phe Gln
65      70      75      80
Asp Asp Asn Leu Ile Ala Glu Leu Thr Asn Thr Glu Asn Ile Ala Leu
      85      90      95
Pro Leu Trp Ala Gln Gly Thr Ser Lys Ser Asp Ala Thr Glu Ile Ala
      100      105      110
His Glu Ala Met Arg Lys Leu Gly Ile Glu Ser Leu Gly Arg Arg Tyr
      115      120      125
Pro Gly Glu Val Ser Gly Gly Gln Arg Gln Arg
      130      135

```

<210> 297
 <211> 378
 <212> DNA
 <213> Homo sapiens

```

<400> 297
tacaccatcg gtgaccagat tgtcgaagct ctgcaggtgc actcgaagat gtccgacaag
60
gacgcttggg cgcgtgccat cgagctgctc gacttggtgg ggattccgaa tcccagggtg
120
cgtgccaaag cttttccgca cgagttttcc ggtggcatga ggcaacgagt cgtcatcgcc
180
atggccatcg cgaacgaccc tgacctcatc atcgccgacg agccgacgac ggccctcgac
240
gtgaccatcc aggcccagat tctcgatttg ctgcgcgtag cccagcgtga aacctatgcg
300
ggcgtcgtaa tgatcaccca cgacctcggg gtggtagctg gtctggctga cagggttgcc
360
gtgatgtatg ccggacgc
378

```

<210> 298
 <211> 126
 <212> PRT
 <213> Homo sapiens

```

<400> 298
Tyr Thr Ile Gly Asp Gln Ile Val Glu Ala Leu Gln Val His Ser Lys
1      5      10      15
Met Ser Asp Lys Asp Ala Trp Ala Arg Ala Ile Glu Leu Leu Asp Leu
      20      25      30
Val Gly Ile Pro Asn Pro Glu Val Arg Ala Lys Ala Phe Pro His Glu
      35      40      45
Phe Ser Gly Gly Met Arg Gln Arg Val Val Ile Ala Met Ala Ile Ala
      50      55      60
Asn Asp Pro Asp Leu Ile Ile Ala Asp Glu Pro Thr Thr Ala Leu Asp
65      70      75      80
Val Thr Ile Gln Ala Gln Ile Leu Asp Leu Leu Arg Val Ala Gln Arg

```

	85		90		95
Glu Thr His	Ala Gly Val Val Met	Ile Thr His Asp	Leu Gly Val Val		
	100	105	110		
Ala Gly Leu	Ala Asp Arg Val Ala Val Met Tyr	Ala Gly Arg			
	115	120	125		

<210> 299
 <211> 368
 <212> DNA
 <213> Homo sapiens

<400> 299
 gtgcacggtt tcgttggcat gcgcaatgac cgggagaact tgcgttttga tccgagactt
 60
 ccagcccaat ggacgtcgat caaacaccac atgctcattg gcgactctca catgctcggt
 120
 ttcttggaac gtgacgccat tacgttccag attctgtcgg gccatgaccg cgacgtgaca
 180
 gtgcgcggtg agctctacca cattgggggtt gagccggtga gggtgccggt gtccgatcag
 240
 gggccggttg gtcttagcct gcgcggtacc catccgatct cgggggttgcg tcgagctgac
 300
 ggttctctta tcaactgcaga agttcccggc agcattgctg agacgattgg gtcttctccg
 360
 atctcgac
 368

<210> 300
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 300
 Val His Gly Phe Val Gly Met Arg Asn Asp Arg Glu Asn Leu Arg Phe
 1 5 10 15
 Asp Pro Arg Leu Pro Ala Gln Trp Thr Ser Ile Lys His His Met Leu
 20 25 30
 Ile Gly Asp Ser His Met Leu Val Phe Leu Glu Arg Asp Ala Ile Thr
 35 40 45
 Phe Gln Ile Leu Ser Gly His Asp Arg Asp Val Thr Val Arg Gly Glu
 50 55 60
 Leu Tyr His Ile Gly Val Glu Pro Val Arg Val Pro Leu Ser Asp Gln
 65 70 75 80
 Gly Pro Leu Arg Pro Ser Leu Arg Val Thr His Pro Ile Ser Gly Leu
 85 90 95
 Arg Arg Ala Asp Gly Ser Leu Ile Thr Ala Glu Val Pro Gly Ser Ile
 100 105 110
 Ala Glu Thr Ile Gly Ser Ser Pro Ile Ser
 115 120

<210> 301
 <211> 456
 <212> DNA
 <213> Homo sapiens

<400> 301

ggccgggtta ttgcccgccc gtttgtcggg gaaacccggc agaccttcga gcgcaccggc
60
aaccggcgcg actattccgt accgccgccc gaaccgacct tgctcgacag gcttacggac
120
gcggggccgga cggatgatcg aatcggcaag attggtgata tctacgcgca caaaggcgtg
180
tctcaggtgc gtaaggcaat ggcaatattg gccttggttcg atgaaacact cattgccatg
240
gacgacgcgc aggacggcga tctggtcttc accaacttcg tggatttcga catgctctac
300
gggcatcgca gggatgtgcc cggctatgcc gccgcgctcg aggttttcga ccggaggctg
360
ccggaagcca tggcgaaatt gcggacgggc gatcttctga tcctgacagc cgatcatggc
420
tgcgaccgca ccctcaaggg aaccgaccac acgcgt
456

<210> 302

<211> 152

<212> PRT

<213> Homo sapiens

<400> 302

Gly	Arg	Val	Ile	Ala	Arg	Pro	Phe	Val	Gly	Glu	Thr	Arg	Gln	Thr	Phe
1				5					10					15	
Glu	Arg	Thr	Gly	Asn	Arg	Arg	Asp	Tyr	Ser	Val	Pro	Pro	Pro	Glu	Pro
			20					25					30		
Thr	Leu	Leu	Asp	Arg	Leu	Thr	Asp	Ala	Gly	Arg	Thr	Val	Ile	Ala	Ile
		35					40					45			
Gly	Lys	Ile	Gly	Asp	Ile	Tyr	Ala	His	Lys	Gly	Val	Ser	Gln	Val	Arg
	50				55					60					
Lys	Ala	Met	Ala	Ile	Leu	Ala	Leu	Phe	Asp	Glu	Thr	Leu	Ile	Ala	Met
65					70				75					80	
Asp	Asp	Ala	Gln	Asp	Gly	Asp	Leu	Val	Phe	Thr	Asn	Phe	Val	Asp	Phe
			85					90					95		
Asp	Met	Leu	Tyr	Gly	His	Arg	Arg	Asp	Val	Pro	Gly	Tyr	Ala	Ala	Ala
			100					105					110		
Leu	Glu	Ala	Phe	Asp	Arg	Arg	Leu	Pro	Glu	Ala	Met	Ala	Lys	Leu	Arg
		115					120					125			
Thr	Gly	Asp	Leu	Leu	Ile	Leu	Thr	Ala	Asp	His	Gly	Cys	Asp	Pro	Thr
	130					135					140				
Leu	Lys	Gly	Thr	Asp	His	Thr	Arg								
145					150										

<210> 303

<211> 402

<212> DNA

<213> Homo sapiens

<400> 303

nncgtgggca tcgaggagtt cctcgacatg aagtatcacg cgacgccgat tcatcgtcgc
60

tgacagcggg tttccggaac acatcagcgt tcagacagga gcgaggagac catgtacctg
 120
 ggtgctcagc tggtcagtga cagcgagtac gagcagcgcc tgagacgtgt ccgtgagctc
 180
 atggaccgtc aggggtctgtc ggcgatcatc gtcaccgatc cggccaacat cttctatctg
 240
 atcggttaca acgcctggtc gttctacacc ccgcagatgc tggtcgtgcc gatcgacgga
 300
 gagatgggtcc tctacgctcg cgagatggat cgcattggcg acatcngcac gacgtcgttg
 360
 cccgccgatc agatcgtcgg ttaccgggag agttatgtgc ac
 402

<210> 304
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 304
 Met Tyr Leu Gly Ala Gln Leu Phe Ser Asp Ser Glu Tyr Glu Gln Arg
 1 5 10 15
 Leu Arg Arg Val Arg Glu Leu Met Asp Arg Gln Gly Leu Ser Ala Ile
 20 25 30
 Ile Val Thr Asp Pro Ala Asn Ile Phe Tyr Leu Ile Gly Tyr Asn Ala
 35 40 45
 Trp Ser Phe Tyr Thr Pro Gln Met Leu Phe Val Pro Ile Asp Gly Glu
 50 55 60
 Met Val Leu Tyr Ala Arg Glu Met Asp Arg Met Ala His Ile Xaa Thr
 65 70 75 80
 Thr Ser Leu Pro Ala Asp Gln Ile Val Gly Tyr Pro Glu Ser Tyr Val
 85 90 95
 His

<210> 305
 <211> 375
 <212> DNA
 <213> Homo sapiens

<400> 305
 nnacgcgtcg gttccgcac gagcgaccgg atcgcatcga cgagcacgct gcaccagtgc
 60
 gtgtcgtcct ggcgaatatg ggcgatcagc cggtagagtt cgggatcgtc gctcacctcg
 120
 gccgccattt cggatgcgac acgcgcgcct gcgcgctcgg cctccagcaa ctcgtcgagc
 180
 gtcgccacca gcgcggcgcg atcttcatgc ggagtcagat cggcgcgggc gtcaggcccg
 240
 tcgccatgcg tcggaatcga catgcagcac cctcctgcca ggatcgatgg cgtaatacgt
 300
 gcgacgggtac acggcgcggtg ttgcacgaac gtgcaaatca gcgcgtgcct cgtgccatat
 360
 acgtcacatc atatg
 375

<210> 306
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 306
 Xaa Arg Val Gly Ser Ala Ser Ser Asp Arg Ile Ala Ser Thr Ser Thr
 1 5 10 15
 Leu His Gln Cys Val Ser Ser Trp Arg Ile Trp Ala Ile Ser Arg Tyr
 20 25 30
 Ser Ser Gly Ser Ser Leu Thr Ser Ala Ala Ile Ser Asp Ala Thr Arg
 35 40 45
 Ala Pro Ala Arg Ser Ala Ser Ser Asn Ser Ser Ser Val Ala Thr Ser
 50 55 60
 Ala Ala Arg Ser Ser Cys Gly Val Arg Ser Ala Arg Ala Ser Gly Pro
 65 70 75 80
 Ser Pro Cys Val Gly Ile Asp Met Gln His Pro Pro Ala Arg Ile Asp
 85 90 95
 Gly Val Ile Arg Ala Thr Val His Gly Ala Cys Cys Thr Asn Val Gln
 100 105 110
 Ile Ser Ala Cys Leu Val Pro Tyr Thr Ser His His Met
 115 120 125

<210> 307
 <211> 685
 <212> DNA
 <213> Homo sapiens

<400> 307
 actagttctg gccgctcccc tggggctttg ggtaacaatt gtcagcccca cccatcctag
 60
 ggtaggaag gctattctct ttggccactc tcatacctaag acctatttgg agaacctctg
 120
 gggtttgagt ctttttttca gcagaatgag gcttgatccc gcattatagc acctcgaca
 180
 tttgatgtct cttcttctca cccactcacc ccacctggg gggtggggca aaaaagtggc
 240
 tcaaagctgc gggtcagagt tccttgtaaa caaggctcct ccctcactgt cctcacctg
 300
 ctccagcaga gggagcagcg gaaggaccac tctgctgcag ccattgcttg ttctaacca
 360
 gcagaactgg acataatggg aacagggctc gaagacaatc aatccagggc tgcagtgggt
 420
 gctgagtctg gggaagcctc cacctggagg ggcagctggg cagtggcagc tcccttgga
 480
 tggtcagcc tctggacatc accccacca accagagccc tggtccttgc tggatgtcca
 540
 cagatgagtg cctgggattg gtctcagcca ctatgggggg gatgtgcagg gagaggtgat
 600
 gagggagtga gcaggactgt ctatgtgcct ctgtcctcat cctgaggctt gggcttgaaa
 660
 ttggtgctgc agcactggca cgcgt
 685

<210> 308
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 308
 Met Leu Val Ser Asn Pro Ala Glu Leu Asp Ile Met Gly Thr Gly Ser
 1 5 10 15
 Glu Asp Asn Gln Ser Arg Ala Ala Val Gly Ala Glu Ser Gly Glu Ala
 20 25 30
 Ser Thr Trp Arg Gly Ser Trp Ala Val Ala Ala Pro Leu Glu Trp Leu
 35 40 45
 Ser Leu Trp Thr Ser Pro His Pro Thr Arg Ala Leu Ala Leu Ala Gly
 50 55 60
 Cys Pro Gln Met Ser Ala Trp Asp Trp Ser Gln Pro Leu Trp Gly Gly
 65 70 75 80
 Cys Ala Gly Arg Gly Asp Glu Gly Val Ser Arg Thr Val Tyr Val Pro
 85 90 95
 Leu Ser Ser Ser
 100

<210> 309
 <211> 432
 <212> DNA
 <213> Homo sapiens

<400> 309
 caggctcgta ctattcgtat ccctgtgcat atggtcgagg tcatcaataa gctggctcgc
 60
 gtccagcgtc agatgctcca ggacctaggt cgtgagccca ccccggaaga gcttgccaac
 120
 gaactcgata tgaccgcaga gaaggtcatt gaggtgcaga aatacggctcg cgagccgatac
 180
 tcgctgcata cccactggg tgaggatggc gattctgagt tcggtgacct tattgaggat
 240
 tccgaggcca tcgtgccagc agacgccgtc aacttcaccc tgttgcagga gcagctgcat
 300
 gatgtcctcg ataccttgtc cgagcgagag gccgggtgtcg tgtcgatgcg attcggcttg
 360
 accgacggac agcccaagac cctggatgag atcggcaaag tctacgggtgt tactcgggag
 420
 cgcacccgcc ag
 432

<210> 310
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 310
 Gln Ala Arg Thr Ile Arg Ile Pro Val His Met Val Glu Val Ile Asn
 1 5 10 15
 Lys Leu Ala Arg Val Gln Arg Gln Met Leu Gln Asp Leu Gly Arg Glu

```

      20      25      30
Pro Thr Pro Glu Glu Leu Ala Asn Glu Leu Asp Met Thr Ala Glu Lys
      35      40      45
Val Ile Glu Val Gln Lys Tyr Gly Arg Glu Pro Ile Ser Leu His Thr
      50      55      60
Pro Leu Gly Glu Asp Gly Asp Ser Glu Phe Gly Asp Leu Ile Glu Asp
      65      70      75      80
Ser Glu Ala Ile Val Pro Ala Asp Ala Val Asn Phe Thr Leu Leu Gln
      85      90      95
Glu Gln Leu His Asp Val Leu Asp Thr Leu Ser Glu Arg Glu Ala Gly
      100      105      110
Val Val Ser Met Arg Phe Gly Leu Thr Asp Gly Gln Pro Lys Thr Leu
      115      120      125
Asp Glu Ile Gly Lys Val Tyr Gly Val Thr Arg Glu Arg Ile Arg Gln
      130      135      140

```

<210> 311
 <211> 358
 <212> DNA
 <213> Homo sapiens

```

<400> 311
acgcgtatcg aaaatatccc tcccattatt accgctcgcc ctgaactgat ggctcatgaa
60
ctgacgccag aatctcttga tgcgagcctg gagtgggccc atgtggtggt cattggtcct
120
ggactgggac aacaagcgtg gggcaaaaaa gcgctacaaa aggtcgagaa ttgtcgtaaa
180
ccgatgctgt gggatgccga cgcgcttaac cttctggcaa tcaatcctga taaacgtcac
240
aatcgcatcc tgacgccaca ccccggcgag gccgcgcggc tgcttagctg cagcgtcgca
300
gaaattgaaa acgatcgctt acttntctgc gcacgtctgg taaaacggta acccgagt
358

```

<210> 312
 <211> 116
 <212> PRT
 <213> Homo sapiens

```

<400> 312
Thr Arg Ile Glu Asn Ile Pro Pro Ile Ile Thr Ala Arg Pro Glu Leu
1      5      10      15
Met Ala His Glu Leu Thr Pro Glu Ser Leu Asp Ala Ser Leu Glu Trp
      20      25      30
Ala Asp Val Val Val Ile Gly Pro Gly Leu Gly Gln Gln Ala Trp Gly
      35      40      45
Lys Lys Ala Leu Gln Lys Val Glu Asn Cys Arg Lys Pro Met Leu Trp
      50      55      60
Asp Ala Asp Ala Leu Asn Leu Leu Ala Ile Asn Pro Asp Lys Arg His
      65      70      75      80
Asn Arg Ile Leu Thr Pro His Pro Gly Glu Ala Ala Arg Leu Leu Ser
      85      90      95
Cys Ser Val Ala Glu Ile Glu Asn Asp Arg Leu Leu Xaa Cys Ala Arg

```

100 105 110
 Leu Val Lys Arg
 115
 <210> 313
 <211> 347
 <212> DNA
 <213> Homo sapiens
 <400> 313
 ncaactgaaa gcattgagat gagcgacgtg ctgtccccct tccacccac caaggccaac
 60
 acccctggtg gcgaaccgcg caccatccgc acctcgaacg cgcacatcat tgccgtcacc
 120
 agtggcaaag gcggcgtggg caagaccttt gtctccgcca acctggccgc cgcgctgacc
 180
 cgcctgggac tgcgctgct ggtactggac gccgacctgg gcctggccaa cttggacgtg
 240
 gtgctgaacc tctaccccaa ggtgacgctg cacgatgtgt tcaccggcaa ggcctcgctg
 300
 caagacgagg tggtcacggc ccccgccggc ttccatgtgc tgctagc
 347

<210> 314
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 314
 Xaa Thr Glu Ser Ile Glu Met Ser Asp Val Leu Ser Pro Phe His Pro
 1 5 10 15
 Thr Lys Ala Asn Thr Pro Gly Gly Glu Pro Arg Thr Ile Arg Thr Ser
 20 25 30
 Asn Ala His Ile Ile Ala Val Thr Ser Gly Lys Gly Gly Val Gly Lys
 35 40 45
 Thr Phe Val Ser Ala Asn Leu Ala Ala Ala Leu Thr Arg Leu Gly Leu
 50 55 60
 Arg Val Leu Val Leu Asp Ala Asp Leu Gly Leu Ala Asn Leu Asp Val
 65 70 75 80
 Val Leu Asn Leu Tyr Pro Lys Val Thr Leu His Asp Val Phe Thr Gly
 85 90 95
 Lys Ala Ser Leu Gln Asp Ala Val Val Thr Ala Pro Gly Gly Phe His
 100 105 110
 Val Leu Leu
 115

<210> 315
 <211> 544
 <212> DNA
 <213> Homo sapiens

<400> 315
 nnacgcgttc gtcaacagga aaacaacaac ggcttctcgc tggagggaac catgcttgcc
 60

gaagatatct acgcgatcat gctgttttca tcgctcatcc tggctgtccc ggggccatcc
 120
 aacaccttgc tgctcagcgc ccgtttccat ttcggctcgc tgcgggcggc gcccttcac
 180
 ctgcttgagg cgttgggcta ctgctatcc atttcggcat ggggctgggt attggcgcgc
 240
 ctgtccgaga gcaatccatg gatcatcagt ctgaccaagg cactctgcgc gctatatgtg
 300
 gcgcttctgg cggtgaagac ctggaatgcc ntcgatccgc agtgcggggc cggtaacttc
 360
 cgccatgggc ccctgcccct gttcgtggca accctgtcga acccgaaggc gctgatcttc
 420
 gccagcgtga tctttcccgg caaggcggtc ctgcacttct ggaacaacta cacgatctcg
 480
 ctgctggcct tcctggttgt gctggcgccc atcgggatgc tttgggtcgg gctggggggc
 540
 ggta
 544

<210> 316
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 316
 Ile Tyr Ala Ile Met Leu Phe Ser Ser Leu Ile Leu Val Val Pro Gly
 1 5 10 15
 Pro Ser Asn Thr Leu Leu Leu Ser Ala Arg Phe His Phe Gly Ser Leu
 20 25 30
 Arg Ala Ala Pro Phe Ile Leu Leu Glu Ala Leu Gly Tyr Ser Leu Ser
 35 40 45
 Ile Ser Ala Trp Gly Trp Val Leu Ala Arg Leu Ser Glu Ser Asn Pro
 50 55 60
 Trp Ile Ile Ser Leu Thr Lys Ala Leu Cys Ala Leu Tyr Val Ala Leu
 65 70 75 80
 Leu Ala Val Lys Thr Trp Asn Ala Xaa Asp Pro Gln Cys Gly Ala Gly
 85 90 95
 Asn Phe Arg His Gly Pro Leu Pro Leu Phe Val Ala Thr Leu Ser Asn
 100 105 110
 Pro Lys Ala Leu Ile Phe Ala Ser Val Ile Phe Pro Gly Lys Ala Phe
 115 120 125
 Leu Asp Phe Trp Asn Asn Tyr Thr Ile Ser Leu Leu Ala Phe Leu Val
 130 135 140
 Val Leu Ala Pro Ile Gly Met Leu Trp Val Gly Leu Gly Ala Gly
 145 150 155

<210> 317
 <211> 343
 <212> DNA
 <213> Homo sapiens

<400> 317
 nggtcagcct ctcgcccagg caattctctt aagatacatg agctgctatg agtaccaaag
 60

ccagaggttt gtccactgag agaagcacat tggaaagggg ggcgtgggccc tgggactgtg
 120
 tggcacttta tgcacggggg gggcctaagg gggnggtcc accaaccatg cactgngggg
 180
 ggggtgtggg taacatgccg tgcatttttg ggggtgtgcca tgagtggcac accatggggg
 240
 tggcatgtgg ggcattgtatg catgtgggtg tggcgcagca aactcagctc ttacctggtc
 300
 ggggccagcc tctaaaactt ctcacattgg gctcccttct gac
 343

<210> 318
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 318
 Met Ser Thr Lys Ala Arg Gly Leu Ser Thr Glu Arg Ser Thr Leu Glu
 1 5 10 15
 Arg Gly Ala Trp Ala Trp Asp Cys Val Ala Leu Tyr Ala Arg Gly Gly
 20 25 30
 Pro Lys Gly Gly Gly Pro Pro Thr Met His Xaa Gly Trp Gly Val Gly
 35 40 45
 Asn Met Pro Cys Ile Leu Gly Val Cys His Glu Trp His Thr Met Gly
 50 55 60
 Val Ala Cys Gly Ala Cys Met His Val Val Leu Ala Gln Gln Thr Gln
 65 70 75 80
 Leu Leu Pro Gly Trp Gly Gln Pro Leu Lys Leu Leu Thr Leu Gly Ser
 85 90 95
 Leu Leu

<210> 319
 <211> 429
 <212> DNA
 <213> Homo sapiens

<400> 319
 gaattctcga tgtacccctt cccggcagtc ctattctcga gctgagcggg cacagtggcc
 60
 ccgttaacag tgtggcttgg ggtccacca gccagagcac gttgcgaaat ggacctagta
 120
 agggcatgat atgtacagga ggcgacgatg ctcagtgcct cgtatatgat ctgactagct
 180
 caactcttcg aacagcatct gctcaaggac ggcgctctcg aaacagtcca tataaacaaa
 240
 gccattcacc gggaaatagac ggatggcgtg tcggcgcaga agtgccggtg ctcgcttata
 300
 cgccccgctc tatgggtcaac aatgctagct ggctcggcat gcctgcgcca tcaaaacgca
 360
 catcgctaca gagcaaacac cgcagccttt accgcagctt actcagtgag tggactgagt
 420
 atacgtccn
 429

<210> 320
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 320
 Met Ile Cys Thr Gly Gly Asp Asp Ala Gln Cys Leu Val Tyr Asp Leu
 1 5 10 15
 Thr Ser Ser Thr Leu Arg Thr Ala Ser Ala Gln Gly Arg Arg Ser Arg
 20 25 30
 Asn Ser Pro Tyr Lys Gln Ser His Ser Pro Gly Ile Asp Gly Trp Arg
 35 40 45
 Val Gly Ala Glu Val Pro Val Leu Ala Tyr Thr Ala Pro Ser Met Val
 50 55 60
 Asn Asn Ala Ser Trp Leu Gly Met Pro Ala Pro Ser Lys Arg Thr Ser
 65 70 75 80
 Leu Gln Ser Lys His Arg Ser Leu Tyr Arg Ser Leu Leu Ser Glu Trp
 85 90 95
 Thr Glu Tyr Thr Ser
 100

<210> 321
 <211> 530
 <212> DNA
 <213> Homo sapiens

<400> 321
 ngtgcacgac gtgctcgcca agtccctcgg gtcctctaata gcatcaacg tggttcacgc
 60
 caccgtcgat gcgttgcagc agctcgagga gcccggaagag gtcgcccgtc gccgcggcaa
 120
 gtccggtgag gagatcgccc cagcagccat gctgcgtgcg cgcaaggagg ccgacgaggc
 180
 cgccgctgct gcccgcatgg aggaaaaggc ggggggtaac tgatgagcaa gctgaagatc
 240
 acccagatca agtctggcat cgctaccaag ccaaatcatc gtgagaccct gcgcagcctc
 300
 ggactgaagc gtattggtga cacggtcac caggaggacc gcccgaggtt ccgcggcatg
 360
 gtccggaccg ttcgtcacct cgtcaccatg gaagagggtg actgacatgg ctattgagct
 420
 ccatgacctc aagcccgtc ctggtgcccc caaggccaag acccgcggtg gtcgtggtga
 480
 gggttccaag ggtaagaccg ctggtcgcgg taccaagggc accggtgcac
 530

<210> 322
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 322
 Met Ser Lys Leu Lys Ile Thr Gln Ile Lys Ser Gly Ile Ala Thr Lys

1	5	10	15
Pro Asn His Arg Glu Thr Leu Arg Ser Leu Gly Leu Lys Arg Ile Gly			
	20	25	30
Asp Thr Val Ile Lys Glu Asp Arg Pro Glu Phe Arg Gly Met Val Arg			
	35	40	45
Thr Val Arg His Leu Val Thr Met Glu Glu Val Asp			
50	55	60	

<210> 323
 <211> 468
 <212> DNA
 <213> Homo sapiens

<400> 323
 ntccggaccc gctgtggcca cgtattctgc cgttctgtga ttgctaccag tctaaagaac
 60
 aacaagtgga cctgtcctta ttgccgggca tatcttcctt cagaaggagt tccagcaact
 120
 gatgtagcca aaagaatgaa atcagagtat aagaactgcg ctgagtgtga caccctggtt
 180
 tgccctcagtg aaatgagggc acatattcgg acttgtcaga agtacataga taagtatgga
 240
 ccactacaag aacttgagga gacagcagca aggtgtgtat gtcccttttg tcagagggaa
 300
 ctgtatgaag acagcttgct ggatcattgt attactcatc acagatcgga acggaggcct
 360
 gtgttctgtc cactttgcca ttaataccc gatgagaatc caagcagctt cagtggcagt
 420
 ttaataagac atctgcaagt tagtcacact ttggtttatg atgatttc
 468

<210> 324
 <211> 156
 <212> PRT
 <213> Homo sapiens

<400> 324
Xaa Arg Thr Arg Cys Gly His Val Phe Cys Arg Ser Cys Ile Ala Thr
1 5 10 15
Ser Leu Lys Asn Asn Lys Trp Thr Cys Pro Tyr Cys Arg Ala Tyr Leu
20 25 30
Pro Ser Glu Gly Val Pro Ala Thr Asp Val Ala Lys Arg Met Lys Ser
35 40 45
Glu Tyr Lys Asn Cys Ala Glu Cys Asp Thr Leu Val Cys Leu Ser Glu
50 55 60
Met Arg Ala His Ile Arg Thr Cys Gln Lys Tyr Ile Asp Lys Tyr Gly
65 70 75 80
Pro Leu Gln Glu Leu Glu Glu Thr Ala Ala Arg Cys Val Cys Pro Phe
85 90 95
Cys Gln Arg Glu Leu Tyr Glu Asp Ser Leu Leu Asp His Cys Ile Thr
100 105 110
His His Arg Ser Glu Arg Arg Pro Val Phe Cys Pro Leu Cys His Leu
115 120 125
Ile Pro Asp Glu Asn Pro Ser Ser Phe Ser Gly Ser Leu Ile Arg His

130 135 140
 Leu Gln Val Ser His Thr Leu Val Tyr Asp Asp Phe
 145 150 155

<210> 325
 <211> 374
 <212> DNA
 <213> Homo sapiens

<400> 325
 acgcgtgaag ggaggacgag gaagtaacgg gaagcacaag gccgctgctg gggagatggc
 60
 actggagccc cctaggaagc atctcacagg ctgtggccct tggcacgggg atctggggcc
 120
 aggtcgagcg caggtctggg tatcatgcga gtgcgggctc gctggggcgg gaaagagttt
 180
 ggagctctgc tcccagggaa tccccactcc cgcagatgac ttgcccgaga gagttctgct
 240
 ggtggatttt gatggaaatt ctatttgatc gcacccactt ggttcactgt gtgcttccgg
 300
 gtccccaggt tttaggtgct tcatgccttg ctgggaacga gacacgctcc tgcctcagt
 360
 gaatcttcag tcta
 374

<210> 326
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 326
 Met Lys His Leu Lys Pro Gly Asp Pro Glu Ala His Ser Glu Pro Ser
 1 5 10 15
 Gly Cys Asp Gln Ile Glu Phe Pro Ser Lys Ser Thr Ser Arg Thr Leu
 20 25 30
 Ser Gly Lys Ser Ser Ala Gly Val Gly Ile Pro Trp Glu Gln Ser Ser
 35 40 45
 Lys Leu Phe Pro Ala Pro Ala Ser Pro His Ser His Asp Thr Gln Thr
 50 55 60
 Cys Ala Arg Pro Gly Pro Arg Ser Pro Cys Gln Gly Pro Gln Pro Val
 65 70 75 80
 Arg Cys Phe Leu Gly Gly Ser Ser Ala Ile Ser Pro Ala Ala Ala Leu
 85 90 95
 Cys Phe Pro Leu Leu Pro Arg Pro Pro Phe Thr Arg
 100 105

<210> 327
 <211> 538
 <212> DNA
 <213> Homo sapiens

<400> 327
 cactataaaa tccagtttgg ggcccgtggt ctttcctatt ggtctgtcag gtgaaaaact
 60

ccggctgggg gaaaagcgtc cggtgggttg ttggtaaaga gggcgctga tgggctctgg
120
ggaatggagg atggcgccacc ggctgtgggt ggactgtgga aacgggggggt ggcagtgccg
180
gggtagttgt cctgctggtc tggttttggg atcctgggct ggagaaatgc gatccaaaag
240
agctcgggat gggctcagag cgacccacga aaataccagg ggccaagtaa aatgaacca
300
ccctttaaca gtgcacaaag cgctggcaca cgggccacgt ctggtgacgc aggctgccc
360
aagcgctcca accattttgc aaacctggga gagcaagagg ggctctgcag gtctagccgc
420
cgccccctgtc ccactctggc cagccggagt ttttcaccta cagaccaata ggaaagaaca
480
cgggcccca actggatttt atagtctgag ctctcagcat ctaaggaatg atatgcc
538

<210> 328

<211> 125

<212> PRT

<213> Homo sapiens

<400> 328

Met	Val	Gly	Ala	Leu	Arg	Ala	Ala	Cys	Val	Thr	Arg	Arg	Gly	Pro	Cys
1				5					10					15	
Ala	Ser	Ala	Leu	Cys	Thr	Val	Lys	Gly	Trp	Val	His	Phe	Thr	Trp	Pro
			20					25					30		
Leu	Val	Phe	Ser	Trp	Val	Ala	Leu	Ser	Pro	Ser	Arg	Ala	Leu	Leu	Asp
		35					40					45			
Arg	Ile	Ser	Pro	Ala	Gln	Asp	Pro	Lys	Thr	Arg	Pro	Ala	Gly	Gln	Leu
	50					55					60				
Pro	Arg	His	Cys	His	Pro	Pro	Phe	Pro	Gln	Ser	Thr	His	Ser	Arg	Cys
65					70					75				80	
Ala	Ile	Leu	His	Ser	Pro	Glu	Pro	Ile	Thr	His	Pro	Leu	Tyr	Gln	Gln
			85						90					95	
Thr	Thr	Gly	Arg	Phe	Ser	Pro	Ser	Arg	Ser	Phe	Ser	Pro	Asp	Arg	Pro
			100					105					110		
Ile	Gly	Lys	Asn	Thr	Gly	Pro	Lys	Leu	Asp	Phe	Ile	Val			
		115					120					125			

<210> 329

<211> 407

<212> DNA

<213> Homo sapiens

<400> 329

tccggagagt tccctcccca ggaattcctt ctaagaatcc atgtggaaat agagcctgaa
60
gctcttcagt ctttctgctc cactgagcag tgttttcctg atacccttgg tatcctgcca
120
gcagcctcgt tatgactcct aactccattg cctccatgg cccctgggcg ctctctctct
180
ctttctctcc aggtagtaga gcactgcttc tggcttcttg tgcacagaag gggttccac
240

agctgagagc tgggctccta ctgacatagt tatttccttt ataccctgcc ccaccttctt
 300
 ctggtagcac acagcaacct tgcatagttag ctggtatcat taccttccca atcaacaggc
 360
 cttgatttct tataggactt tttctctcag atttacattg cttcttt
 407

<210> 330
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 330
 Met Ile Pro Ala Thr Met Gln Gly Cys Cys Val Leu Pro Glu Glu Gly
 1 5 10 15
 Gly Ala Gly Tyr Lys Gly Asn Asn Tyr Val Ser Arg Ser Pro Ala Leu
 20 25 30
 Ser Cys Gly Lys Pro Phe Cys Ala Gln Glu Ala Arg Ser Ser Ala Leu
 35 40 45
 Leu Pro Gly Glu Lys Glu Arg Glu Ser Ala Gln Gly Pro Trp Arg Ala
 50 55 60
 Met Glu Leu Gly Val Ile Thr Arg Leu Leu Ala Gly Tyr Gln Gly Tyr
 65 70 75 80
 Gln Glu Asn Thr Ala Gln Trp Ser Arg Lys Thr Glu Glu Leu Gln Ala
 85 90 95
 Leu Phe Pro His Gly Phe Leu Glu Gly Ile Pro Gly Glu Gly Thr Leu
 100 105 110
 Arg

<210> 331
 <211> 523
 <212> DNA
 <213> Homo sapiens

<400> 331
 tgtaccgaac ctgctggtct cgagggcctt gctgggctcg tcgtacgcac agctgacgaa
 60
 tccaccggcc cccatcccgg cgccactttc gctgaggcca tggagtcgat cggagccagc
 120
 tacgacggat cggccggggtt ggccggaagt cacgtcggcg tcgatgtgcc cgtgacaagg
 180
 ttcgacgcag cggctgaact cttcgtcgaa ttgttgaaca ccacgagcct ggttgaagag
 240
 gacatcgccc gtcagatcga cgcggcgcca gcctccctgg cccagaccag ccagcgcgga
 300
 tcggccctag ccgagatggc agcagcacgt gcgctatggc cagtggggtc acggtcgtcc
 360
 ctgcccacga tcggtaccct ctcgtcgggtg gaaaagctca acgccgcagc cgcacgagaa
 420
 ttctgggccc cgcactggac gatctccgat gccgtgctgg tggttgccgg agagggagtc
 480
 gaggacctcg acttgtcaat attcaaggag tggacgacca gct
 523

<210> 332
 <211> 174
 <212> PRT
 <213> Homo sapiens

<400> 332
 Cys Thr Glu Pro Ala Gly Leu Glu Gly Leu Ala Gly Leu Val Val Arg
 1 5 10 15
 Thr Ala Asp Glu Ser Thr Gly Pro His Pro Gly Ala Thr Phe Ala Glu
 20 25 30
 Ala Met Glu Ser Ile Gly Ala Ser Tyr Asp Gly Ser Ala Gly Leu Ala
 35 40 45
 Gly Ser His Val Gly Val Asp Val Pro Val Thr Arg Phe Asp Ala Ala
 50 55 60
 Ala Glu Leu Phe Val Glu Leu Leu Asn Thr Thr Ser Leu Val Glu Glu
 65 70 75 80
 Asp Ile Ala Arg Gln Ile Asp Ala Ala Arg Ala Ser Leu Ala Gln Thr
 85 90 95
 Ser Gln Arg Gly Ser Ala Leu Ala Glu Met Ala Ala Ala Arg Ala Leu
 100 105 110
 Trp Pro Val Gly Ser Arg Ser Ser Leu Pro Thr Ile Gly Thr Leu Ser
 115 120 125
 Ser Val Glu Lys Leu Asn Ala Ala Ala Arg Glu Phe Trp Ala Ala
 130 135 140
 His Trp Thr Ile Ser Asp Ala Val Leu Val Val Ala Gly Glu Gly Val
 145 150 155 160
 Glu Asp Leu Asp Leu Ser Ile Phe Lys Glu Trp Thr Thr Ser
 165 170

<210> 333
 <211> 372
 <212> DNA
 <213> Homo sapiens

<400> 333
 nntgttcgtc gtgtcgaccc ggaactcaag gcccgaggca tgacgggtgaa ggtgcccaacc
 60
 gatcccatc accgcccggg agttccattg aagtctgcca aggaccgtat ggacatcatt
 120
 tctgcttacc gagaactcgg aagctatcgc gccgcagccg aggtgtgcgg caccacccac
 180
 aagaccgtca agcgggtggt cgatcggttt gaagccggcg atccacccac cgggtggcaag
 240
 gaacgggccc gcaactacga tgcggtggcc cagctcgtcg cgcagcgagt cgcgcggtca
 300
 cacggccgga tcaactgcaa acggctgcta ccggtagcgc gagcggcagg atatgagggg
 360
 tcggcgcgga at
 372

<210> 334
 <211> 88
 <212> PRT

<213> Homo sapiens

<400> 334

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Met Asp Ile Ile Ser Ala Tyr Arg Glu Leu Gly Ser Tyr Arg Ala Ala
 1           5           10           15
Ala Glu Val Cys Gly Thr Thr His Lys Thr Val Lys Arg Val Val Asp
           20           25           30
Arg Phe Glu Ala Gly Asp Pro Pro Thr Gly Gly Lys Glu Arg Ala Arg
           35           40           45
Asn Tyr Asp Ala Val Ala Gln Leu Val Ala Gln Arg Val Ala Arg Ser
           50           55           60
His Gly Arg Ile Thr Ala Lys Arg Leu Leu Pro Val Ala Arg Ala Ala
65           70           75           80
Gly Tyr Glu Gly Ser Ala Arg Asn
           85

```

<210> 335

<211> 356

<212> DNA

<213> Homo sapiens

<400> 335

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gtgcacgcct tgctgggcga gggcgatgcg cctgcgcgca ccttcgtgga cggtaccttt
60
ggcaggggag ggcattcgcg gctcatcctg cagcgggttg ggccgcaagg ccgcctgggtg
120
gcgttcgaca aggacaccga agccattcaa gcagcggcgc gcatcacgga tgcgcgcttt
180
tccatcnggc accagggggtt cagccatctc ggggaactgc ccgccgccag cgtgtccggt
240
gtgctgctgg acctgggcgt gagctccccg cagatcgacg acccccagcg cgggttcagt
300
tttcgtttcg atggtccgct ggacatgcgc atggacacca ctccgatgca tggatg
356

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<210> 336

<211> 118

<212> PRT

<213> Homo sapiens

<400> 336

```

Val His Ala Leu Leu Gly Glu Gly Asp Ala Pro Ala Arg Thr Phe Val
 1           5           10           15
Asp Gly Thr Phe Gly Arg Gly Gly His Ser Arg Leu Ile Leu Gln Arg
           20           25           30
Leu Gly Pro Gln Gly Arg Leu Val Ala Phe Asp Lys Asp Thr Glu Ala
           35           40           45
Ile Gln Ala Ala Ala Arg Ile Thr Asp Ala Arg Phe Ser Ile Xaa His
           50           55           60
Gln Gly Phe Ser His Leu Gly Glu Leu Pro Ala Ala Ser Val Ser Gly
65           70           75           80
Val Leu Leu Asp Leu Gly Val Ser Ser Pro Gln Ile Asp Asp Pro Gln
           85           90           95
Arg Gly Phe Ser Phe Arg Phe Asp Gly Pro Leu Asp Met Arg Met Asp

```

100 105 110
 Thr Thr Pro Met His Gly
 115
 <210> 337
 <211> 447
 <212> DNA
 <213> Homo sapiens
 <400> 337
 cagcctctct ccgaccgcgc cgggtgtgaag cacgggcatg ccgggtgtgca agtggcacca
 60
 cagccaaaac agcgagctca cacttcaaac tccttcaaag accccaggcc tctgtaagaa
 120
 ccgctcatct ctgtgcccac agctcccccg cttccatgtg acccagaaat ggaaccacgc
 180
 agcagaggcg gggatcacag gtgaagcagc tgtgaacatt tgcttcaggc ttctgtgcaa
 240
 acaggcgcca tcatgtcagc cggtgagcag gagcaacgtg cgtgggtcag ggggtggcca
 300
 cacgtccaac tttataagaa atgacagatt ccctgatggc catagggatc tgcagggcca
 360
 gcagcaggca taggacttcc ggtggccctg cgtcttcatc aacactgagt attgtcaggg
 420
 tttctgtact gtttttacag ccaattg
 447

<210> 338
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 338
 Met Pro Val Cys Lys Trp His His Ser Gln Asn Ser Glu Leu Thr Leu
 1 5 10 15
 Gln Thr Pro Ser Lys Thr Pro Gly Leu Cys Lys Asn Arg Ser Ser Leu
 20 25 30
 Cys Pro Gln Leu Pro Arg Phe His Val Thr Gln Lys Trp Asn His Ala
 35 40 45
 Ala Glu Ala Gly Ile Thr Gly Glu Ala Ala Val Asn Ile Cys Phe Arg
 50 55 60
 Leu Leu Cys Lys Gln Ala Pro Ser Cys Gln Pro Val Ser Arg Ser Asn
 65 70 75 80
 Val Arg Gly Ser Gly Gly Gly His Thr Ser Asn Phe Ile Arg Asn Asp
 85 90 95
 Arg Phe Pro Asp Gly His Arg Asp Leu Gln Gly Gln Gln Gln Ala
 100 105 110

<210> 339
 <211> 588
 <212> DNA
 <213> Homo sapiens

<400> 339

tctagaatga agcgctgtat cctagcaccg gcagacgtac caagactatc aagggcgtca
60
gatcgtttat cctgcagttg ccattcatca gacaaatcca gtggaaccca atggaagaca
120
ccgacctgca agcgctgatg gccagactcg aattgctaata tgatcgggtc gagcaactta
180
agagtcaaaa cggactccta ttagctcagg aaaagacctg ggcgcganaa cgcgctcacc
240
tcattgaaaa aaacgaaatc gcccggcgta aggtcgaatc gatgatttcg cgcctgaagg
300
ccctggagca agactatgag ttaagcaata gcgttacgtg cagatcctcg acaaagaata
360
ttcgatcatc tgcccccagg aagaacgcag cacctgggtga gtgctgcccg ctacctggaa
420
ggccaaaagg cgtgaaatcc gcagcagcgg caaagtcatc ggtgccgacc gcatcgccgt
480
gatggccgcg ctgaacatca cccacgatct gctgcataag caggaacggc ctgacgttca
540
ggccagcggc tcaacgcgcg agcaagtgcg tgacctgctg gaacgcgt
588

<210> 340
<211> 123
<212> PRT
<213> Homo sapiens

<400> 340
Met Glu Asp Thr Asp Leu Gln Ala Leu Met Ala Arg Leu Glu Leu Leu
1 5 10 15
Ile Asp Arg Val Glu Gln Leu Lys Ser Gln Asn Gly Leu Leu Leu Ala
20 25 30
Gln Glu Lys Thr Trp Ala Arg Xaa Arg Ala His Leu Ile Glu Lys Asn
35 40 45
Glu Ile Ala Arg Arg Lys Val Glu Ser Met Ile Ser Arg Leu Lys Ala
50 55 60
Leu Glu Gln Asp Tyr Glu Leu Ser Asn Ser Val Thr Cys Arg Ser Ser
65 70 75 80
Thr Lys Asn Ile Arg Ser Ser Ala Pro Arg Lys Asn Ala Ala Pro Gly
85 90 95
Glu Cys Cys Pro Leu Pro Gly Arg Pro Lys Gly Val Lys Ser Ala Ala
100 105 110
Ala Ala Lys Ser Ser Val Pro Thr Ala Ser Pro
115 120

<210> 341
<211> 401
<212> DNA
<213> Homo sapiens

<400> 341
ngccgcgcgg cctacctgct gtacctggcc tatgccacct ggcgtgaccg ctccggccttt
60
gcaatgaacg acacgccgac agttgcgacc gcgcgcagcc tgatcctgcg tggcttcttg
120

ctgaacattc ttaaccccaa gctgacaatt ttcttcctgg ccttcctgcc tcaattcgta
 180
 acgccaggcg gcaccgcgcc ggccttgacg atgctggtac tgagcggcgt gttcatggcg
 240
 atgacgcttg cagtgtttgt gctgtatggc ctgttggcga atgtgtttcg tcgtgcagtg
 300
 gtcgagtcgc cacgtgtgca gaactggctg cgacgcagtt ttgccacggc ctttgccggg
 360
 ctgggggtga acctggcggt tgcgcagcgc tgaggacgcg t
 401

<210> 342
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 342
 Xaa Arg Ala Ala Tyr Leu Leu Tyr Leu Ala Tyr Ala Thr Trp Arg Asp
 1 5 10 15
 Arg Ser Ala Phe Ala Met Asn Asp Thr Pro Thr Val Ala Thr Ala Arg
 20 25 30
 Ser Leu Ile Leu Arg Gly Phe Leu Leu Asn Ile Leu Asn Pro Lys Leu
 35 40 45
 Thr Ile Phe Phe Leu Ala Phe Leu Pro Gln Phe Val Thr Pro Gly Gly
 50 55 60
 Thr Ala Pro Ala Leu Gln Met Leu Val Leu Ser Gly Val Phe Met Ala
 65 70 75 80
 Met Thr Leu Ala Val Phe Val Leu Tyr Gly Leu Leu Ala Asn Val Phe
 85 90 95
 Arg Arg Ala Val Val Glu Ser Pro Arg Val Gln Asn Trp Leu Arg Arg
 100 105 110
 Ser Phe Ala Thr Ala Phe Ala Gly Leu Gly Leu Asn Leu Ala Phe Ala
 115 120 125
 Gln Arg
 130

<210> 343
 <211> 389
 <212> DNA
 <213> Homo sapiens

<400> 343
 gtgttgcgca actacatggc gtccttgccg ttcagcgtgg tcgagtcggc gcgcacgcac
 60
 ggggtgctcca acttccagat cttctggaag ctgacgcgcc cgatggcgat gccggcgatg
 120
 gcggcgcttcg cgaccctgca gttcctgtgg gtgtggaacg acctgctcat cgccaagctc
 180
 ttctcacca acgacaaccc cacggatgac gtcaagctcc aacagctttc cnngggcccc
 240
 aaggcccagg gtgcggagct gctgacggcg ggcgccttca tctccatcgt gctacccatg
 300
 atcgtcttct tcgtgctcca gaacttctg gtgcgcggta tgacgtcggg tgccgtcaag
 360

gggtgaccgc tcaactgcag tggcccggg
389

<210> 344
<211> 121
<212> PRT
<213> Homo sapiens

<400> 344
Val Leu Arg Asn Tyr Met Ala Ser Leu Pro Phe Ser Val Val Glu Ser
1 5 10 15
Ala Arg Ile Asp Gly Cys Ser Asn Phe Gln Ile Phe Trp Lys Leu Ile
20 25 30
Ala Pro Met Ala Met Pro Ala Met Ala Ala Phe Ala Thr Leu Gln Phe
35 40 45
Leu Trp Val Trp Asn Asp Leu Leu Ile Ala Lys Leu Phe Leu Thr Asn
50 55 60
Asp Asn Pro Thr Val Ile Val Lys Leu Gln Gln Leu Ser Xaa Gly Pro
65 70 75 80
Lys Ala Gln Gly Ala Glu Leu Leu Thr Ala Gly Ala Phe Ile Ser Ile
85 90 95
Val Leu Pro Met Ile Val Phe Phe Val Leu Gln Asn Phe Leu Val Arg
100 105 110
Gly Met Thr Ser Gly Ala Val Lys Gly
115 120

<210> 345
<211> 360
<212> DNA
<213> Homo sapiens

<400> 345
ctagtacttt atgctgatgg tgaacgtcgt tacatccttg cccctaaagg catggttgct
60
ggtgatgtga tccaatctgg tgaagatgca tcaattaaag taggtaactg cttaccgatg
120
cgtaatatcc cagttggtac aacagtacac gctgtagaaa tgaaacctgc taaagggtgca
180
caaattgcac gttctgctgg ttcttacagc caaattatag ctgctgatgg tgcttacggt
240
actctacggt tacgtagtgg tgaaatgcgt aaaatccctg ctgagtgtcg tgcaacaatc
300
ggtgaagttg gtaatgcaga acatatgcta cgtcaactag gtaaagctgg tgctacgcgt
360

<210> 346
<211> 120
<212> PRT
<213> Homo sapiens

<400> 346
Leu Val Leu Tyr Ala Asp Gly Glu Arg Arg Tyr Ile Leu Ala Pro Lys
1 5 10 15
Gly Met Val Ala Gly Asp Val Ile Gln Ser Gly Glu Asp Ala Ser Ile

```

      20      25      30
Lys Val Gly Asn Cys Leu Pro Met Arg Asn Ile Pro Val Gly Thr Thr
      35      40      45
Val His Ala Val Glu Met Lys Pro Ala Lys Gly Ala Gln Ile Ala Arg
      50      55      60
Ser Ala Gly Ser Tyr Ser Gln Ile Ile Ala Arg Asp Gly Ala Tyr Val
65      70      75      80
Thr Leu Arg Leu Arg Ser Gly Glu Met Arg Lys Ile Pro Ala Glu Cys
      85      90      95
Arg Ala Thr Ile Gly Glu Val Gly Asn Ala Glu His Met Leu Arg Gln
      100      105      110
Leu Gly Lys Ala Gly Ala Thr Arg
      115      120

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<210> 347
 <211> 565
 <212> DNA
 <213> Homo sapiens

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<400> 347
accggtgatg ccaaaggtgc tgtgacaagg ggattcatcg gttcgggcaa ggtcgtcacg
60
gcagctgccg tcatcatgat ttcggtgttc gtcttcttca tccccgaggg catgaacgcc
120
atcaaggaaa tcgccctggc cctggccgctc gggatcctca cggatgcctt ctgtgtgcgg
180
atgaccctcg tcccggccgt gatggccctg ctaggtgaca aggcattggtg gttgcccggg
240
tggtctggatc gacgcctacc ccgcctcgac atcgagggag aagggatcac ccacgaggaa
300
aagctggccg cctggcccac agcggatcac accgaggccc tgcacgccga ggggatcggg
360
gtggaggggc tcttcgaagg cctcgatctg cacgtcgaac cgcgtcaggt gcaagccgtc
420
gtcggatcgc agaacagtgt ctcgccgctc ctgctggcga tcgggggacg gctgcccttg
480
gatcacggcc ggatgaggtc gggaggattg ctgctacccg agcgggcttc cagagtgcgt
540
cgggtgacgt ggttcctcga cgcgt
565

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<210> 348
 <211> 188
 <212> PRT
 <213> Homo sapiens

```

<400> 348
Thr Gly Asp Ala Lys Gly Ala Val Thr Arg Gly Phe Ile Gly Ser Gly
1      5      10      15
Lys Val Val Thr Ala Ala Ala Val Ile Met Ile Ser Val Phe Val Phe
      20      25      30
Phe Ile Pro Glu Gly Met Asn Ala Ile Lys Glu Ile Ala Leu Ala Leu
      35      40      45
Ala Val Gly Ile Leu Thr Asp Ala Phe Leu Val Arg Met Thr Leu Val

```



```

      50              55              60
Pro Ala Val Met Ala Leu Leu Gly Asp Lys Ala Trp Trp Leu Pro Gly
65              70              75              80
Trp Leu Asp Arg Arg Leu Pro Arg Leu Asp Ile Glu Gly Glu Gly Ile
      85              90              95
Thr His Glu Glu Lys Leu Ala Ala Trp Pro Thr Ala Asp His Thr Glu
      100             105             110
Ala Leu His Ala Glu Gly Ile Gly Val Glu Gly Leu Phe Glu Gly Leu
      115             120             125
Asp Leu His Val Glu Pro Arg Gln Val Gln Ala Val Val Gly Ser Gln
      130             135             140
Asn Ser Val Ser Ala Val Leu Leu Ala Ile Gly Gly Arg Leu Pro Leu
145             150             155             160
Asp His Gly Arg Met Arg Ser Gly Gly Leu Leu Leu Pro Glu Arg Ala
      165             170             175
Ser Arg Val Arg Arg Val Thr Trp Phe Leu Asp Ala
      180             185

```

<210> 349

<211> 339

<212> DNA

<213> Homo sapiens

<400> 349

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ntgctggcca cggataatga ccgtactctg cgtgatgtcg ttgccgctga ccctacccat
60
gagctcgggtt cggctaccgc tcatacgttt gcggacaatt tgccgttcct tcttaaactg
120
ctcgcggcag aagagccact atcgttgcag gctcatccca gtttggcgca agcacaggaa
180
gggtacgggc gggagaatcg caaaggggtg ccattagatg cccagaccg gaattaccac
240
gatcccaacc ataaaccgga gcttattgtt gggctgacgc gattccacgc actagccggc
300
ttccgtgaac cacaacgcac acttgagctt tttgacgcg
339

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<210> 350

<211> 113

<212> PRT

<213> Homo sapiens

<400> 350

```

Xaa Leu Ala Thr Asp Asn Asp Arg Thr Leu Arg Asp Val Val Ala Ala
1      5      10      15
Asp Pro Thr His Glu Leu Gly Ser Ala Thr Ala His Thr Phe Ala Asp
      20      25      30
Asn Leu Pro Phe Leu Leu Lys Leu Leu Ala Ala Glu Glu Pro Leu Ser
      35      40      45
Leu Gln Ala His Pro Ser Leu Ala Gln Ala Gln Glu Gly Tyr Gly Arg
      50      55      60
Glu Asn Arg Lys Gly Val Pro Leu Asp Ala Pro Asp Arg Asn Tyr His
65      70      75      80
Asp Pro Asn His Lys Pro Glu Leu Ile Val Gly Leu Thr Arg Phe His

```

	85		90		95										
Ala	Leu	Ala	Gly	Phe	Arg	Glu	Pro	Gln	Arg	Thr	Leu	Glu	Leu	Phe	Asp
	100				105						110				
Ala															

<210> 351
 <211> 354
 <212> DNA
 <213> Homo sapiens

<400> 351
 gcgcgccccca gtgccgagac ccggggcttc aggagccggc cccgggagag aagagtgcgg
 60
 cggcggacgg agaaaacaac tccaaagttg gcgaaaggca ccgcccctac tcccgggctg
 120
 ccgcgcctc cccgccccca gccctggcat ccagagtacg ggtcgagccc gnggccatgg
 180
 agccccctg gggaggcggc accagggagc ctggggccccg gggctccgcc gcgaccccat
 240
 cgggtagacc acagaagctc cgggaccctt ccggcacctc tggacagccc aggatgctgt
 300
 tggccaccn ntctctctcc tctctcttgg aggcgctctg gcccatccag accg
 354

<210> 352
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 352
 Ala Arg Pro Ser Ala Glu Thr Arg Gly Phe Arg Ser Arg Pro Arg Glu
 1 5 10 15
 Arg Arg Val Arg Arg Arg Thr Glu Lys Thr Thr Pro Lys Leu Ala Lys
 20 25 30
 Gly Thr Ala Pro Thr Pro Gly Leu Pro Pro Pro Pro Arg Pro Gln Pro
 35 40 45
 Trp His Pro Glu Tyr Gly Ser Ser Pro Xaa Pro Trp Ser Pro Pro Gly
 50 55 60
 Glu Ala Ala Pro Gly Ser Leu Gly Pro Gly Ala Pro Pro Arg Pro His
 65 70 75 80
 Arg Val Asp His Arg Ser Ser Gly Thr Leu Pro Ala Pro Leu Asp Ser
 85 90 95
 Pro Gly Cys Cys Trp Pro Pro Xaa Pro Pro Pro Pro Pro Trp Arg Arg
 100 105 110
 Ser Gly Pro Ser Arg Pro
 115

<210> 353
 <211> 1469
 <212> DNA
 <213> Homo sapiens

<400> 353

nntcatgaag gcttgaactt gcgtgatctt cagcctgcgg acctggcggg tgacggcggt
60
attgagccgg tggacctcgt ggtcggagat gtctctttta tctccttgac gatgatecctt
120
gaacccattt cagctgttgt cagcccacac ggcctcatgc tgttgctggg gaagcctcaa
180
tttgagggtg gttgcaaggc tttgggagcc catggcggtg tcacggaccc ggccctgcgc
240
ttgcaggcca tcgcgggtgt catggcagca gcggtagatt tgggttggcg tatgcgtgac
300
gagtgcgata gcccgttgcc cgggcaggat ggaaacgttg agcacttcgt cttgctggaa
360
cgtacgggtc ggtgacagac gtccgggcat atcatgggcc gctactgtgg tcttgtgaac
420
gacacgagcc cttcgagata cgttgctgctc gtcacccatg ccacgcggga cgacgctttt
480
gacgcggctg ccgaattcat ctctgaaatg gcggggcgag acattgggtg cgcgggtccg
540
gatgatcagg tgaagccgat gtcaagcaag ctgccaggga tcgatcttga aagcttggga
600
gagttcgccc acgaggcgga ggtggtcgtc gtctttggcg gcgacggcac gatcttgca
660
gctgctgaat ggtcattacc tcgccacgtt cccatgattg gcgtcaacct tggccatgct
720
ggttttctgg ctgagctgga gcgctccgat atggcggatc tagtgaacaa ggtgtgttcg
780
cgcgactaca ccgttgagga tcgcctcgtg cttaaaaacca ccgtcacga gcattccgga
840
caacaccgtt ggagttcttt tgccgtcaac gagttgtctc tggaaaaggc agcccggcgg
900
cgcgtgctcg acgttctggc gtctgtcgac gagttgccgg tgcaacgctg gagttgcgac
960
gggatcctgg tctcgacccc gaccggatcg acggcctacg cgttctcagc tggcggcccg
1020
gtcatgtggc ccgatctcga cgccatgctc atggtgccgt tgagcgctca cgtctctttt
1080
gctcgaccgc tggatcatgag ccagctgct cgagtggacc ttgacatcca gccagacggt
1140
tcagaatcgg cggttctgtg gtgcgacggg cgccgatcgt gcaccgtacg accgggggaa
1200
agaatcaccg tcgtccgcca tcccgaacct ctgcgcattg ctcgtctggc cgcgcagccc
1260
ttcacatcgc gtctgggtcaa gaagtttgag ctcccgggtca gcgggtggcg tcagggtcgt
1320
gaccgtcatc acctagagga gacttcgtga tacgtagtgt gcgaattcgt ggactcggcg
1380
tcacgatga gacggtcctc gaaccctcat ccgcgctgac ggcagtcacc ggcgagaccg
1440
gcgccggaaa gaccatggtg gtcaccggt
1469

<210> 354

<211> 318

<212> PRT

<213> Homo sapiens

<400> 354

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Met Gly Arg Tyr Cys Gly Leu Val Asn Asp Thr Ser Pro Ser Arg Tyr
 1           5           10           15
Val Val Val Val Thr His Ala Thr Arg Asp Asp Ala Phe Asp Ala Ala
          20           25           30
Ala Glu Phe Ile Ser Glu Met Ala Gly Arg Asp Ile Gly Cys Ala Val
          35           40           45
Pro Asp Asp Gln Val Lys Pro Met Ser Ser Lys Leu Pro Gly Ile Asp
          50           55           60
Leu Glu Ser Leu Gly Glu Phe Ala His Glu Ala Glu Val Val Val Val
65           70           75           80
Phe Gly Gly Asp Gly Thr Ile Leu Arg Ala Ala Glu Trp Ser Leu Pro
          85           90           95
Arg His Val Pro Met Ile Gly Val Asn Leu Gly His Val Gly Phe Leu
          100          105          110
Ala Glu Leu Glu Arg Ser Asp Met Ala Asp Leu Val Asn Lys Val Cys
          115          120          125
Ser Arg Asp Tyr Thr Val Glu Asp Arg Leu Val Leu Lys Thr Thr Val
          130          135          140
Thr Glu His Ser Gly Gln His Arg Trp Ser Ser Phe Ala Val Asn Glu
145          150          155          160
Leu Ser Leu Glu Lys Ala Ala Arg Arg Arg Met Leu Asp Val Leu Ala
          165          170          175
Ser Val Asp Glu Leu Pro Val Gln Arg Trp Ser Cys Asp Gly Ile Leu
          180          185          190
Val Ser Thr Pro Thr Gly Ser Thr Ala Tyr Ala Phe Ser Ala Gly Gly
          195          200          205
Pro Val Met Trp Pro Asp Leu Asp Ala Met Leu Met Val Pro Leu Ser
          210          215          220
Ala His Ala Leu Phe Ala Arg Pro Leu Val Met Ser Pro Ala Ala Arg
225          230          235          240
Val Asp Leu Asp Ile Gln Pro Asp Gly Ser Glu Ser Ala Val Leu Trp
          245          250          255
Cys Asp Gly Arg Arg Ser Cys Thr Val Arg Pro Gly Glu Arg Ile Thr
          260          265          270
Val Val Arg His Pro Asp Arg Leu Arg Ile Ala Arg Leu Ala Ala Gln
          275          280          285
Pro Phe Thr Ser Arg Leu Val Lys Lys Phe Glu Leu Pro Val Ser Gly
          290          295          300
Trp Arg Gln Gly Arg Asp Arg His His Leu Glu Glu Thr Ser
305          310          315

```

<210> 355

<211> 558

<212> DNA

<213> Homo sapiens

<400> 355

```

nggatccac ctctggaat ggaaaccac ataccagttc tcttcctcga tttgaatgcg
60
gatgacctca gtgccaatga gcagcttggt ggcccccatg catccggcgt gaactccatc
120

```

ctgcccaagg agcatggcag ccagtttttc tacctgcca tcataaagca cagtgatgat
 180
 gaggtttcag ccacagcctc ttgggattcc tcggtgcatg attctgttca cttgaatggg
 240
 gtcacaccac agaatgaaag gatttaccta attgtgaaaa ccacagttca actcagccac
 300
 cctgctgcta tggagttagt attacgaaaa cgaattgcag ccaatattta caacaaacag
 360
 agtttcacgc agagtttgaa gaggagaata tcctgaaaa atatatttta ttcctgtggt
 420
 gtaacctatg aaatagtatc caatatacca aaggcaactg aggagataga ggaccgggaa
 480
 acgctggctc tcctggcagc aaggagtga aacgaaggca catcagatgg gaagacgtac
 540
 attgagaagt acactcga
 558

<210> 356
 <211> 186
 <212> PRT
 <213> Homo sapiens

<400> 356
 Xaa Ile Pro Pro Pro Gly Met Glu Thr His Ile Pro Val Leu Phe Leu
 1 5 10 15
 Asp Leu Asn Ala Asp Asp Leu Ser Ala Asn Glu Gln Leu Val Gly Pro
 20 25 30
 His Ala Ser Gly Val Asn Ser Ile Leu Pro Lys Glu His Gly Ser Gln
 35 40 45
 Phe Phe Tyr Leu Pro Ile Ile Lys His Ser Asp Asp Glu Val Ser Ala
 50 55 60
 Thr Ala Ser Trp Asp Ser Ser Val His Asp Ser Val His Leu Asn Gly
 65 70 75 80
 Val Thr Pro Gln Asn Glu Arg Ile Tyr Leu Ile Val Lys Thr Thr Val
 85 90 95
 Gln Leu Ser His Pro Ala Ala Met Glu Leu Val Leu Arg Lys Arg Ile
 100 105 110
 Ala Ala Asn Ile Tyr Asn Lys Gln Ser Phe Thr Gln Ser Leu Lys Arg
 115 120 125
 Arg Ile Ser Leu Lys Asn Ile Phe Tyr Ser Cys Gly Val Thr Tyr Glu
 130 135 140
 Ile Val Ser Asn Ile Pro Lys Ala Thr Glu Glu Ile Glu Asp Arg Glu
 145 150 155 160
 Thr Leu Ala Leu Leu Ala Ala Arg Ser Glu Asn Glu Gly Thr Ser Asp
 165 170 175
 Gly Lys Thr Tyr Ile Glu Lys Tyr Thr Arg
 180 185

<210> 357
 <211> 323
 <212> DNA
 <213> Homo sapiens

<400> 357

acgcgtgcgt gtgttgtgtg agtcgggtgt gtgcatgcgt gtgggtgtgc agcaggtggg
 60
 gtacgatcag gctgaaggct gatcaggcac aaggctctgg gggagagccc tggttccagc
 120
 cctgggggtca gagcagcagg ggccagaaag acggcagggg tgagcactgc acccgctggg
 180
 cagggcaggg ccacagaagg cagggcatgg aggccacgtg aagggttga cagagtggat
 240
 ggatgtctcc ggaagcacct gcgtggccca gtcagcagga tcagactcgc atgtgtcagg
 300
 gtcaccatgg gtcagcgagg atn
 323

<210> 358

<211> 102

<212> PRT

<213> Homo sapiens

<400> 358

Met	Val	Thr	Leu	Thr	His	Ala	Ser	Leu	Ile	Leu	Leu	Thr	Gly	Pro	Arg
1				5					10					15	
Arg	Cys	Phe	Arg	Arg	His	Pro	Ser	Thr	Leu	Ser	Ser	Pro	Ser	Arg	Gly
			20					25					30		
Leu	His	Ala	Leu	Pro	Ser	Val	Ala	Leu	Pro	Cys	Pro	Ala	Gly	Ala	Val
		35					40					45			
Leu	Thr	Pro	Ala	Val	Phe	Leu	Ala	Pro	Ala	Ala	Leu	Thr	Pro	Gly	Leu
	50					55					60				
Glu	Pro	Gly	Leu	Ser	Pro	Arg	Ala	Leu	Cys	Leu	Ile	Ser	Leu	Gln	Pro
65					70				75					80	
Asp	Arg	Thr	Pro	Pro	Ala	Ala	His	Pro	His	Ala	Cys	Thr	His	Pro	Thr
				85					90					95	
His	Thr	Thr	His	Ala	Arg										
															100

<210> 359

<211> 265

<212> DNA

<213> Homo sapiens

<400> 359

acgcgtaccg acaagcgccc ggtgatggcc gaccttcgcg aatcgggctgc aatcgagcag
 60
 gatgcggaca tgatcgtctt catctaccgc gacgattact acaacaagga aaattcgccg
 120
 gacaaggggc tggccgagat catcatcggc aagcatcggg ggggccccac cggctcgtgc
 180
 aagctgaagt tcttcggcga gtacacccgt ttcgacaacc tggcccacaa ctcggttggt
 240
 tcgttcgaat aacggatgat tccgg
 265

<210> 360

<211> 83

<212> PRT

<213> Homo sapiens

<400> 360

```

Thr Arg Thr Asp Lys Arg Pro Val Met Ala Asp Leu Arg Glu Ser Gly
 1           5           10          15
Ala Ile Glu Gln Asp Ala Asp Met Ile Val Phe Ile Tyr Arg Asp Asp
          20          25          30
Tyr Tyr Asn Lys Glu Asn Ser Pro Asp Lys Gly Leu Ala Glu Ile Ile
          35          40          45
Ile Gly Lys His Arg Gly Gly Pro Thr Gly Ser Cys Lys Leu Lys Phe
          50          55          60
Phe Gly Glu Tyr Thr Arg Phe Asp Asn Leu Ala His Asn Ser Val Gly
65          70          75          80
Ser Phe Glu

```

<210> 361

<211> 453

<212> DNA

<213> Homo sapiens

<400> 361

```

gctttgcagg aggaaatctc tatctctggc tgcaagatga ggctgagcta cctgagcagc
60
cggacccctg gctacaaatc tgtcctgagg atcagcctca cccacccgac catccccttc
120
aacctcatga aggtgcacct catggtagcg gtggagggcc gcctcttcag gaagtgggtc
180
gctgcagccc cagacctgtc ctattatttc atttgggaca agacagacgt ctacaaccag
240
aaggtgtttg ggctttcaga agcctttggt tccgtggggt atgaatatga atcctgccc
300
gatctaattc tgtgggaaaa aagaacaaca gtgctgcagg gctatgaaat tgacgcgtcc
360
aagcttggag gatggagcct agacaaacat catgccctca acattcaaag tggcatcctg
420
cacaaaggga atgngagaa ccagtttgtg tct
453

```

<210> 362

<211> 151

<212> PRT

<213> Homo sapiens

<400> 362

```

Ala Leu Gln Glu Glu Ile Ser Ile Ser Gly Cys Lys Met Arg Leu Ser
 1           5           10          15
Tyr Leu Ser Ser Arg Thr Pro Gly Tyr Lys Ser Val Leu Arg Ile Ser
          20          25          30
Leu Thr His Pro Thr Ile Pro Phe Asn Leu Met Lys Val His Leu Met
          35          40          45
Val Ala Val Glu Gly Arg Leu Phe Arg Lys Trp Phe Ala Ala Ala Pro
          50          55          60
Asp Leu Ser Tyr Tyr Phe Ile Trp Asp Lys Thr Asp Val Tyr Asn Gln

```

```

65          70          75          80
Lys Val Phe Gly Leu Ser Glu Ala Phe Val Ser Val Gly Tyr Glu Tyr
          85          90          95
Glu Ser Cys Pro Asp Leu Ile Leu Trp Glu Lys Arg Thr Thr Val Leu
          100          105          110
Gln Gly Tyr Glu Ile Asp Ala Ser Lys Leu Gly Gly Trp Ser Leu Asp
          115          120          125
Lys His His Ala Leu Asn Ile Gln Ser Gly Ile Leu His Lys Gly Asn
          130          135          140
Gly Glu Asn Gln Phe Val Ser
145          150

```

```

<210> 363
<211> 502
<212> DNA
<213> Homo sapiens

```

```

<400> 363
ggtaacaaaa aagtttgcca cagtattcac actccaggtc tccataaacc ttccagatcc
60
gctcacacaa gctggtgttc atttgcttct tctgtaaact gttcaggacc ttcataaaag
120
cggtgatgcc tgaccggtgc tcaggggcag ctttgcaaga gtcaggctga tgtgtgatgg
180
tgtccccacc accagctact ggagggagga ggtctgaggc ctcagctggg ttgacctga
240
gacacctgct gggatctggg tcaccagctg aaagcacagc catgttctgc cttccccta
300
gggggctctg ggcgccatgg ctttcctgat ctgaccagc actctgggccc ttggacagca
360
gtagtgtgat cacttcacct tgcgtctgga ctgagcttct gtgctgcatg tctgggggct
420
tctcaggagc agcatgagcc tctgcggagg aggtatcatt tttcaacaaa aaatcatctg
480
aaaccacctc ttgagaatgc ag
502

```

```

<210> 364
<211> 136
<212> PRT
<213> Homo sapiens

```

```

<400> 364
Met Gln His Arg Ser Ser Val Gln Thr Gln Gly Glu Val Ile Thr Leu
1          5          10          15
Leu Leu Ser Lys Ala Gln Ser Ala Gly Ser Asp Gln Glu Ser His Gly
          20          25          30
Ala Gln Ser Pro Leu Gly Glu Gly Gln Asn Met Ala Val Leu Ser Ala
          35          40          45
Gly Asp Pro Asp Pro Ser Arg Cys Leu Arg Ser Asn Pro Ala Glu Ala
          50          55          60
Ser Asp Leu Leu Pro Pro Val Ala Gly Gly Gly Asp Thr Ile Thr His
65          70          75          80
Gln Pro Asp Ser Cys Lys Ala Ala Pro Glu His Arg Ser Gly Ile Thr

```

				85					90					95					
Ala	Phe	Met	Lys	Val	Leu	Asn	Ser	Leu	Gln	Lys	Lys	Gln	Met	Asn	Thr				
			100						105					110					
Ser	Leu	Cys	Glu	Arg	Ile	Trp	Lys	Val	Tyr	Gly	Asp	Leu	Glu	Cys	Glu				
		115					120					125							
Tyr	Cys	Gly	Lys	Leu	Phe	Trp	Tyr												
	130					135													

<210> 365
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 365
 atctcaacgg atgcatccat caaggagatg atccccccag gtgctcttgt tatgctcaca
 60
 ccactgatcg ttgggattct atttgggggt gagaccctct ctggagtcct tgctggtgcc
 120
 cttgtctctg gtgttcagat tgccatttct gcatccaaca ctggtggtgc ctgggacaac
 180
 gccaagaagt acattgaggc tggagtttca gagcatgccca ggacccttgg cccaaaaggt
 240
 tctgaccctc acaaggcggc tgtcattggt gacaccattg gagatcctct caaggacacg
 300
 tctggccctt ccctcaacat cctcatcaag ctt
 333

<210> 366
 <211> 111
 <212> PRT
 <213> Homo sapiens

Ile	Ser	Thr	Asp	Ala	Ser	Ile	Lys	Glu	Met	Ile	Pro	Pro	Gly	Ala	Leu				
1				5					10					15					
Val	Met	Leu	Thr	Pro	Leu	Ile	Val	Gly	Ile	Leu	Phe	Gly	Val	Glu	Thr				
			20					25					30						
Leu	Ser	Gly	Val	Leu	Ala	Gly	Ala	Leu	Val	Ser	Gly	Val	Gln	Ile	Ala				
		35				40					45								
Ile	Ser	Ala	Ser	Asn	Thr	Gly	Gly	Ala	Trp	Asp	Asn	Ala	Lys	Lys	Tyr				
	50				55			60											
Ile	Glu	Ala	Gly	Val	Ser	Glu	His	Ala	Arg	Thr	Leu	Gly	Pro	Lys	Gly				
65				70				75					80						
Ser	Asp	Pro	His	Lys	Ala	Ala	Val	Ile	Gly	Asp	Thr	Ile	Gly	Asp	Pro				
			85					90					95						
Leu	Lys	Asp	Thr	Ser	Gly	Pro	Ser	Leu	Asn	Ile	Leu	Ile	Lys	Leu					
		100				105							110						

<210> 367
 <211> 381
 <212> DNA
 <213> Homo sapiens

<400> 367

gcgttcgtcg cactacccgg cggcggcgga acccttgacg agctactcga agcatggaca
60
tggcagcagc tcggtgtaca cagcaaaccg gtgngccttg tacgactcga cnncttctgg
120
gcaccgctga ccgcgctact caaccacatg accatcgaaa gcttcattcg ccctgaggac
180
cgcgcctcgc tcgtgatcgc cgataccata catcagctga tggccgatct tgagggatgg
240
acccaccac caccgaagtg gcgctcgtga catagaacaa atgattctga ctatggctca
300
ttgacatctg cgcagcggct actagctcca ttgacttcaa atcgggcctt ggccgaggct
360
cngttcaggt ggcccgaat g
381

<210> 368
<211> 89
<212> PRT
<213> Homo sapiens

<400> 368
Ala Phe Val Ala Leu Pro Gly Gly Gly Gly Thr Leu Asp Glu Leu Leu
1 5 10 15
Glu Ala Trp Thr Trp Gln Gln Leu Gly Val His Ser Lys Pro Val Xaa
20 25 30
Leu Val Arg Leu Asp Xaa Phe Trp Ala Pro Leu Thr Ala Leu Leu Asn
35 40 45
His Met Thr Ile Glu Ser Phe Ile Arg Pro Glu Asp Arg Ala Ser Leu
50 55 60
Val Ile Ala Asp Thr Ile His Gln Leu Met Ala Asp Leu Glu Gly Trp
65 70 75 80
Thr Pro Pro Pro Pro Lys Trp Arg Ser
85

<210> 369
<211> 313
<212> DNA
<213> Homo sapiens

<400> 369
gatacatgat cctctcatat cgcacacaca ccgctcccct ctgccgcaat tcgcagacaa
60
acttgcgag gcttcacagc aagccgtcaa ggctgcttcc tgtgggctac cgatagtctc
120
gtacgcgagt tctcggacat caacgccaac gtcgggcaag atactgtcaa cgccatctac
180
acattctacg agcagcaagc gaccagtttc cttegccagc tgaacgacct cccacccgaa
240
gagcttcccg acgtcatcga ggacttcttc cgctgtcca ctgatgtcct tctttaccat
300
ttccagcaag ctt
313

<210> 370

<211> 101
 <212> PRT
 <213> Homo sapiens

<400> 370
 Ser Ser His Thr Ala His Thr Pro Leu Pro Ser Ala Ala Ile Arg Arg
 1 5 10 15
 Gln Thr Cys Ala Gly Phe Thr Ala Ser Arg Gln Gly Cys Phe Leu Trp
 20 25 30
 Ala Thr Asp Ser Leu Val Arg Glu Phe Ser Asp Ile Asn Ala Asn Val
 35 40 45
 Gly Gln Asp Thr Val Asn Ala Ile Tyr Thr Phe Tyr Glu Gln Gln Ala
 50 55 60
 Thr Ser Phe Leu Arg Gln Leu Asn Asp Leu Pro Pro Glu Glu Leu Pro
 65 70 75 80
 Asp Val Ile Glu Asp Phe Phe Arg Leu Ser Thr Asp Val Leu Leu Tyr
 85 90 95
 His Phe Gln Gln Ala
 100

<210> 371
 <211> 380
 <212> DNA
 <213> Homo sapiens

<400> 371
 atgacggggtc acgtcatcct ggcgattcca caggtggtga cgtcatggat cggcctcatc
 60
 tgcacgcgcca ttggcacggg ctttatcaag ccgaacctct ccacgggtggt aggaggtctt
 120
 tacgatgacg gtgacccccg ccgcgatcag ggtttcctgt acttctacat gtcgatcagt
 180
 attggatctc tcttcgcgcc gatcgtcacc ggcctcctca aggaccatta cggctaccac
 240
 gtaggtttca ttgccgctgc tatcggtatg gctctgggtc tgatcgctt cttccacggt
 300
 cgttccaaac tgcgtgagct cgccttcgac atccccaatc cgctggcccc cggcgagggt
 360
 cgccggatgg tgctccgcgg
 380

<210> 372
 <211> 126
 <212> PRT
 <213> Homo sapiens

<400> 372
 Met Thr Gly His Val Ile Leu Ala Ile Pro Gln Val Val Thr Ser Trp
 1 5 10 15
 Ile Gly Leu Ile Cys Ile Ala Ile Gly Thr Gly Phe Ile Lys Pro Asn
 20 25 30
 Leu Ser Thr Val Val Gly Gly Leu Tyr Asp Asp Gly Asp Pro Arg Arg
 35 40 45
 Asp Gln Gly Phe Leu Tyr Phe Tyr Met Ser Ile Ser Ile Gly Ser Leu

50		55		60											
Phe	Ala	Pro	Ile	Val	Thr	Gly	Leu	Leu	Lys	Asp	His	Tyr	Gly	Tyr	His
65				70				75						80	
Val	Gly	Phe	Ile	Ala	Ala	Ala	Ile	Gly	Met	Ala	Leu	Gly	Leu	Ile	Ala
		85						90					95		
Phe	Phe	His	Gly	Arg	Ser	Lys	Leu	Arg	Glu	Leu	Ala	Phe	Asp	Ile	Pro
		100					105						110		
Asn	Pro	Leu	Ala	Pro	Gly	Glu	Gly	Arg	Arg	Met	Val	Leu	Arg		
		115					120						125		

<210> 373
 <211> 475
 <212> DNA
 <213> Homo sapiens

<400> 373
 acatgttgga aaaattgcct cccactctgg tgctacaggt atgaatctca gccacagtga
 60
 tgactgtggc agctacaggc ctgatgaaca cccaccaag aaaaggagca tcatgtgcct
 120
 gcttctctct ggttcctaaa tcctttggcc aaacattttc cccacaaccc tccactccag
 180
 ttggctggtc actgcctctc agaaagaagt cccaggtccc tgtcagcccc agagcgcctg
 240
 catggactct gccactgtc cctttccaac acggaggccc ccaattctgg ggacccctac
 300
 accctaccct gtaccaccac atccccatgc ctgctccaga cagcactaac ctcccatgac
 360
 agtgggacca aagcagttct taaaggcca atccactcag ttcttaaagt aaaaacagtt
 420
 gcccatgagt ccccccaaa gacgtccgca catatgccaa acattcggtg tgcac
 475

<210> 374
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 374
 Met Gly Met Trp Trp Tyr Arg Val Gly Cys Arg Gly Pro Gln Asn Trp
 1 5 10 15
 Gly Pro Pro Cys Trp Lys Gly Thr Val Gly Arg Val His Ala Gly Ala
 20 25 30
 Leu Gly Leu Thr Gly Thr Trp Asp Phe Phe Leu Arg Gly Ser Asp Gln
 35 40 45
 Pro Thr Gly Val Glu Gly Cys Gly Glu Asn Val Trp Pro Lys Asp Leu
 50 55 60
 Gly Thr Arg Glu Lys Gln Ala His Asp Ala Pro Phe Leu Gly Gly Val
 65 70 75 80
 Phe Ile Arg Pro Val Ala Ala Thr Val Ile Thr Val Ala Glu Ile His
 85 90 95
 Thr Cys Ser Thr Arg Val Gly Gly Asn Phe Ser Asn Met
 100 105

<210> 375
 <211> 332
 <212> DNA
 <213> Homo sapiens

<400> 375
 nnacgcgtcg cctccacctc gaaacccgcc ggcggtcgtt ttttcaccat ggccgaccgc
 60
 aaggcccaag ttgcgacggt cacggacacg ctgtatttca cgccgtcgca atgggatgga
 120
 tgcattggcac ggatgcgtgg ggataagata tcagcactga agtggaatca gatgcagatg
 180
 gcggcatgct ccttcatagc ggcagtgggt gcgaagctgg gctgcccgc ggcactatg
 240
 ggcacggcgc agctgctgta ccagcgtttc catctatttc atgcgccgac tgagttttcg
 300
 ttacatgagg tggctttgac gtgtctcttc ac
 332

<210> 376
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 376
 Xaa Arg Val Ala Ser Thr Ser Lys Pro Ala Gly Gly Arg Phe Phe Thr
 1 5 10 15
 Met Ala Asp Arg Lys Ala Gln Val Ala Thr Val Thr Asp Thr Leu Tyr
 20 25 30
 Phe Thr Pro Ser Gln Trp Asp Gly Cys Met Ala Arg Met Arg Gly Asp
 35 40 45
 Lys Ile Ser Ala Leu Lys Trp Asn Gln Met Gln Met Ala Ala Cys Ser
 50 55 60
 Phe Ile Ala Ala Val Gly Ala Lys Leu Gly Cys Pro Gln Arg Thr Met
 65 70 75 80
 Gly Thr Ala Gln Leu Leu Tyr Gln Arg Phe His Leu Phe His Ala Pro
 85 90 95
 Thr Glu Phe Ser Leu His Glu Val Ala Leu Thr Cys Leu Phe
 100 105 110

<210> 377
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 377
 cgcgtgccag gtatgtcaac tgatctgtcg gatatttccg aggttgagta ccgtcaactg
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 aggctggaac gagtgggtgct gtgttcgggtg tggactcagg gaactgccgc agacgccgag
 120
 aacgctatgg cggagctgaa agcccttgct gaaacggcgg gatctcaggt actcgaagct
 180
 gtcattgcaac gtcggactac cccggatccg gcgacgtaca ttgggttcggg caaggtggct
 240

gagcttgccg aggtggtgcg ggcgactggt gccgatactg tcatttgtga cgggtgaactt
 300
 gacgccgctc agttgcgcaa cctcgaggat cgggtcaagn gcaaagttgt ggaccggtcg
 360
 gtctgattc
 369

<210> 378
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 378
 Arg Val Pro Gly Met Ser Thr Asp Leu Ser Asp Ile Ser Glu Val Glu
 1 5 10 15
 Tyr Arg Gln Leu Arg Leu Glu Arg Val Val Leu Cys Ser Val Trp Thr
 20 25 30
 Gln Gly Thr Ala Ala Asp Ala Glu Asn Ala Met Ala Glu Leu Lys Ala
 35 40 45
 Leu Ala Glu Thr Ala Gly Ser Gln Val Leu Glu Ala Val Met Gln Arg
 50 55 60
 Arg Thr Thr Pro Asp Pro Ala Thr Tyr Ile Gly Ser Gly Lys Val Ala
 65 70 75 80
 Glu Leu Ala Glu Val Val Arg Ala Thr Gly Ala Asp Thr Val Ile Cys
 85 90 95
 Asp Gly Glu Leu Asp Ala Ala Gln Leu Arg Asn Leu Glu Asp Arg Val
 100 105 110
 Lys Xaa Lys Val Val Asp Arg Ser Val
 115 120

<210> 379
 <211> 408
 <212> DNA
 <213> Homo sapiens

<400> 379
 acgcgttact taaacttata tgtaaataat aaattcatta tttctagttg gtttaggtact
 60
 atgggctgtg gtttaccagg tgctatggca gctaaaattg cttatccaaa ccgtcaagca
 120
 gtagctatca caggcgacgg tgcgttccaa atggtaatgc aagactttgc tacagctgtt
 180
 caatataact taccaatgac aatctttgta ttaaataaca aacaattgtc attcattaata
 240
 tatgaacaac aagctgctgg tgaattagag tatgccattg atttctctga tatggatcat
 300
 gctaaatttg ctgaagctgc tggtggtaaa ggctatgttg tgagagatgt aagtcgtctt
 360
 gacgacatcg ttgaagaggc aatggctcaa gatgttccaa caatcggt
 408

<210> 380
 <211> 136
 <212> PRT

<213> Homo sapiens

<400> 380

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Thr Arg Tyr Leu Asn Leu Ser Val Asn Asn Lys Phe Ile Ile Ser Ser
 1           5           10           15
Trp Leu Gly Thr Met Gly Cys Gly Leu Pro Gly Ala Met Ala Ala Lys
      20           25           30
Ile Ala Tyr Pro Asn Arg Gln Ala Val Ala Ile Thr Gly Asp Gly Ala
      35           40           45
Phe Gln Met Val Met Gln Asp Phe Ala Thr Ala Val Gln Tyr Asn Leu
      50           55           60
Pro Met Thr Ile Phe Val Leu Asn Asn Lys Gln Leu Ser Phe Ile Lys
65           70           75           80
Tyr Glu Gln Gln Ala Ala Gly Glu Leu Glu Tyr Ala Ile Asp Phe Ser
      85           90           95
Asp Met Asp His Ala Lys Phe Ala Glu Ala Ala Gly Gly Lys Gly Tyr
      100          105          110
Val Val Arg Asp Val Ser Arg Leu Asp Asp Ile Val Glu Glu Ala Met
      115          120          125
Ala Gln Asp Val Pro Thr Ile Val
      130          135

```

<210> 381

<211> 613

<212> DNA

<213> Homo sapiens

<400> 381

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nacgcgtcat aggcggggccc agtggaagac cacgccaaca cagttggttg agatccgcgt
60
tgagggcaag gtcctgcgcg tcccgcgaaa tctggtcaag gcctaccact ctgggctgat
120
cgacgtcgag gactgaaccc tgggagcctg ggcggtccag catgactgct caggctcatt
180
acaaaaacgc gtcgatcccc tagggttgtc gtcatgagca agcccgaagt gaccctgccc
240
gattccgccc ccgacgacct cgtcgttgag gacatcacca tcggcgacgg ccctgaagcg
300
tccgctggca acctcgtcga agtgcactac gtcggcgtgg ccttaagcaa tggtcgtgag
360
ttcgattctt cctggaaccg cggggagccg ctgaccttcc aactaggggc tggccagggtg
420
atccccgagt gggatgaagg tgtccaaggt atgaaggtcg gtggacgacg caaactcgtc
480
atccccacc accttgctta cggtccgcaa ggaatctccg gtgtgatcgc tggcggtgag
540
acgctggtct tcgtctgcga ccttgtaaac atcatctgac gtgacccccg ctcaagcagt
600
cttcgcgccc ggg
613

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<210> 382

<211> 137

<212> PRT

<213> Homo sapiens

<400> 382

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Leu Leu Arg Leu Ile Thr Lys Thr Arg Arg Ser Arg Arg Val Val Val
 1           5           10           15
Met Ser Lys Pro Glu Val Thr Leu Pro Asp Ser Ala Pro Asp Asp Leu
      20           25           30
Val Val Glu Asp Ile Thr Ile Gly Asp Gly Pro Glu Ala Ser Ala Gly
      35           40           45
Asn Leu Val Glu Val His Tyr Val Gly Val Ala Leu Ser Asn Gly Arg
 50           55           60
Glu Phe Asp Ser Ser Trp Asn Arg Gly Glu Pro Leu Thr Phe Gln Leu
65           70           75           80
Gly Ala Gly Gln Val Ile Pro Glu Trp Asp Glu Gly Val Gln Gly Met
      85           90           95
Lys Val Gly Gly Arg Arg Lys Leu Val Ile Pro His His Leu Ala Tyr
      100           105           110
Gly Pro Gln Gly Ile Ser Gly Val Ile Ala Gly Gly Glu Thr Leu Val
      115           120           125
Phe Val Cys Asp Leu Val Asn Ile Ile
      130           135

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<210> 383

<211> 352

<212> DNA

<213> Homo sapiens

<400> 383

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nggagcaaca cctggtcctt gggaatgaag tgtaggagtt gcatttgctg aggttggtgt
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ttgccaaaga gatgccagct tcttcgaact actgctgtgc aactcttcat gttcaaaacc
120
cagttttctg tttttcacac ctgaacatac acccccctgc agttgggtgg ctcccccggt
180
accagctggg ctctatctac agagagagca atggcttccc ttcccttgaa ggaagtctca
240
ccctcacaag gacacttgat ccgctgcaaa gcagaaagtg tgcggaccct ttgggaaggg
300
cgttcttttc ttgttttagaa cctaggattc tgtttttccc aaacaggatc an
352

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<210> 384

<211> 93

<212> PRT

<213> Homo sapiens

<400> 384

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Met Pro Ala Ser Ser Asn Tyr Cys Cys Ala Thr Leu His Val Gln Asn
 1           5           10           15
Pro Val Phe Cys Phe Ser His Leu Asn Ile His Pro Pro Ala Val Gly
      20           25           30
Trp Leu Pro Arg Tyr Gln Leu Gly Ser Ile Tyr Arg Glu Ser Asn Gly
      35           40           45
Phe Pro Ser Leu Glu Gly Ser Leu Thr Leu Thr Arg Thr Leu Asp Pro

```

50	55	60
Leu Gln Ser Arg Lys Cys Ala Asp Pro Leu Gly Arg Ala Phe Phe Ser		
65	70	75
Cys Leu Glu Pro Arg Ile Leu Phe Phe Pro Asn Arg Ile		80
85	90	

<210> 385
 <211> 342
 <212> DNA
 <213> Homo sapiens

<400> 385
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 gcacctcggg caatgtcctg ggctgactg gcacacgcaa tcaaagcgag caacaacaca
 120
 caaaaacgca tcatgaggca gacgccaggg aagtgcaga agccgcagca ggcgcgcggc
 180
 gattggaaat atcggtgagg ctaatggtca ccagcgcttg caggttgat tccgtggcca
 240
 attcgcgga cgacagcacc gccagttcca gctcgccgcg cagcaccagg cgacgcaagc
 300
 tgcggcgcaa ctccgggtgc accaacaaca ccgcactgtt ca
 342

<210> 386
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 386
 Met Gln Asn Ala Pro Phe Thr Gly Arg Gln Val Asp Arg Ala Ala Ser
 1 5 10 15
 Thr Ser Gly Asn Val Leu Gly Leu Thr Gly Thr Arg Asn Gln Ser Glu
 20 25 30
 Gln Gln His Thr Lys Thr His His Glu Ala Asp Ala Arg Glu Val Thr
 35 40 45
 Glu Ala Ala Ala Gly Ala Arg Arg Leu Glu Ile Ser Val Arg Leu Met
 50 55 60
 Val Thr Ser Ala Cys Arg Leu Tyr Ser Val Ala Asn Ser Arg Asn Asp
 65 70 75 80
 Ser Thr Ala Ser Ser Ser Ser Pro Arg Ser Thr Arg Arg Arg Lys Leu
 85 90 95
 Arg Arg Asn Ser Gly Cys Thr Asn Asn Thr Ala Leu Phe
 100 105

<210> 387
 <211> 379
 <212> DNA
 <213> Homo sapiens

<400> 387
 acgcgtgacg cgccggcatc ggaagcgttg actgcagaga agaccgcgca cgtggctgtg
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ggacgtgctg gcacgtctga catggtgcgt ggacccgcct tctcttcgcc tgcgcatgcc
 120
 atgcaagagg agcttgacaa tgtgcgtgat ctgcgccatg cgcggcagca agcgctcgat
 180
 gctgttcggt ccgagctgct cgaagcgcag caagcatgtg cctcgtgcca gctgcagctg
 240
 cagcatgtgc cagatgatcg tgtgcgagcg catcccatat accaggcgct ccatgcggac
 300
 gttgcttaca tgcagcaaga acttgatcac gtacgagacg cattggcttc ggcagaatct
 360
 gagaatgcga gcctgcgcg
 379

<210> 388
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 388
 Met Arg Leu Val Arg Asp Gln Val Leu Ala Ala Cys Lys Gln Arg Pro
 1 5 10 15
 His Gly Ala Pro Gly Ile Trp Asp Ala Leu Ala His Asp His Leu Ala
 20 25 30
 His Ala Ala Ala Ala Ala Gly Thr Arg His Met Leu Ala Ala Leu Arg
 35 40 45
 Ala Ala Arg Asn Glu Gln His Arg Ala Leu Ala Ala Ala His Gly Arg
 50 55 60
 Asp His Ala His Cys Gln Ala Pro Leu Ala Trp His Ala Gln Ala Lys
 65 70 75 80
 Arg Arg Arg Val His Ala Pro Cys Gln Thr Cys Gln His Val Pro Gln
 85 90 95
 Pro Arg Ala Arg Ser Ser Leu Gln Ser Thr Leu Pro Met Pro Ala Arg
 100 105 110
 His Ala

<210> 389
 <211> 382
 <212> DNA
 <213> Homo sapiens

<400> 389
 ngatggccga ctgtcccact gtcagtacgc gaagctcgcc gtcgagtcgg tccacgtccg
 60
 ggcctccac gtgctccgca accctccgaa gcgatgacct ggcccggggg cggcaacgag
 120
 gtattgcgtt tggagacgct tgggggtcaat tacggccagg tgcgcgccgt cgatgccctg
 180
 acgaccaccg tagagcgcgg caccatcacc tgcctcatgg gtcgaaatgg atcaggcaag
 240
 tcgtctctga tgtgggcgat ccaaggggca acaaagtcct cagggagggt actgggtcaac
 300
 cagaggggtt cttgggctga ccccgcaaa gccgacgccg cgaccgctcg acgaatggtg
 360

agcttagtcc cgcagtcagc cn
382

<210> 390
<211> 127
<212> PRT
<213> Homo sapiens

<400> 390
Xaa Trp Pro Thr Val Pro Leu Ser Val Arg Glu Ala Arg Arg Arg Val
1 5 10 15
Gly Pro Arg Pro Gly Leu Pro Arg Ala Pro Gln Pro Ser Glu Ala Met
20 25 30
Thr Trp Pro Gly Gly Gly Asn Glu Val Leu Arg Leu Glu Thr Leu Gly
35 40 45
Val Asn Tyr Gly Gln Val Arg Ala Val Asp Ala Leu Thr Thr Thr Val
50 55 60
Glu Arg Gly Thr Ile Thr Cys Leu Met Gly Arg Asn Gly Ser Gly Lys
65 70 75 80
Ser Ser Leu Met Trp Ala Ile Gln Gly Ala Thr Lys Ser Ser Gly Arg
85 90 95
Val Leu Val Asn His Glu Gly Ser Trp Ala Asp Pro Arg Lys Ala Asp
100 105 110
Ala Ala Thr Ala Arg Arg Met Val Ser Leu Val Pro Gln Ser Ala
115 120 125

<210> 391
<211> 456
<212> DNA
<213> Homo sapiens

<400> 391
nnacgcgttg ccgctctgtg aggcgcctat cacggtgaca ctctcggtgc tatgagcgtg
60
tgcgacccta tcggtggcat gcaagccntg ttcagcgact ctattcccca gcagatcttc
120
ctgcccgcgc cctccttctt tcgccgccga cgaggccgac gtggagacgt ggtgcagcga
180
ggccgatgaa tcctggacac ccaccgcgac gacctggccg ggatcattgt cgagcccatc
240
ttgcaaggag ccggaggcat gtggccgtgg tctccgtcct gtctgaagca cctgcgccgt
300
cgtgctgatg aacttgacct agttcttata gccgacgagg tcgctactgg atttgggcgg
360
actggcaaac ttttcgcatg cgagtgggcc gatatcggtc ctgacatcat ggtgggttggg
420
aatccatga ctggcggata cctgacccag tcggcc
456

<210> 392
<211> 55
<212> PRT
<213> Homo sapiens

<400> 392

Gly Ala Tyr His Gly Asp Thr Leu Gly Ala Met Ser Val Cys Asp Pro
 1 5 10 15
 Ile Gly Gly Met His Ala Xaa Phe Ser Asp Ser Ile Pro Gln Gln Ile
 20 25 30
 Phe Leu Pro Ala Pro Ser Phe Phe Arg Arg Arg Arg Gly Arg Arg Gly
 35 40 45
 Asp Val Val Gln Arg Gly Arg
 50 55

<210> 393

<211> 371

<212> DNA

<213> Homo sapiens

<400> 393

nacgcgttgc tcgtcattgg tggctactcg gcctacgaag gtatctacac catgatgact
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 gacgaggacc ggtaccgggc ttcccgattt ccgacgggtg gcacccgggc ttctatcgac
 120
 aacaacctcc ccggttcgga actgtccatc ggcaccgaca ccgctctcaa cgtcatcgtc
 180
 gaggcgatgg acaagattaa ggagtcgggt atcgcgcca gacgctgctt cgtcgtcgag
 240
 acgatgggtc gtgactgcgg atacctcgcg ttgatgtcgg gtatcgcagc tggcgctgag
 300
 cggatctata ccaacgagga cggatatctc ctggacgata tagccaacga cgtccattgg
 360
 ttgcgggagt c
 371

<210> 394

<211> 123

<212> PRT

<213> Homo sapiens

<400> 394

Xaa Ala Leu Leu Val Ile Gly Gly Tyr Ser Ala Tyr Glu Gly Ile Tyr
 1 5 10 15
 Thr Met Met Thr Glu Arg Asp Arg Tyr Pro Ala Phe Arg Ile Pro Thr
 20 25 30
 Val Cys Ile Pro Ala Ser Ile Asp Asn Asn Leu Pro Gly Ser Glu Leu
 35 40 45
 Ser Ile Gly Thr Asp Thr Ala Leu Asn Val Ile Val Glu Ala Met Asp
 50 55 60
 Lys Ile Lys Glu Ser Gly Ile Ala Ser Arg Arg Cys Phe Val Val Glu
 65 70 75 80
 Thr Met Gly Arg Asp Cys Gly Tyr Leu Ala Leu Met Ser Gly Ile Ala
 85 90 95
 Ala Gly Ala Glu Arg Ile Tyr Thr Asn Glu Asp Gly Ile Ser Leu Asp
 100 105 110
 Asp Leu Ala Asn Asp Val His Trp Leu Arg Glu
 115 120

<210> 395
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 395
 gaattctagt tgggagattc attgaccaga cttttggaat aaacactagt catcatgcta
 60
 gcgacaggtg gtcttgtgca tggtagaaag gcagtccaag cctatgtctc tgaaacctgc
 120
 tctcatttct gttttctact ttacgattta tgttatctca tactccccat gttgcctggt
 180
 ctccagtttt tttacttggtg ttatttccat tcttctattc ctgctcaatt tctgcctcag
 240
 ggcagaattg tgtccaacag ctcttaaagt cagcgcagaa actgtgatgt taaaaacatc
 300
 ttgttatccg gccccaaaac atgttgtcct tggtaactct tactggtttg t
 351

<210> 396
 <211> 90
 <212> PRT
 <213> Homo sapiens

<400> 396
 Met Val Glu Arg Gln Ser Lys Pro Met Ser Leu Lys Pro Ala Leu Ile
 1 5 10 15
 Ser Val Phe Tyr Phe Thr Ile Tyr Val Ile Ser Tyr Ser Pro Cys Cys
 20 25 30
 Leu Phe Ser Ser Phe Phe Thr Cys Val Ile Ser Ile Leu Leu Phe Leu
 35 40 45
 Leu Asn Phe Cys Leu Arg Ala Glu Leu Cys Pro Thr Ala Leu Lys Cys
 50 55 60
 Ser Ala Glu Thr Val Met Leu Lys Thr Ser Cys Tyr Pro Ala Pro Lys
 65 70 75 80
 His Val Val Leu Gly Asn Ser Tyr Trp Phe
 85 90

<210> 397
 <211> 483
 <212> DNA
 <213> Homo sapiens

<400> 397
 gccgtcatta aagagatcac ccctctctc caacctggtg atgtcctcgt cgacggtggt
 60
 aatgcttatt ttggtgatac ccgccgccgt gaggaggaaa tacgtccac cggcattcac
 120
 tatgttggtg ctggcatctc cgggtggggga gtcggggccc tgagggtccc atcaattatg
 180
 cctggcgggg ttaaggaatc ttacgaaatc atcggaccgg tcttagaaaa aatctccgcc
 240
 cacgtcgacg gtgaaccctg ctgcgcatgg atgggtactg acggcgccgg acacttcgtc
 300

aagatgggtcc ataatggcat cgagtacgcc gatatgcagt tcattggcga ggcgcccttc
 360
 ctttttgcgn tgcccgcggg ttgaccaat gctgaggccg ccgatgcctt cgagtcgtgg
 420
 aaccatggcg acctcaattc ctacctcgtc gaaatcactt ctcgggtact gcgtgccaaag
 480
 gat
 483

<210> 398
 <211> 161
 <212> PRT
 <213> Homo sapiens

<400> 398
 Ala Val Ile Lys Glu Ile Thr Pro Leu Leu Gln Pro Gly Asp Val Leu
 1 5 10 15
 Val Asp Gly Gly Asn Ala Tyr Phe Gly Asp Thr Arg Arg Arg Glu Glu
 20 25 30
 Glu Ile Arg Pro Thr Gly Ile His Tyr Val Gly Thr Gly Ile Ser Gly
 35 40 45
 Gly Gly Val Gly Ala Leu Arg Val Pro Ser Ile Met Pro Gly Gly Val
 50 55 60
 Lys Glu Ser Tyr Glu Ile Ile Gly Pro Val Leu Glu Lys Ile Ser Ala
 65 70 75 80
 His Val Asp Gly Glu Pro Cys Cys Ala Trp Met Gly Thr Asp Gly Ala
 85 90 95
 Gly His Phe Val Lys Met Val His Asn Gly Ile Glu Tyr Ala Asp Met
 100 105 110
 Gln Phe Ile Gly Glu Ala Pro Phe Leu Phe Ala Xaa Pro Ala Gly Leu
 115 120 125
 Thr Asn Ala Glu Ala Ala Asp Ala Phe Glu Ser Trp Asn His Gly Asp
 130 135 140
 Leu Asn Ser Tyr Leu Val Glu Ile Thr Ser Arg Val Leu Arg Ala Lys
 145 150 155 160
 Asp

<210> 399
 <211> 314
 <212> DNA
 <213> Homo sapiens

<400> 399
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 60
 ggctcatcca cccatccact cattcaccca tctatccatc cactcatcca cccatccagt
 120
 cattcactca ttgtccatc cactcatgta cccatccact cattcgccca tttatccatc
 180
 cactcaacca tccactcatc caccatcca nctcatcatc cgtccagtca cccatctatc
 240
 caccatgta tccatccact catccaccca tccactcatc tgtccatcca cttatccacc
 300

catctactca ccca
314

<210> 400
<211> 104
<212> PRT
<213> Homo sapiens

<400> 400
Xaa Gly Met Lys Thr Thr Gln Pro Phe Leu Ser Ser Asn Leu Leu Gln
1 5 10 15
Ala Ser Val His Gly Ser Ser Thr His Pro Leu Ile His Pro Ser Ile
20 25 30
His Pro Leu Ile His Pro Ser Ser His Ser Leu Ile Cys Pro Ser Thr
35 40 45
His Val Pro Ile His Ser Phe Ala His Leu Ser Ile His Ser Thr Ile
50 55 60
His Ser Ser Thr His Pro Xaa His His Pro Ser Ser His Pro Ser Ile
65 70 75 80
His Pro Cys Ile His Pro Leu Ile His Pro Ser Thr His Leu Ser Ile
85 90 95
His Leu Ser Thr His Leu Leu Thr
100

<210> 401
<211> 2165
<212> DNA
<213> Homo sapiens

<400> 401
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agaagcaaat atatacagtc aatttaacag tgtttacttc tctggattgt ttaatgggtg
120
caaaatgaaa gatctattga agtttcacta tacattgcat tgattgaacc ttggagagtt
180
ttatgaaaaa gaggggcatc ccttgccatc tgtttgccag tcttccttgc cccttccttt
240
gaaatgcctg cctctttttt gccagattg tttcctgacc atccgaactc agatggggtc
300
ctctaagttc ttcctggata ttcacaaatc ccttcacaag gccacgtgc gaagtgaatg
360
atctggaggt gcctgggcat ctgtgttgga agggagtcaa gactcaccag ccagtcagtt
420
tgtgggctac agttgtccca caaaaatcag gcatgttcac ctcccctctg ggcccctaca
480
gctgggactg atcatagcct cagattagaa gaaatactga cttctaactc tataagccag
540
cactcctggg taaggagtga agctctgttg gccatgccgc tttggactgc tgggcagagc
600
tgagcctaca gttttgtact ggggtgcacg gatgacagct gggaagatgg aaaggcagct
660
tgaggattta tagcagctaa agggtaaagt ctgttatgca aaagggtccc atatgaactt
720

cctacaggtg tagccgcagc caagtgtctg tacagctgct gagaatttgt cggatgatgta
780
aaaattcctc tttgcatcac aagcgagtgg aaagccaggg gctgcatgag tggagaaagc
840
acagtctggg ttttcaagta ctgcagagaa tgagaatacc cagccgggag cctggagttg
900
aggcccgagt tacacaggct cccggaatac agacctggga agatagggga ggagagggga
960
agcttgtggc cttttgatec gcccccgaa tgcccaccgt gcgctgcttt gctgccttca
1020
tctcctgctc agaggccttc tccttcccag agacctcctt ggatgggtct aaggagagaca
1080
ctgcccgggc ctttttccct gcaatcacia ggtccaaatc ctccaggctg cgcttgatcg
1140
gccgcgccgc cccaatgttc tacgggctca ttttccgggt caggattggg tggaccatgc
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1260
attcagggtg ttttttaggg cctgacatgg tcatgggtga taccgacag gctttggggt
1320
gacagtctcg actctggctg cctaagacct ggaactggga gatgcctttg ctctcctggg
1380
gccctgtggg ggaatgagcc aggcccagga ccttgccggg aggtttgtgc gggttcttgg
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1500
cttgacaggt cagggacgtg agataattta catggagctt ttcttggtgt ctgtgggaag
1560
gaaaagaact gttttccgat tccctgtaca tgtccctgga agggatattg gatgtctgtt
1620
cattatgaag atgggtgctg gtgtgtctgt agaggctatg gagatgaggg gacgagtaga
1680
agtcagccag gaagctaggg atgtgggaat gggggagggc ctttttctct aagagtttat
1740
ccttgccctc ctgaatttct tgcttcagga cgtaggagtc agcaaggggg ttaaggatg
1800
gcttgagaga gctgcagcgg tggggatctg atcgactcag tttctcatgc ttaaagatgt
1860
cattgatggg ctttctctct tccgagggtc tgcttctgaa actctggacg tgctgaatca
1920
ctgatggccg gctgaccgcc atatggctcag tgctttggcc atgggtgggtc tgggacaaac
1980
tggaacacaa gtcaccccta gcaatcagtt tctttttgct gatcaaaggg ggtggggagc
2040
cataagggtg gctgctggag aggctggccc cactcacttg ggacaaaagc tttttcttgg
2100
ccagtgggga catcatgcct gggttgcccc tagagtagag caggggctg taattaagtc
2160
catgg
2165

<210> 402

<211> 87

<212> PRT

<213> Homo sapiens

<400> 402

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Glu Tyr Pro Ala Gly Ser Leu Glu Leu Arg Pro Glu Leu His Arg Leu
 1           5           10           15
Pro Glu Tyr Arg Pro Gly Lys Ile Gly Glu Glu Arg Gly Ser Leu Trp
           20           25           30
Pro Phe Asp Pro Pro Pro Glu Cys Pro Pro Cys Ala Ala Leu Leu Pro
           35           40           45
Ser Ser Pro Ala Gln Arg Pro Ser Pro Ser Gln Arg Pro Pro Trp Met
           50           55           60
Gly Leu Arg Glu Thr Leu Pro Gly Pro Phe Ser Leu Gln Ser Gln Gly
65           70           75           80
Pro Asn Pro Pro Gly Cys Ala
           85

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<210> 403

<211> 369

<212> DNA

<213> Homo sapiens

<400> 403

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cccatgggtg tgtcccagga cggcgtcatg aagcgtcagg taaatgacaa ggaaacggtc
60
gcgcacttgt tcgaatacac gacgcaagtg tctgtcgact cgacgccgca actcgtccag
120
ccttcgccca cgtcgcacga caacctcgtg cctgtccaga tgatcttttg cttcaagcag
180
cgcaacgcga aaaagatcaa tagccaccgc tgggtatttc atgcactggg ccgcatgcta
240
cagcccgaca tggtcgtctt ggtggacgtc ggcacgaagc ccggccacct cgccctatac
300
catctatggc aggcattcta tcaccgacct accttgggcg gtgcttgcg cgaaattcat
360
gctatgatc
369

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<210> 404

<211> 123

<212> PRT

<213> Homo sapiens

<400> 404

```

Pro Met Gly Val Ser Gln Asp Gly Val Met Lys Arg Gln Val Asn Asp
 1           5           10           15
Lys Glu Thr Val Ala His Leu Phe Glu Tyr Thr Thr Gln Val Ser Val
           20           25           30
Asp Ser Thr Pro Gln Leu Val Gln Pro Ser Pro Thr Ser His Asp Asn
           35           40           45
Leu Val Pro Val Gln Met Ile Phe Cys Phe Lys Gln Arg Asn Ala Lys
           50           55           60
Lys Ile Asn Ser His Arg Trp Val Phe His Ala Leu Gly Arg Met Leu
65           70           75           80
Gln Pro Asp Met Val Val Leu Val Asp Val Gly Thr Lys Pro Gly His

```

				85						90					95				
Leu	Ala	Leu	Tyr	His	Leu	Trp	Gln	Ala	Phe	Tyr	His	Arg	Pro	Thr	Leu				
				100				105					110						
Gly	Gly	Ala	Cys	Gly	Glu	Ile	His	Ala	Met	Ile									
				115				120											

<210> 405
 <211> 840
 <212> DNA
 <213> Homo sapiens

<400> 405
 gaattcccgc gcaccagctc gaagctggag cactttgtgt ctatcctgct gaagtgttc
 60
 gactcgccct ggaccacgag ggcctgtcg gagacagtgg tggaggagag cgacccaag
 120
 ccggccttca gcaagatgaa tgggtccatg gacaaaaagt catcgaccgt cagtgaggac
 180
 gtggaggcca ccgtgcccac gctgcagcgg accaagtcac ggatcgagca gggatatcgtg
 240
 gaccgctcag agacgggctg gctggacaag aaggaggggg agcaagccaa ggcgctgttt
 300
 gagaaggtga agaagttccg gacccatgtg gaggaggggg acattgtgta ccgcctctac
 360
 atgcggcaga ccatcatcaa ggtgatcaag ttcattcctca tcattctgta caccgtctac
 420
 tacgtgcaca acatcaagtt cgacgtggac tgcaccgtgg acattgagag cctgacgggc
 480
 taccgcacct accgctgtgc ccacccctg gccacactct tcaagatcct ggcgtccttc
 540
 tacatcagcc tagtcatctt ctacggcctc atctgcatgt atacactgtg gtggatgcta
 600
 cggcgctccc tcaagaagta ctcgtttgag tcgatccgtg aggagagcag ctacagcgac
 660
 atccccgacg tcaagaacga cttcgccctc atgctgcacc tcattgacca atacgaccg
 720
 ctctactcca agcgcttcgc cgtcttcctg tcggaggtga gtgagaacaa gctgcggcag
 780
 ctgaacctca acaacgagtg gacgctggac aagctccggt acggagagaa gacaacgcgt
 840

<210> 406
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 406
 Leu Ile Cys Met Tyr Thr Leu Trp Trp Met Leu Arg Arg Ser Leu Lys
 1 5 10 15
 Lys Tyr Ser Phe Glu Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile
 20 25 30
 Pro Asp Val Lys Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln
 35 40 45
 Tyr Asp Pro Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val

50		55		60											
Ser	Glu	Asn	Lys	Leu	Arg	Gln	Leu	Asn	Leu	Asn	Asn	Glu	Trp	Thr	Leu
65					70					75					80
Asp	Lys	Leu	Arg	Tyr	Gly	Glu	Lys	Thr	Thr	Arg					
				85					90						

<210> 407
 <211> 535
 <212> DNA
 <213> Homo sapiens

<400> 407
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 60
 aggctctact ttgctctgcc tggctctcagg gtgtagggga tggagagctg gacttccagc
 120
 ctgtcttcttg gctgtctagg ggccaggggc tcgggacaca gagctcctgg aggccgagca
 180
 caagccttgg gcagaggtga ggcagagctc tgactgtttc attcgactac gttgccaagg
 240
 agatgctcgc tcggagtggg tgctctgggt ctgggattcc aaaccaagct gccttctctg
 300
 atgtggcctt agtgctctgg gcggatgtac cttggctctg cctggaccct ctctctcttc
 360
 caggcctctg tcccaccagg atgatgccta tccagagctc attgtcctct cccacttcct
 420
 ccccgagctt cccattccgt gtctctctgg agggcccatc atcatcctgg tggaggtggt
 480
 gcactgagga ccacagcagc cctcgcattc ccacgggcaa aggggtatgt gtagg
 535

<210> 408
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 408
 Met Leu Ala Arg Ser Gly Cys Ser Gly Ser Gly Ile Pro Asn Gln Ala
 1 5 10 15
 Ala Phe Ser Asp Val Ala Leu Val Leu Trp Ala Asp Val Pro Trp Leu
 20 25 30
 Cys Leu Asp Pro Leu Ser Leu Pro Gly Leu Cys Pro Thr Arg Met Met
 35 40 45
 Pro Ile Gln Ser Ser Leu Ser Ser Pro Thr Ser Ser Pro Ser Phe Pro
 50 55 60
 Phe Arg Val Ser Leu Glu Gly Pro Ser Ser Ser Trp Trp Arg Cys Cys
 65 70 75 80
 Thr Glu Asp His Ser Ser Pro Arg Ile Pro Thr Gly Lys Gly Val Cys
 85 90 95
 Val

<210> 409
 <211> 375

<212> DNA

<213> Homo sapiens

<400> 409

ngtgtcatgg gtgtctatac cagcgatgag gccaaagactg ccaagacttt tggatttggg
 60
 ggacttccga ttacgactaa tattttctctt gccacaact tcaatatgga tgaaatttct
 120
 gatattgtct tccgtgtcaa tgataccagt ttgacaccaa ctgtgggacc agaattagct
 180
 agaaaattga ccgaaattgc tggctctcag caaggggagt atcaggtgtc agatgcgact
 240
 gcagccttcc aagaagtgc acaattgttc ggctttataa ctacgattat tagtgccatt
 300
 gcaggaattt ccctttttgt tggagggact ggtgttatga acatcatgct ggtttcgggtg
 360
 acggagcgta cgcgt
 375

<210> 410

<211> 125

<212> PRT

<213> Homo sapiens

<400> 410

Xaa	Val	Met	Gly	Val	Tyr	Thr	Ser	Asp	Glu	Ala	Lys	Thr	Ala	Lys	Thr
1				5					10					15	
Phe	Gly	Ile	Gly	Gly	Leu	Pro	Ile	Thr	Thr	Asn	Ile	Ser	Leu	Ala	Asn
			20					25					30		
Asn	Phe	Asn	Met	Asp	Glu	Ile	Ser	Asp	Ile	Val	Phe	Arg	Val	Asn	Asp
		35					40					45			
Thr	Ser	Leu	Thr	Pro	Thr	Val	Gly	Pro	Glu	Leu	Ala	Arg	Lys	Leu	Thr
	50					55					60				
Glu	Ile	Ala	Gly	Leu	Gln	Gln	Gly	Glu	Tyr	Gln	Val	Ser	Asp	Ala	Thr
65					70				75					80	
Ala	Ala	Phe	Gln	Glu	Val	Gln	Gln	Leu	Phe	Gly	Phe	Ile	Thr	Thr	Ile
			85						90					95	
Ile	Ser	Ala	Ile	Ala	Gly	Ile	Ser	Leu	Phe	Val	Gly	Gly	Thr	Gly	Val
		100						105					110		
Met	Asn	Ile	Met	Leu	Val	Ser	Val	Thr	Glu	Arg	Thr	Arg			
		115					120					125			

<210> 411

<211> 409

<212> DNA

<213> Homo sapiens

<400> 411

ccacatactt caccctcctc acccctcca cctactccac cacctggcag tcgccatcga
 60
 ggatgggacg caactccacg tccacatgct ccggaccacg cggcgtgtgg tggatgtgca
 120
 gcacgcggtc ggggcccctt gagctcgaag gcgcggcgca tcgggcagtg ctcgccggcc
 180

tggctcgacagg gcacgtcgta ctggtgagac acgcggaagc acttgtggcc gatgtaggcg
 240
 cgatecggctg tcccgaactg gcgctgatag gccgtgtaca caacacaaac tgttgtactc
 300
 ccggtccacc acgatcatgg gctgggactc gtgttccagg tggggggcca gggcttgggc
 360
 ctgcggtgag cgcgtggggg ggatggggca tagcgtcggg gaggagggtg
 409

<210> 412
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 412
 Met Pro His Pro Pro His Ala Leu Thr Ala Gly Pro Ser Pro Gly Pro
 1 5 10 15
 Pro Pro Gly Thr Arg Val Pro Ala His Asp Arg Gly Gly Pro Gly Val
 20 25 30
 Gln Gln Phe Val Leu Cys Thr Arg Pro Ile Ser Ala Ser Ser Gly Gln
 35 40 45
 Pro Ile Ala Pro Thr Ser Ala Thr Ser Ala Ser Ala Ser Arg Thr Ser
 50 55 60
 Thr Thr Cys Pro Ala Thr Arg Pro Ala Ser Thr Ala Arg Cys Ala Ala
 65 70 75 80
 Pro Ser Ser Ser Arg Gly Pro Asp Arg Val Leu His Ile His His Thr
 85 90 95
 Pro Arg Gly Pro Glu His Val Asp Val Glu Leu Arg Pro Ile Leu Asp
 100 105 110
 Gly Asp Cys Gln Val Val Glu
 115

<210> 413
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 413
 ccgggcatcc caccaccggg tgtcatgaac caagtagtgg cccctatggt agggactcca
 60
 gcaccgggtg gaagtccata tggacaacag gtgggagttt tggggcctcc agggcagcag
 120
 gcaccacctc catatcccgg cccacatcca gctggacccc ctgtcataca gcagccaaca
 180
 acacccatgt ttgtagctcc cccccaaag acccagcggc ttcttcaactc agaggcctac
 240
 ctgaaataca ttgaaggact cagtgcggag tccaacagca ttagcaagtg ggatcagaca
 300
 ctggcagctc ggagacgcga cgtccatttg tcgaaagaac aggagagccg cctaccc
 357

<210> 414
 <211> 119
 <212> PRT

<213> Homo sapiens

<400> 414

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Pro Gly Ile Pro Pro Pro Gly Val Met Asn Gln Val Val Ala Pro Met
 1           5           10           15
Val Gly Thr Pro Ala Pro Gly Gly Ser Pro Tyr Gly Gln Gln Val Gly
          20           25           30
Val Leu Gly Pro Pro Gly Gln Gln Ala Pro Pro Pro Tyr Pro Gly Pro
          35           40           45
His Pro Ala Gly Pro Pro Val Ile Gln Gln Pro Thr Thr Pro Met Phe
          50           55           60
Val Ala Pro Pro Pro Lys Thr Gln Arg Leu Leu His Ser Glu Ala Tyr
65           70           75           80
Leu Lys Tyr Ile Glu Gly Leu Ser Ala Glu Ser Asn Ser Ile Ser Lys
          85           90           95
Trp Asp Gln Thr Leu Ala Ala Arg Arg Arg Asp Val His Leu Ser Lys
          100          105          110
Glu Gln Glu Ser Arg Leu Pro
          115

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<210> 415

<211> 332

<212> DNA

<213> Homo sapiens

<400> 415

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tctagagcca acttggttat cgtaatgaat agagagacta catctatatac aattattacg
60
ctctatagta atcatgaagc ttgggttata tgtatgacaa aaattgcaga aaaatcgaaa
120
caagaatatg gcgacttact aaaagaaaaa gaccatttac aagatatgga acagcttgag
180
atgactatcg tctcgatcca tacgccgtat ccgtccattg tcagaattca aggaaaaatc
240
aacacattac agccagagct ttggcaagct cccaatttag caattcggtt aattgtgagc
300
aatccgccag agggacaacc catctcacgc gt
332

```

<210> 416

<211> 102

<212> PRT

<213> Homo sapiens

<400> 416

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Met Asn Arg Glu Thr Thr Ser Ile Ser Ile Ile Thr Leu Tyr Ser Asn
 1           5           10           15
His Glu Ala Trp Val Ile Cys Met Thr Lys Ile Ala Glu Lys Ser Lys
          20           25           30
Gln Glu Tyr Gly Asp Leu Leu Lys Glu Lys Asp His Leu Gln Asp Met
          35           40           45
Glu Gln Leu Glu Met Thr Ile Val Ser Ile His Thr Pro Tyr Pro Ser
          50           55           60
Ile Val Arg Ile Gln Gly Lys Ile Asn Thr Leu Gln Pro Glu Leu Trp

```



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<210> 417
<211> 483
<212> DNA
<213> Homo sapiens
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<210> 418
<211> 161
<212> PRT
<213> Homo sapiens

639

130	135	140
Gly Pro Arg Ala Leu Asn Ala Asn Gly Ile Lys Val Leu Ala Asp Pro		
145	150	155
Arg		160

<210> 419
 <211> 797
 <212> DNA
 <213> Homo sapiens

<400> 419
 atttcacccc aggaaaacca gtaaggacca atgattaagc ccaagggttg gtaccgagtt
 60
 cggatccata agtaccggcc gccaggggtg ctggaatttg ggctcccccc ggtgaaaata
 120
 tccatgcagc cgcgttgtct taggtagaaa agggagactg ggggtggggtg ggctgagctc
 180
 aagcccctgc ctacatactt tagtagtaac gactcccgat ctgcatccaa cacatttacc
 240
 gaacttctag taagcgcccc ccgctgcaag cgaaagcact ccctgccaa gaaacagatc
 300
 ttttccactt aaaattccca aactcagacc ttccactttt tactgaacaa aaagcgtgta
 360
 catgatctga agggttgaca tgacattttc taaattgggc gaatcaggaa gaggttgatg
 420
 aaaatccttg acgttttctg gggataggac atttgtgtgt gataacgttc ttaagtcgaa
 480
 tttcagtgtg gcagtgcacg cagattcttc attgggtgta gtgtatttcc atacgggatg
 540
 tattagtaca agaaatagtg ttccctttga cactcgaacc caaggagtgg tccgaggctt
 600
 tttgaggcaa cgtaggatca atgtctctga agcagatttg gtgaaggatg caggtctcat
 660
 aatttacaga gcaatcacag ctttctttga aacggagaaa ttagattcta tgaaattttg
 720
 tcagtgcaga tagatatgat gtggagaaac ggggaaaatt gagtacaaaa agatgaggct
 780
 tgaatgatgg ctggcca
 797

<210> 420
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 420
 Met Arg Pro Ala Ser Phe Thr Lys Ser Ala Ser Glu Thr Leu Ile Leu
 1 5 10 15
 Arg Cys Leu Lys Lys Pro Arg Thr Thr Pro Trp Val Arg Val Ser Lys
 20 25 30
 Gly Thr Leu Phe Leu Val Leu Ile His Thr Val Trp Lys Tyr Thr Asn
 35 40 45
 Thr Asn Glu Glu Ser Ala Cys Thr Ala Thr Leu Lys Phe Asp Leu Arg

50		55		60											
Thr	Leu	Ser	His	Thr	Asn	Val	Leu	Ser	Pro	Glu	Asn	Val	Lys	Asp	Phe
65					70					75					80
His	Gln	Pro	Leu	Pro	Asp	Ser	Pro	Asn	Leu	Glu	Asn	Val	Met	Ser	Thr
			85						90					95	
Leu	Gln	Ile	Met	Tyr	Thr	Leu	Phe	Val	Gln						
			100					105							

<210> 421
 <211> 406
 <212> DNA
 <213> Homo sapiens

<400> 421
 ggatccacca tgatggagcc caccaccca tcctcagtc acctgctgca gcttctccat
 60
 aaccaaacac aggtcaatct tgtctcccta aacacaccat gtgctctcat gctgccatgg
 120
 ttgacctggg gccctctcta cctcctctgc tttctggaga acccttgac tcctcccaag
 180
 ccttcaagtt ggaaagtga cagtcagcat atgtctctag ctcagccctt actgcgtgga
 240
 ttcatagaaga ttggttcact gtcagcccct gaccagaacg tgtgttttag gaaagcagga
 300
 accaagtctt accaatgtct gtagtcccag cctccaccct ggcatacagt aggtgctcat
 360
 tgaatgtggg agggaaagag gagacacatg gaagggaatg tcattc
 406

<210> 422
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 422
Met Met Glu Pro Thr His Pro Ser Ser Val His Leu Leu Gln Leu Leu
1 5 10 15
His Asn Pro Thr Gln Val Asn Leu Val Ser Leu Asn Thr Pro Cys Ala
20 25 30
Leu Met Leu Pro Trp Phe Ala Trp Gly Pro Leu Tyr Leu Leu Cys Phe
35 40 45
Leu Glu Asn Pro Cys Thr Pro Pro Lys Pro Ser Ser Trp Lys Val Asn
50 55 60
Ser Gln His Met Ser Leu Ala Gln Pro Leu Leu Arg Gly Phe Met Lys
65 70 75 80
Ile Gly Ser Leu Ser Ala Pro Asp Gln Asn Val Cys Phe Arg Lys Ala
85 90 95
Gly Thr Lys Ser Tyr Gln Cys Leu
100

<210> 423
 <211> 628
 <212> DNA
 <213> Homo sapiens

<400> 423

ngccacccta cgcctcgcct gcaatggcaa cttcagatcc ccggtggcac cgtagtctta
 60
 gagccaccgg ttctgagcgg ggaggacgac ggggttgggg cgagggaagg agagggagaa
 120
 ggagatgggg atttgctgac gcagacccaa gcccaaacgc cgactccagc acccgcttgg
 180
 ccggcgcccc cagccacacc gcgcttcctg gccctcgcaa atggctccct gttggtgccc
 240
 ctctgagtg ccaaggaggc gggcgtctac acttgccgtg cacacaatga gctgggcgcc
 300
 aactctacgt caatacgcgt ggcggtggca gcaaccgggc ccccaaaaca cgcgcctggc
 360
 gccgggggag aacccgacgg acaggccccg acctctgagc gcaagtccac agccaagggc
 420
 cggggcaaca gcgtcctgcc ttccaaaccc gagggcaaaa tcaaaggcca aggcctggcc
 480
 aaggtcagca ttctcgggga gaccgagacg gagccggagg aggacacaag tgagggagag
 540
 gaggccgaag accagatcct cgcggacccg gcggaggagc agcgtgtgg caacggggac
 600
 ccctctcggc acgttttctaa ccacgcgt
 628

<210> 424

<211> 209

<212> PRT

<213> Homo sapiens

<400> 424

Xaa	His	Pro	Thr	Pro	Arg	Leu	Gln	Trp	Gln	Leu	Gln	Ile	Pro	Gly	Gly
1				5				10						15	
Thr	Val	Val	Leu	Glu	Pro	Pro	Val	Leu	Ser	Gly	Glu	Asp	Asp	Gly	Val
			20					25						30	
Gly	Ala	Glu	Glu	Gly	Glu	Gly	Glu	Gly	Asp	Gly	Asp	Leu	Leu	Thr	Gln
		35					40					45			
Thr	Gln	Ala	Gln	Thr	Pro	Thr	Pro	Ala	Pro	Ala	Trp	Pro	Ala	Pro	Pro
	50					55					60				
Ala	Thr	Pro	Arg	Phe	Leu	Ala	Leu	Ala	Asn	Gly	Ser	Leu	Leu	Val	Pro
65				70					75					80	
Leu	Leu	Ser	Ala	Lys	Glu	Ala	Gly	Val	Tyr	Thr	Cys	Arg	Ala	His	Asn
				85					90					95	
Glu	Leu	Gly	Ala	Asn	Ser	Thr	Ser	Ile	Arg	Val	Ala	Val	Ala	Ala	Thr
			100					105					110		
Gly	Pro	Pro	Lys	His	Ala	Pro	Gly	Ala	Gly	Gly	Glu	Pro	Asp	Gly	Gln
		115					120						125		
Ala	Pro	Thr	Ser	Glu	Arg	Lys	Ser	Thr	Ala	Lys	Gly	Arg	Gly	Asn	Ser
		130				135					140				
Val	Leu	Pro	Ser	Lys	Pro	Glu	Gly	Lys	Ile	Lys	Gly	Gln	Gly	Leu	Ala
145				150						155				160	
Lys	Val	Ser	Ile	Leu	Gly	Glu	Thr	Glu	Thr	Glu	Pro	Glu	Glu	Asp	Thr
			165					170						175	
Ser	Glu	Gly	Glu	Glu	Ala	Glu	Asp	Gln	Ile	Leu	Ala	Asp	Pro	Ala	Glu

			180						185					190	
Glu	Gln	Arg	Cys	Gly	Asn	Gly	Asp	Pro	Ser	Arg	Tyr	Val	Ser	Asn	His
			195				200					205			

Ala

<210> 425
 <211> 471
 <212> DNA
 <213> Homo sapiens

<400> 425
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 60
 tacgtggatt tgaccccagg cactnaagtg cgcgtcatcg ccattgacac cgtgttccta
 120
 ggatcgtgca cgaatggccg tgaggactta cggctggctg ctgaggttcc caaaggacga
 180
 catatcgcag cgggcacccg gatgctcgtc gcccctggat ctgctcgtgt ccgtctgcag
 240
 gctatggagg aaggcctcga cgagatcggg tcccggtttg ctgacatctt tcgcaataac
 300
 tctgcgaaca atggcttggt actggctcag gttgaccccg aggtcgtcga agagttgtgg
 360
 gactttgccg agcagcatcc tggtagagcag ctcaccgtct ccctcgagaa tcggacgatc
 420
 aaccttccgg gtcgcacgac ctaccggttc catattgatg acgtcacgcg t
 471

<210> 426
 <211> 157
 <212> PRT
 <213> Homo sapiens

<400> 426
 Pro Ala Val Glu Asp Phe Glu Asp Asp Val Ala Arg Ser Ala Ala Leu
 1 5 10 15
 Arg Ala Leu Glu Tyr Val Asp Leu Thr Pro Gly Thr Xaa Val Arg Val
 20 25 30
 Ile Ala Ile Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Gly Arg Glu
 35 40 45
 Asp Leu Arg Leu Ala Ala Glu Val Pro Lys Gly Arg His Ile Ala Ala
 50 55 60
 Gly Thr Arg Met Leu Val Ala Pro Gly Ser Ala Arg Val Arg Leu Gln
 65 70 75 80
 Ala Met Glu Glu Gly Leu Asp Glu Ile Gly Ser Arg Phe Ala Asp Ile
 85 90 95
 Phe Arg Asn Asn Ser Ala Asn Asn Gly Leu Leu Leu Ala Gln Val Asp
 100 105 110
 Pro Glu Val Val Glu Glu Leu Trp Asp Phe Ala Glu Gln His Pro Gly
 115 120 125
 Glu Gln Leu Thr Val Ser Leu Glu Asn Arg Thr Ile Asn Leu Pro Gly
 130 135 140
 Arg Thr Thr Tyr Pro Phe His Ile Asp Asp Val Thr Arg

145

150

155

<210> 427

<211> 546

<212> DNA

<213> Homo sapiens

<400> 427

ctagcggtag tagaaggtat gcagtttgat cgcggctact tgtctccgta tttcatcaac
60
aatcaagaaa caatgaatgc agagctagaa aaccatttta ttcttcttgt tgataagaaa
120
atttctaata tccgtgactt gctaccaatt ttggaagggtg ttgctaaagc atcgcgcccc
180
ttgttgatca ttgcggaaga cgttgaaggc gaagcgttgg caaccttggg ttgtaacact
240
atgcgcggca tcgtaaaagt agcggcagcg aaagcgccag gttttgggtga tcgccgtaaa
300
gcaatgcttc aagacattgc tgtgctaacg ggttcaactg ttatttcaga agaaattggc
360
attaagcttg aagaagcgac aattgaacag ttgggtacag cgaagcgcgt tacattgaca
420
aaagaaagta caacgattgt tgatgggtgcg ggtggtgcag ctaatattac tggtcgtggt
480
gagcaaattc gtgcagaaat tgctaactct tcttctggct acgataaaga gaaattgcaa
540
gaacgc
546

<210> 428

<211> 182

<212> PRT

<213> Homo sapiens

<400> 428

Leu	Ala	Val	Val	Glu	Gly	Met	Gln	Phe	Asp	Arg	Gly	Tyr	Leu	Ser	Pro
1				5					10					15	
Tyr	Phe	Ile	Asn	Asn	Gln	Glu	Thr	Met	Asn	Ala	Glu	Leu	Glu	Asn	Pro
			20					25					30		
Phe	Ile	Leu	Leu	Val	Asp	Lys	Lys	Ile	Ser	Asn	Ile	Arg	Asp	Leu	Leu
		35				40						45			
Pro	Ile	Leu	Glu	Gly	Val	Ala	Lys	Ala	Ser	Arg	Pro	Leu	Leu	Ile	Ile
	50					55					60				
Ala	Glu	Asp	Val	Glu	Gly	Glu	Ala	Leu	Ala	Thr	Leu	Val	Val	Asn	Thr
65				70					75					80	
Met	Arg	Gly	Ile	Val	Lys	Val	Ala	Ala	Ala	Lys	Ala	Pro	Gly	Phe	Gly
			85						90					95	
Asp	Arg	Arg	Lys	Ala	Met	Leu	Gln	Asp	Ile	Ala	Val	Leu	Thr	Gly	Ser
			100					105					110		
Thr	Val	Ile	Ser	Glu	Glu	Ile	Gly	Ile	Lys	Leu	Glu	Glu	Ala	Thr	Ile
		115					120						125		
Glu	Gln	Leu	Gly	Thr	Ala	Lys	Arg	Val	Thr	Leu	Thr	Lys	Glu	Ser	Thr
	130					135						140			
Thr	Ile	Val	Asp	Gly	Ala	Gly	Val	Ala	Ala	Asn	Ile	Thr	Gly	Arg	Val

145 150 155 160
 Glu Gln Ile Arg Ala Glu Ile Ala Asn Ser Ser Ser Gly Tyr Asp Lys
 165 170 175
 Glu Lys Leu Gln Glu Arg
 180

<210> 429
 <211> 425
 <212> DNA
 <213> Homo sapiens

<400> 429
 gctagcagcc cttacaggag acgggctaata aataatgcag cagtggctcc gacaacttgc
 60
 ccgttgcagc cggtcacgga tccatttgct tttagtagac aggcgctcca aagtacacca
 120
 ctgggcagtt cgtccaaaag cagtccacct gtcttgcaag gccagcccc cgcagggttt
 180
 tctcaacacc ccggtttgct tgtgccttac acacaatgca aaaaatagct ctcagggacc
 240
 ctgtgagccc ctgcctggac ctctgacaca gccagagca catgccagtc cgttttctgg
 300
 tgcattgaca ccttcagcac ctctggggcc tgagatgaac aggagtgcag aggtcgggtcc
 360
 cagttcagag cctgaagttc agactctgcc atatcttcct cactacattc caggagtgga
 420
 tcctg
 425

<210> 430
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 430
 Met Gln Gln Trp Leu Arg Gln Leu Ala Arg Cys Ser Arg Ser Arg Ile
 1 5 10 15
 His Leu Leu Leu Val Asp Arg Arg Ser Lys Val His His Trp Ala Val
 20 25 30
 Arg Pro Lys Ala Val His Leu Ser Cys Lys Ala Gln Pro Pro Gln Gly
 35 40 45
 Phe Leu Asn Thr Pro Val Cys Leu Cys Leu Thr His Asn Ala Lys Asn
 50 55 60
 Ser Ser Gln Gly Pro Cys Glu Pro Leu Pro Gly Pro Leu Thr Gln Pro
 65 70 75 80
 Arg Ala His Ala Ser Pro Phe Ser Gly Ala Leu Thr Pro Ser Ala Pro
 85 90 95
 Pro Gly Pro Glu Met Asn Arg Ser Ala Glu Val Gly Pro Ser Ser Glu
 100 105 110
 Pro Glu Val Gln Thr Leu Pro Tyr Leu Pro His Tyr Ile Pro Gly Val
 115 120 125
 Asp Pro
 130

<210> 431
 <211> 192
 <212> DNA
 <213> Homo sapiens

<400> 431
 ctagccatcc accagcgtac acacacggga gagaggccct acactggcct cgggtgcaac
 60
 cgccgcttcc gccagcgcac ggccctcgtc atccaccagc gcatccacac gggcgagaag
 120
 cctnaccgt gcccgactg cgagcggcgc ttctcctcct cctctcgctt ggtcagtcac
 180
 cggcgtgtgc ac
 192

<210> 432
 <211> 64
 <212> PRT
 <213> Homo sapiens

<400> 432
 Leu Ala Ile His Gln Arg Thr His Thr Gly Glu Arg Pro Tyr Thr Gly
 1 5 10 15
 Leu Gly Cys Asn Arg Arg Phe Arg Gln Arg Thr Ala Leu Val Ile His
 20 25 30
 Gln Arg Ile His Thr Gly Glu Lys Pro Xaa Pro Cys Pro Asp Cys Glu
 35 40 45
 Arg Arg Phe Ser Ser Ser Ser Arg Leu Val Ser His Arg Arg Val His
 50 55 60

<210> 433
 <211> 635
 <212> DNA
 <213> Homo sapiens

<400> 433
 nngccggcgg ctgcgttggg atacgacgtc gctgcgattg ggcgtgagta tctttggtac
 60
 ctcatggagg agcgtggcgc gtatgcggag gccgccgcgc tcatgccgct gctgctccgg
 120
 accgaccgag gcgcgtggga cacgtttgtg tgctgctacc tcgagcggca ccaaagggat
 180
 gcgatactcc cgcacattcc gacgcaggac cccagctga gtgagatggt gtacgatctc
 240
 gtgctggtgc atctgctgca gcacgatccc acgcagctgt tggcgacgct ccgcgcatgg
 300
 ccgagtcaca tctactcgaa gcaggcgggtg gctgcggcga tcggcgatca cgcacgaacc
 360
 agccgcacgc tgctcgagt cctcgcacag ctgtacatgg ccgcacatca gcccggaag
 420
 gctctgacat actacatgcy cctgcgtgat ccatgcgtgt ttgatctcat tcgcgagtac
 480
 gatctgctga tcgatgtgca gcaccacatc ggcacgctcg tcgagctcga tcaggaatgc
 540

gccggctcca ctgagccgcg ctccagcgcg cttatgccgc tgctcgtgcc atataccac
600

tcgattccca tccagcgcgc catggcgcag ctcga
635

<210> 434

<211> 211

<212> PRT

<213> Homo sapiens

<400> 434

Xaa	Pro	Ala	Ala	Ala	Leu	Gly	Tyr	Asp	Val	Ala	Ala	Ile	Gly	Arg	Glu
1				5					10					15	
Tyr	Leu	Trp	Tyr	Leu	Met	Glu	Glu	Arg	Gly	Ala	Tyr	Ala	Glu	Ala	Ala
			20					25					30		
Ala	Leu	Met	Pro	Leu	Leu	Leu	Arg	Thr	Asp	Arg	Gly	Ala	Trp	Asp	Thr
		35				40					45				
Phe	Val	Cys	Cys	Tyr	Leu	Glu	Arg	His	Gln	Arg	Asp	Ala	Ile	Leu	Pro
	50					55				60					
His	Ile	Pro	Thr	Gln	Asp	Pro	Gln	Leu	Ser	Glu	Met	Val	Tyr	Asp	Leu
65				70					75					80	
Val	Leu	Val	His	Leu	Leu	Gln	His	Asp	Pro	Thr	Gln	Leu	Leu	Ala	Thr
			85					90						95	
Leu	Arg	Ala	Trp	Pro	Ser	His	Ile	Tyr	Ser	Lys	Gln	Ala	Val	Ala	Ala
		100						105					110		
Ala	Ile	Gly	Asp	His	Ala	Arg	Thr	Ser	Arg	Thr	Leu	Leu	Glu	Cys	Leu
	115					120					125				
Ala	Gln	Leu	Tyr	Met	Ala	Ala	His	Gln	Pro	Gly	Lys	Ala	Leu	Thr	Tyr
	130					135				140					
Tyr	Met	Arg	Leu	Arg	Asp	Pro	Cys	Val	Phe	Asp	Leu	Ile	Arg	Glu	Tyr
145				150				155					160		
Asp	Leu	Leu	Ile	Asp	Val	Gln	His	His	Ile	Gly	Thr	Leu	Val	Glu	Leu
			165					170					175		
Asp	Gln	Glu	Cys	Ala	Gly	Ser	Thr	Glu	Pro	Arg	Ser	Ser	Ala	Leu	Met
		180						185					190		
Pro	Leu	Leu	Val	Pro	Tyr	Thr	His	Ser	Ile	Pro	Ile	Gln	Arg	Ala	Met
	195					200						205			
Ala	Gln	Leu													
	210														

<210> 435

<211> 493

<212> DNA

<213> Homo sapiens

<400> 435

nncgtacgtt cgcgtatattt ccgcgcccgg gaagctatcg ataataaagt tcaaccgctg
60
atccagcgtt agcaatggcg ggcacaggaa gggtagcttag gcatgcagaa agaaaagctt
120
tccgctctga tggatgggtga atcggttcgac agcgagctgt tgagttctct gtcgcaagat
180
cgaacgcttc aacaaagctg gcagggttat cacctgatac gtgacacact gcgaggtgat
240

gtcgggcaag tgatgcatct cgacatcgcc gatcgcgtag ccgctgcact tgagaaagaa
 300
 cccgcccggc tgggtgccttc cgccgttcag gaatctcagc cgcagcctca cacctggcag
 360
 aaaatgccgt tctgggacaa agtgcgtccc tgggcgagcc agattacgca aatcggtatg
 420
 gcggcctgcy tgtcgctggc ggtgatcgtc ggcgtgcagc agtacaacca gccttctgcy
 480
 ccatcgaacg cgt
 493

<210> 436
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 436
 Met Gln Lys Glu Lys Leu Ser Ala Leu Met Asp Gly Glu Ser Phe Asp
 1 5 10 15
 Ser Glu Leu Leu Ser Ser Leu Ser Gln Asp Arg Thr Leu Gln Gln Ser
 20 25 30
 Trp Gln Gly Tyr His Leu Ile Arg Asp Thr Leu Arg Gly Asp Val Gly
 35 40 45
 Gln Val Met His Leu Asp Ile Ala Asp Arg Val Ala Ala Ala Leu Glu
 50 55 60
 Lys Glu Pro Ala Arg Leu Val Pro Ser Ala Val Gln Glu Ser Gln Pro
 65 70 75 80
 Gln Pro His Thr Trp Gln Lys Met Pro Phe Trp Asp Lys Val Arg Pro
 85 90 95
 Trp Ala Ser Gln Ile Thr Gln Ile Gly Met Ala Ala Cys Val Ser Leu
 100 105 110
 Ala Val Ile Val Gly Val Gln Gln Tyr Asn Gln Pro Ser Ala Pro Ser
 115 120 125
 Asn Ala
 130

<210> 437
 <211> 447
 <212> DNA
 <213> Homo sapiens

<400> 437
 ntggtaaccg gtgtccctga tatggaccct gctgtggttag agcgtaaatt atttatttta
 60
 cgtaattatg taacacgcat ctgtttggag tctgttaatg gaattaagga caacttttac
 120
 attaatacat tctcatacaa aacaatcggt tataaagggtc agttaaccac tgaacaagtg
 180
 ccacaatatt tcttagattt acaaaatcca agtatggtaa cggcattagc gcttggttcat
 240
 tcacgtttct caacaaatac atttctcgt tggcgtttag cacaaccatt ccgttacatc
 300
 gtcataatg gcgaaatcaa tacggttcgc ggtaatatca attggatgaa agcacgtgaa
 360

gcgttacttg aagctgaatt tttcactcgc tcagaattag atatgttaat gccaatctgt
 420
 acggatggta tgtctgactc ggcaagg
 447

<210> 438
 <211> 149
 <212> PRT
 <213> Homo sapiens

<400> 438
 Xaa Val Thr Gly Val Pro Asp Met Asp Pro Ala Val Leu Glu Arg Lys
 1 5 10 15
 Leu Phe Ile Leu Arg Asn Tyr Val Thr Arg Ile Cys Leu Glu Ser Val
 20 25 30
 Asn Gly Ile Lys Asp Asn Phe Tyr Ile Asn Thr Phe Ser Tyr Lys Thr
 35 40 45
 Ile Val Tyr Lys Gly Gln Leu Thr Thr Glu Gln Val Pro Gln Tyr Phe
 50 55 60
 Leu Asp Leu Gln Asn Pro Ser Met Val Thr Ala Leu Ala Leu Val His
 65 70 75 80
 Ser Arg Phe Ser Thr Asn Thr Phe Pro Arg Trp Arg Leu Ala Gln Pro
 85 90 95
 Phe Arg Tyr Ile Ala His Asn Gly Glu Ile Asn Thr Val Arg Gly Asn
 100 105 110
 Ile Asn Trp Met Lys Ala Arg Glu Ala Leu Leu Glu Ala Glu Phe Phe
 115 120 125
 Thr Arg Ser Glu Leu Asp Met Leu Met Pro Ile Cys Thr Asp Gly Met
 130 135 140
 Ser Asp Ser Ala Arg
 145

<210> 439
 <211> 395
 <212> DNA
 <213> Homo sapiens

<400> 439
 nacgcgtgaa gggagagtgg ggccgagccc caggaggctg tectgcagca gctgcaccag
 60
 cttcccaggg gccggctgga cctggccacg caaagcctga cggtggagac ctgcagggcc
 120
 ctgggcaagc tgctgccgag ggagacgctg tgcacggagc tggtcctgag tgactgcatg
 180
 ctcagcgagg aagggggccac actgctgctc cgaggcctgt gtgccaacac cgtgctgcgc
 240
 tttctggact taaagggcaa caaccttcgg gctgcagggg ccgaggctct gggaaaactc
 300
 ctccaacaga acaagtccat tcagagcctc acgctggagt ggaacagcct gggcacgtgg
 360
 gacgatgcct tcgccacctt ctgcggggggc ctggc
 395

<210> 440

<211> 128
 <212> PRT
 <213> Homo sapiens

<400> 440
 Arg Glu Ser Gly Ala Glu Pro Gln Glu Ala Val Leu Gln Gln Leu His
 1 5 10 15
 Gln Leu Pro Arg Gly Arg Leu Asp Leu Ala Thr Gln Ser Leu Thr Val
 20 25 30
 Glu Thr Cys Arg Ala Leu Gly Lys Leu Leu Pro Arg Glu Thr Leu Cys
 35 40 45
 Thr Glu Leu Val Leu Ser Asp Cys Met Leu Ser Glu Glu Gly Ala Thr
 50 55 60
 Leu Leu Leu Arg Gly Leu Cys Ala Asn Thr Val Leu Arg Phe Leu Asp
 65 70 75 80
 Leu Lys Gly Asn Asn Leu Arg Ala Ala Gly Ala Glu Ala Leu Gly Lys
 85 90 95
 Leu Leu Gln Gln Asn Lys Ser Ile Gln Ser Leu Thr Leu Glu Trp Asn
 100 105 110
 Ser Leu Gly Thr Trp Asp Asp Ala Phe Ala Thr Phe Cys Gly Gly Leu
 115 120 125

<210> 441
 <211> 364
 <212> DNA
 <213> Homo sapiens

<400> 441
 gccagtgact acgtgaacat gttcgatgcc gagcagggt tcttcgacag gcgcagccc
 60
 ggcgggcaggt tccaagccgg cttggatccg gaatcctggg gcggtctgtt cactgagacc
 120
 gacggttgga acttcgcctt ccacgctcca caggacggcc gggggctggc cgcgctctac
 180
 ggcggtccga aaggcttgga gaacaagctc gatgcctttt tcgcgacgcc ggaaaacgcg
 240
 gacaagccgg cgtacggcgg aatccacgaa atgggtcgagg ccagagcggg ccggatgggc
 300
 caattgggca tgtccaacga gccctcgac catattcct acatctacaa ctatgccggc
 360
 gcgc
 364

<210> 442
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 442
 Ala Gln Tyr Tyr Val Asn Met Phe Asp Ala Glu Gln Gly Phe Phe Asp
 1 5 10 15
 Arg Arg Ser Pro Gly Gly Glu Phe Gln Ala Gly Leu Asp Pro Glu Ser
 20 25 30
 Trp Gly Gly Leu Phe Thr Glu Thr Asp Gly Trp Asn Phe Ala Phe His

35	40	45
Ala Pro Gln Asp Gly Arg Gly Leu Ala Ala Leu Tyr Gly Gly Pro Lys		
50	55	60
Gly Leu Glu Asn Lys Leu Asp Ala Phe Phe Ala Thr Pro Glu Asn Ala		
65	70	75
Asp Lys Pro Ala Tyr Gly Gly Ile His Glu Met Val Glu Ala Arg Ala		80
85	90	95
Val Arg Met Gly Gln Leu Gly Met Ser Asn Glu Pro Ser His His Ile		
100	105	110
Pro Tyr Ile Tyr Asn Tyr Ala Gly Ala		
115	120	

<210> 443
 <211> 430
 <212> DNA
 <213> Homo sapiens

<400> 443
 accggttacg gctcagtgc acaagagatg ttcgccaaca acctcgtgcg gatgccgctg
 60
 ctcattggtgc tggcaatccc cttcgccaag atcctctcga cgacctgtc catcggatcg
 120
 ggcgggtccgg cggcgtcttc cggccctggc atgggtcatcg gcggagccac tggcgcgga
 180
 ctgtggcgcc tcctcgaggg gctgccaggt atcccatcct caccgatgag tttcgtcatt
 240
 gtcggcatga tcgcctgctt cgggtgcggtt gcccatgccc cactcggcgt gctgctcatg
 300
 gttggcgaga tgaccggaaa cctgtcgctg ctcgctcctg gcatgatcgc cgtcgccgtc
 360
 gctggccgag ttgtcgggga cacttcgata tacacctctc agctcaagga tcgcctggag
 420
 ggcgacgcgt
 430

<210> 444
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 444
Thr Gly Tyr Gly Ser Val Gln Gln Glu Met Phe Ala Asn Asn Leu Val
1 5 10 15
Arg Met Pro Leu Leu Met Val Leu Ala Ile Pro Phe Ala Lys Ile Leu
20 25 30
Ser Thr Thr Leu Ser Ile Gly Ser Gly Gly Pro Ala Ala Ser Ser Gly
35 40 45
Pro Gly Met Val Ile Gly Gly Ala Thr Gly Ala Ala Leu Trp Arg Leu
50 55 60
Leu Glu Gly Leu Pro Gly Ile Pro Ser Ser Pro Met Ser Phe Val Ile
65 70 75 80
Val Gly Met Ile Ala Cys Phe Gly Ala Val Ala His Ala Pro Leu Gly
85 90 95
Val Leu Leu Met Val Gly Glu Met Thr Gly Asn Leu Ser Leu Leu Ala

	100		105		110
Pro Gly Met Ile Ala Val Ala Val Ala Gly Arg Val Val Gly Asp Thr					
	115		120		125
Ser Ile Tyr Thr Ser Gln Leu Lys Asp Arg Leu Glu Gly Asp Ala					
	130		135		140

<210> 445
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 445
 ccattggggct gcctagcctc tggggaggcc cctcagctgg tgacaccagc agggcagatt
 60
 tcttgcttta ttgctcacc tgtccagggt tccctctggt tgtgaggag ctgctgccac
 120
 cttgggtcca ggaagcatga agctccgcag gtcagcctcc tgggtgggagg acttttcctt
 180
 agttttcttt gctcttctgc tctgagtcca gccctggctg gacctttgat cccttctctc
 240
 tttatcagga aattttctga ctttcttctt ttgccttttc aagatctgtg atgccatctc
 300
 caagtgggaa caagccatga aggagctgca ccccggaag tctgagggtg ggacacgcgt
 360

<210> 446
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 446
 Met Ala Cys Ser His Leu Glu Met Ala Ser Gln Ile Leu Lys Arg Gln
 1 5 10 15
 Lys Lys Lys Val Arg Lys Phe Pro Asp Lys Glu Arg Arg Asp Gln Arg
 20 25 30
 Ser Ser Gln Gly Trp Thr Gln Ser Arg Arg Ala Lys Lys Thr Lys Glu
 35 40 45
 Lys Ser Ser His Gln Glu Ala Asp Leu Arg Ser Phe Met Leu Pro Gly
 50 55 60
 Pro Lys Val Ala Ala Ala Pro Ser Gln Thr Glu Gly Thr Leu Asp Arg
 65 70 75 80
 Val Ser Asn Lys Ala Arg Asn Leu Pro Cys Trp Cys His Gln Leu Arg
 85 90 95
 Gly Leu Pro Arg Gly
 100

<210> 447
 <211> 487
 <212> DNA
 <213> Homo sapiens

<400> 447
 acgcgtgaag ggggaaattg ctcgtgccac ctgaggatta atcattaccc tggaaccctt
 60

cccaaggcca tcaaggaaca cgcacccctt accagacctt ccagctgctg ggggctctcc
 120
 gagtgaggct gaggtcatgg agaaggggaat ggggggcccc catggccagc tggacctgat
 180
 cactgcctcc ccactcagcc acagccctca gggccctgtg ccagtccaga agcccattca
 240
 gggacacctt tggccaatgt tctgtttcat ctgcgaggca accttcccca gtgccccaac
 300
 catagcgttt tccccaaac accctcagga aggagggacc actacctgtg cagggggggc
 360
 caggagcctc ctgagagcct catatgggga ggaagtggta ccatctcacc cccattgcct
 420
 ttctctccta ctccacctg gccagcttcc ctcaagtccc ctctgcctc agtgccctt
 480
 cacgcgt
 487

<210> 448
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 448
 Met Glu Lys Gly Met Gly Gly Pro His Gly Gln Leu Asp Leu Ile Thr
 1 5 10 15
 Ala Ser Pro Leu Ser His Ser Pro Gln Gly Pro Val Pro Val Gln Lys
 20 25 30
 Pro Ile Gln Gly His Leu Trp Pro Met Phe Cys Phe Ile Cys Glu Ala
 35 40 45
 Thr Phe Pro Ser Ala Pro Thr Ile Ala Phe Ser Pro Lys His Pro Gln
 50 55 60
 Glu Gly Gly Thr Thr Thr Cys Ala Gly Gly Ala Arg Ser Leu Leu Arg
 65 70 75 80
 Ala Ser Tyr Gly Glu Glu Val Val Pro Ser His Pro His Cys Leu Ser
 85 90 95
 Leu Leu Leu Pro Pro Gly Gln Leu Pro Ser Val Pro Leu Leu Pro Gln
 100 105 110
 Cys Pro Phe Thr Arg
 115

<210> 449
 <211> 353
 <212> DNA
 <213> Homo sapiens

<400> 449
 gagctcagcc agttggagtt tgagaagcgg cagctgcaca gggacttgga gcaggccaag
 60
 gagaaggggg agcgggcaga gaagctggag agggagctac agcgactcca ggaggagaac
 120
 gggaggctgg ccaggaaggt gacctccctg gagacagcca ccgagaaagt cgaggccctg
 180
 gagcatgaga gccagggcct gcagctggag aaccggactc tgaggaagtc tctggacacc
 240

ttgcagaacg tgtccctgca gcttgagggc ctggagcgtg acaacaagca gctggacgca
 300
 gagaacctgg agctgcgcag gctggtggag accatgcgga gacgacaacg cgt
 353

<210> 450
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 450
 Glu Leu Ser Gln Leu Glu Phe Glu Lys Arg Gln Leu His Arg Asp Leu
 1 5 10 15
 Glu Gln Ala Lys Glu Lys Gly Glu Arg Ala Glu Lys Leu Glu Arg Glu
 20 25 30
 Leu Gln Arg Leu Gln Glu Glu Asn Gly Arg Leu Ala Arg Lys Val Thr
 35 40 45
 Ser Leu Glu Thr Ala Thr Glu Lys Val Glu Ala Leu Glu His Glu Ser
 50 55 60
 Gln Gly Leu Gln Leu Glu Asn Arg Thr Leu Arg Lys Ser Leu Asp Thr
 65 70 75 80
 Leu Gln Asn Val Ser Leu Gln Leu Glu Gly Leu Glu Arg Asp Asn Lys
 85 90 95
 Gln Leu Asp Ala Glu Asn Leu Glu Leu Arg Arg Leu Val Glu Thr Met
 100 105 110
 Arg Arg Arg Gln Arg
 115

<210> 451
 <211> 444
 <212> DNA
 <213> Homo sapiens

<400> 451
 gtgatgcggc tgactaagcc tactttattc accaatatcc cagtaacatg tgaagagaaa
 60
 gacttacctg gagatctctt taaccagctg atgagagatg atccttcaac cgttaatggt
 120
 gcagaagttt taatggtggg agaaatgctg actttaccac agaattttgg gaatatattt
 180
 ttgggagaga ccttttccag ttatatcagc gttcataatg atagcaatca agttgtaaaa
 240
 gacatattag taaaagctga tcttcagaca agttctcagc gtttaaactt ttcagcctcc
 300
 aatgctgcag tggctgaact taaaccggat tgttggtattg atgatgtcat acatcatgaa
 360
 gtcaaagaaa ttggaacaca catcttggtg tgtgctgtga gttatacaac tcaggctgga
 420
 gaaaaaatgt atttcagaaa attt
 444

<210> 452
 <211> 148
 <212> PRT

<213> Homo sapiens

<400> 452

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Val Met Arg Leu Thr Lys Pro Thr Leu Phe Thr Asn Ile Pro Val Thr
 1           5           10           15
Cys Glu Glu Lys Asp Leu Pro Gly Asp Leu Phe Asn Gln Leu Met Arg
           20           25           30
Asp Asp Pro Ser Thr Val Asn Gly Ala Glu Val Leu Met Leu Gly Glu
           35           40           45
Met Leu Thr Leu Pro Gln Asn Phe Gly Asn Ile Phe Leu Gly Glu Thr
           50           55           60
Phe Ser Ser Tyr Ile Ser Val His Asn Asp Ser Asn Gln Val Val Lys
65           70           75           80
Asp Ile Leu Val Lys Ala Asp Leu Gln Thr Ser Ser Gln Arg Leu Asn
           85           90           95
Leu Ser Ala Ser Asn Ala Ala Val Ala Glu Leu Lys Pro Asp Cys Cys
           100          105          110
Ile Asp Asp Val Ile His His Glu Val Lys Glu Ile Gly Thr His Ile
           115          120          125
Leu Val Cys Ala Val Ser Tyr Thr Thr Gln Ala Gly Glu Lys Met Tyr
           130          135          140
Phe Arg Lys Phe
145

```

<210> 453

<211> 373

<212> DNA

<213> Homo sapiens

<400> 453

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gctagctctg accccacctt tgccaagtgg cactaggggtg gccaatgggg actaggggtg
60
tataattgga aaatacagtc tcccctgttg tccaagaaag gccccagatg acctggggct
120
tgaaaggcac tcccgctggg tgcttctctg gagcaggtgg ggggcagcgg ggcggcgggg
180
cctgtctgtg ctgagcatcc ccagctccag ggcaggtgct gggctctgag cccactggt
240
gcgttttggg atgggctggc ctgcgcggct gtcgtttcag agcacacaga agagaccctg
300
ccacaggagg agtgggagga gaagctgttg atgttctctg gagacaccct ggccatcatt
360
tctgacaacg cgt
373

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<210> 454

<211> 108

<212> PRT

<213> Homo sapiens

<400> 454

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Met Met Ala Arg Val Ser Arg Arg Asn Ile Asn Ser Phe Ser Ser His
 1           5           10           15
Ser Ser Cys Gly Arg Val Ser Ser Val Cys Ser Glu Thr Thr Ala Ala

```

	20		25		30										
Gln	Ala	Ser	Pro	Ser	Gln	Asn	Ala	Pro	Val	Gly	Leu	Arg	Ala	Gln	His
	35		40		45										
Leu	Pro	Trp	Ser	Trp	Gly	Cys	Ser	Ala	Gln	Thr	Gly	Pro	Ala	Ala	Pro
	50		55		60										
Leu	Pro	Pro	Thr	Cys	Ser	Gln	Glu	Ala	Pro	Ser	Gly	Ser	Ala	Phe	Gln
65			70		75									80	
Ala	Pro	Gly	His	Leu	Gly	Pro	Phe	Leu	Asp	Asn	Arg	Gly	Asp	Cys	Ile
		85			90									95	
Phe	Gln	Leu	Tyr	Asn	Pro	Ser	Pro	His	Trp	Pro	Pro				
	100				105										

<210> 455

<211> 602

<212> DNA

<213> Homo sapiens

<400> 455

cctaggcaaa gcatgcccac cctacctccc cttaccctta cccttcattt tcccctaage
60
accatcacc accgatgtta ctgtatgtgt ttgcttacgc tgacagccca ccaccacac
120
tggaatgtcc gcacgacaaa ggcaggactc ttggctgcct tagccacagc tggatcccca
180
gagctttgta ggggtgttggg cacagagtgg agtgggtact taataagtat ctgtggaatg
240
aacatgtaca gagtgaagcc ctgtgcccag aacaggctca aaataagctc aattcctttc
300
cttgccactt actaagtcct ttttctctcg cccctctca ctgacctggt tttgatgcca
360
gacagcacag atgggctagg gaggcaggtg gggaagcaga gatctgcgtc tcttggagct
420
ggagctggtg ggtggggctc cttcctggtg ctgcggaggc tcattgggga ggtggcagcg
480
acccctcag gaggctctgt cgcctgcact cagatctgtg cttttccaca gcgcccggag
540
gaagacttgc tcaggagata aattcaaaga caacaggaag ctggacgtgg tggctcacgc
600
gt
602

<210> 456

<211> 100

<212> PRT

<213> Homo sapiens

<400> 456

Met	Pro	Thr	Leu	Pro	Pro	Leu	Thr	Leu	Thr	Leu	His	Phe	Pro	Leu	Ser
1			5				10							15	
Thr	His	His	His	Arg	Cys	Tyr	Cys	Met	Cys	Leu	Leu	Thr	Leu	Thr	Ala
		20					25					30			
His	His	Pro	His	Trp	Asn	Val	Arg	Thr	Thr	Lys	Ala	Gly	Leu	Leu	Ala
	35				40						45				
Ala	Leu	Ala	Thr	Ala	Gly	Ser	Pro	Glu	Leu	Cys	Arg	Val	Leu	Gly	Thr

50 55 60
 Glu Trp Ser Gly Tyr Leu Ile Ser Ile Cys Gly Met Asn Met Tyr Arg
 65 70 75 80
 Val Lys Pro Cys Ala Gln Asn Arg Leu Lys Ile Ser Ser Ile Pro Phe
 85 90 95
 Leu Ala Thr Tyr
 100

<210> 457
 <211> 324
 <212> DNA
 <213> Homo sapiens

<400> 457
 acgcgtcatg tggatattcc tgggaggttc ccaggaacgt ttctggacgg gccccgacc
 60
 agaggtcagg gaacttttct tattattctg cacgtgcccc gggatagtca aaccaggtct
 120
 tccccttctg ctggccgcaa cacgccagcc gccgccacga ccgcacgctg aattcatgac
 180
 ccgacacgcg acgtggcagc gagcacaccc accgctagga gaaagagcgc tcatcgaaga
 240
 tcgttttctg tccactggcc agcgccacta tgatcaggtg gggatatccgc ccggcgggcg
 300
 gagcaccggg acgccggggc gccg
 324

<210> 458
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 458
 Met Trp Ile Phe Leu Gly Gly Ser Gln Glu Arg Phe Trp Thr Gly Pro
 1 5 10 15
 Arg Pro Glu Val Arg Glu Leu Phe Leu Leu Phe Cys Thr Cys Pro Gly
 20 25 30
 Ile Val Lys Pro Gly Leu Pro Leu Leu Leu Ala Ala Thr Arg Gln Pro
 35 40 45
 Pro Pro Arg Pro His Ala Glu Phe Met Thr Arg His Ala Thr Trp Gln
 50 55 60
 Arg Ala His Pro Pro Leu Gly Glu Arg Ala Leu Ile Glu Asp Arg Phe
 65 70 75 80
 Leu Ser Thr Gly Gln Arg His Tyr Asp Gln Val Gly Tyr Pro Pro Gly
 85 90 95
 Gly Gly Ser Thr Gly Thr Pro Gly Arg
 100 105

<210> 459
 <211> 415
 <212> DNA
 <213> Homo sapiens

<400> 459

acgcgttcat tcggcatctg cttccatgga tttcctgcgg ggaggcgcgg ccgagagtgc
60
gggtgtcgaa cacgacactt cagtgategt ttcaaccacc ggccgagatg ggtcctgacg
120
ctgggcttca agccgcttgc gctcgcgctc ctgatctcgg gcagcgcgat tccgggtggtt
180
tatgctgccg gcagacgact gcgcacgccc ctcacgaggt atctgcacat gcttaaaggg
240
agaggcctca cccgacagct gggcatcgga tttacgaagc ccacgacgaa ttttcctcgc
300
ctcctcaaag ccgatcatcg gcatgccagg tttgtggttg aatgcttcga tcaacacact
360
aggatcggtg gggtcacca catacaccga gcggcaatcg agcggatagc acctc
415

<210> 460
<211> 105
<212> PRT
<213> Homo sapiens

<400> 460
Met Pro Met Ile Gly Phe Glu Glu Ala Arg Lys Ile Arg Arg Gly Leu
1 5 10 15
Arg Lys Ser Asp Ala Gln Leu Ser Gly Glu Ala Ser Pro Phe Lys His
20 25 30
Val Gln Ile Pro Arg Glu Gly Arg Ala Gln Ser Ser Ala Gly Ser Ile
35 40 45
Asn His Arg Asn Arg Ala Ala Arg Asp Gln Glu Arg Glu Arg Lys Arg
50 55 60
Leu Glu Ala Gln Arg Gln Asp Pro Ser Arg Pro Val Val Glu Thr Ile
65 70 75 80
Thr Glu Val Ser Cys Ser Thr Pro Ala Leu Ser Ala Ala Pro Pro Arg
85 90 95
Arg Lys Ser Met Glu Ala Asp Ala Glu
100 105

<210> 461
<211> 357
<212> DNA
<213> Homo sapiens

<400> 461
acgcgttcga ggtcggctaa atttatcatg cgcacgacaa agagagtagt ggctcacaac
60
cgggtcacat gcatgatgac aaaaactggc agaataagagt tgatgtcatc ccgtctacca
120
gtccttagaa ccagctcaga gagtcccggg gtcgggtaccg tcgagactca gtacacaact
180
gtcgcgatac cggacgaccc tcttcatctg gttgcagatg ggcgtctcaa tcacgtcact
240
gtcgcttacg aaacctacgg gaagctcaat acgtccagcg acaatgcggg ctatacctgt
300
catgcgctta ctggtgatgc ccatgcagcc ggatttcacc ccggtgtagt ccgtccg
357

<210> 462
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 462
 Thr Arg Ser Arg Ser Ala Lys Phe Ile Met Arg Thr Thr Lys Arg Val
 1 5 10 15
 Val Ala His Asn Arg Val Thr Cys Met Met Thr Lys Thr Gly Arg Ile
 20 25 30
 Glu Leu Met Ser Ser Arg Leu Pro Ala Pro Arg Thr Ser Ser Glu Ser
 35 40 45
 Pro Gly Val Gly Thr Val Glu Thr Gln Tyr Thr Thr Val Ala Ile Pro
 50 55 60
 Asp Asp Pro Leu His Leu Val Ala Asp Gly Arg Leu Asn His Val Thr
 65 70 75 80
 Val Ala Tyr Glu Thr Tyr Gly Lys Leu Asn Thr Ser Ser Asp Asn Ala
 85 90 95
 Val Tyr Thr Cys His Ala Leu Thr Gly Asp Ala His Ala Ala Gly Phe
 100 105 110
 His Pro Gly Val Val Arg Pro
 115

<210> 463
 <211> 434
 <212> DNA
 <213> Homo sapiens

<400> 463
 gtgcacgggg tatgcgaggg atgcggcatt gccaccaatg ccgctgacct gcgcagatac
 60
 gaggcagctg gtgacgatga agtgggtgcga tgcgaggaat gcgatcgtat cctgggtgcgt
 120
 accggagagt ccatctgagc ccttcttggtg gcgggtgatgc cgggatatcc gtagaattag
 180
 cggtcggacg agccatccgg gtgatcgcgg cagcgggtgag ttgtcgagga aagtcggggc
 240
 tccatagagc aggggtggtgg gtaacgcca cccgggggtga cccgcgggaa agtgccacag
 300
 agaacagact gccggtttcg agccgggtgag ggtgaaacgg tggagtaagt gcccaccgcg
 360
 tcatcggtga cggtgacggc atggcaaacc ccacctggag caaggccaag aagaccgtga
 420
 ggtcgcggac gcgt
 434

<210> 464
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 464
 Met Pro Ser Pro Ser Pro Met Thr Arg Trp Ala Leu Thr Pro Pro Phe

```

      1           5           10           15
His Pro His Arg Leu Glu Thr Gly Ser Leu Phe Ser Val Ala Leu Ser
      20           25           30
Arg Gly Ser Pro Arg Val Gly Val Thr His His Pro Ala Leu Trp Ser
      35           40           45
Pro Asp Phe Pro Arg Gln Leu Thr Ala Ala Ala Ile Thr Arg Met Ala
      50           55           60
Arg Pro Thr Ala Asn Ser Thr Asp Ile Pro Ala Ser Pro Pro Gln Glu
      65           70           75           80
Gly Leu Arg Trp Thr Leu Arg Tyr Ala Pro Gly Tyr Asp Arg Ile Pro
      85           90           95
Arg Ile Ala Pro Leu His Arg His Gln Leu Pro Arg Ile Cys Ala Gly
      100          105          110
Gln Arg His Trp Trp Gln Cys Arg Ile Pro Arg Ile Pro Arg Ala
      115          120          125

```

<210> 465
 <211> 438
 <212> DNA
 <213> Homo sapiens

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<400> 465
gatcatttag aatttatgga agaagctgat gtgaaagcta tgggtcaaatac tggcactgtg
60
gctgtattgc taccaggagc attttacacc ttgaaagaaa ctcaacttcc accgatgaat
120
ttgttacgtc agtacggagt agacattgct atttcgacgg atgctaatacc agggacgtcg
180
ccagcggtat cattacgggt aatgatgaat atggcatgta ccttgtttgg tatgacacct
240
gaaaccgccc ttgcaggggt aacaattcat gcggcaaaaag cgttggggat tagcgattct
300
catggcactt tagaagttgg caaggtagct gattttgtct gctgggatgt ggaaagcccc
360
ggtgaacttt gttattgggt aggagagcag ttagtaaagc aacgtattca gcacggagta
420
tcccatgaat aatctaga
438

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<210> 466
 <211> 143
 <212> PRT
 <213> Homo sapiens

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<400> 466
Asp His Leu Glu Phe Met Glu Glu Ala Asp Val Lys Ala Met Val Lys
      1           5           10           15
Ser Gly Thr Val Ala Val Leu Leu Pro Gly Ala Phe Tyr Thr Leu Lys
      20           25           30
Glu Thr Gln Leu Pro Pro Met Asn Leu Leu Arg Gln Tyr Gly Val Asp
      35           40           45
Ile Ala Ile Ser Thr Asp Ala Asn Pro Gly Thr Ser Pro Ala Leu Ser
      50           55           60
Leu Arg Leu Met Met Asn Met Ala Cys Thr Leu Phe Gly Met Thr Pro

```

```

65          70          75          80
Glu Thr Ala Leu Ala Gly Val Thr Ile His Ala Ala Lys Ala Leu Gly
          85          90          95
Ile Ser Asp Ser His Gly Thr Leu Glu Val Gly Lys Val Ala Asp Phe
          100          105          110
Val Cys Trp Asp Val Glu Ser Pro Gly Glu Leu Cys Tyr Trp Leu Gly
          115          120          125
Glu Gln Leu Val Lys Gln Arg Ile Gln His Gly Val Ser His Glu
          130          135          140

```

<210> 467
 <211> 460
 <212> DNA
 <213> Homo sapiens

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<400> 467
ntttccctgg ctattggcca tgtgggacac aacgttccgc ctaccccaga gcggttaagc
60
tgcattccctg caccttcttc tcccaccgct tcaaagccac agtgaggaac ttcggagctt
120
ctcgcagtga agatggcggt ggaggaatgg atgccctggc tagaagaggc ggaatatctg
180
ttgatttgtt ggaccgacca caaaaacctg gagtatctcc acacaaccaa gtgcctcaac
240
tccaggcaag caagaagggc ccagctgttt acctggttcc acttttccct ctctaccgg
300
ccgggggtcca agaaccatcag gctggatgcc ctttcttgcc actttatggg catgggcca
360
ttcctccagg cttgcctgtc acccgggctc ccgtcaaacc ctggccttcg tgcgacaaca
420
ctcttggtgc cttctatggt tctgtatggt gccgcaattg
460

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<210> 468
 <211> 118
 <212> PRT
 <213> Homo sapiens

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<400> 468
Gly Thr Ser Glu Leu Leu Ala Val Lys Met Ala Leu Glu Glu Trp Met
1          5          10          15
Pro Trp Leu Glu Glu Ala Glu Tyr Leu Leu Ile Val Trp Thr Asp His
          20          25          30
Lys Asn Leu Glu Tyr Leu His Thr Thr Lys Cys Leu Asn Ser Arg Gln
          35          40          45
Ala Arg Arg Ala Gln Leu Phe Thr Trp Phe His Phe Ser Leu Ser Tyr
          50          55          60
Arg Pro Gly Ser Lys Asn Ile Arg Leu Asp Ala Leu Ser Cys His Phe
65          70          75          80
Met Gly Met Gly Pro Phe Leu Gln Ala Cys Leu Ser Pro Gly Leu Pro
          85          90          95
Ser Asn Pro Gly Leu Arg Ala Thr Thr Leu Leu Val Pro Ser Met Val
          100          105          110
Leu Tyr Val Ala Ala Ile

```

115

<210> 469
 <211> 381
 <212> DNA
 <213> Homo sapiens

<400> 469
 cttgtgcaca cgttatTTTT ccaatacaaa tagtttaaaa agtaaactcc aaatacctat
 60
 aagccccctc aaagcacctt ccaaatatga accttggttaa tgcccaaggt ccagaggggt
 120
 cccccagaaa ggcccaggag cctggggcat gggaaagctg tcgggggtccc catgctgact
 180
 ccctggactc caagcgatat tccataaagc cagggcctcc tggctgcggg agggaggcct
 240
 tgacccaaaa tccattcggc cctggatact ggagaggcag aggcctctgc tgatgagaag
 300
 ccctgagttc ctggctagct gtggttaacc acaaaaaatg cgggggggtga tgattttcga
 360
 agtccatcgg caaagaaaga c
 381

<210> 470
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 470
 Met Asp Phe Glu Asn His His Pro Pro His Phe Leu Trp Leu Thr Thr
 1 5 10 15
 Ala Ser Gln Glu Leu Arg Ala Ser His Gln Gln Arg Pro Leu Pro Leu
 20 25 30
 Gln Tyr Pro Gly Pro Asn Gly Phe Trp Val Lys Ala Ser Leu Pro Gln
 35 40 45
 Pro Gly Gly Pro Gly Phe Met Glu Tyr Arg Leu Glu Ser Arg Glu Ser
 50 55 60
 Ala Trp Gly Pro Arg Gln Leu Ser His Ala Pro Gly Ser Trp Ala Phe
 65 70 75 80
 Leu Gly Asp Pro Ser Gly Pro Trp Ala Leu Thr Arg Phe Ile Phe Gly
 85 90 95
 Arg Cys Phe Glu Gly Ala Tyr Arg Tyr Leu Glu Phe Thr Phe
 100 105 110

<210> 471
 <211> 378
 <212> DNA
 <213> Homo sapiens

<400> 471
 accggtgact acctgcagca ctggattgac atgggtaaaa agggcggcga ccgcatgcc
 60
 gaggtcttcc tggttaactg gttccgccgc ggcgacgatg gccgcttcct gtggccgngg
 120

cttggcgaaa acttcccggg cctanagtgg atcatcgacc gcattgaagg caacgtagag
180
gccgaggaca cgggtggtcgg acgcaccgcc cgcgccgagg acatcgactt gcaaggcctt
240
gacttcgatg tcgacgacgt tcgcgccgca ctcgccgttg acccgaagga atgggaaggc
300
gatatgcaag acaacgccga gtacctgaac ttcttgggct cccgcgtgcc cgaggaagtg
360
tggaaccagt tccgcgcc
378

<210> 472
<211> 126
<212> PRT
<213> Homo sapiens

<400> 472
Thr Gly Asp Tyr Leu Gln His Trp Ile Asp Met Gly Lys Lys Gly Gly
1 5 10 15
Asp Arg Met Pro Glu Val Phe Leu Val Asn Trp Phe Arg Arg Gly Asp
20 25 30
Asp Gly Arg Phe Leu Trp Pro Xaa Leu Gly Glu Asn Phe Pro Val Leu
35 40 45
Xaa Trp Ile Ile Asp Arg Ile Glu Gly Asn Val Glu Ala Glu Asp Thr
50 55 60
Val Val Gly Arg Thr Ala Arg Ala Glu Asp Ile Asp Leu Gln Gly Leu
65 70 75 80
Asp Phe Asp Val Asp Asp Val Arg Ala Ala Leu Ala Val Asp Pro Lys
85 90 95
Glu Trp Glu Gly Asp Met Gln Asp Asn Ala Glu Tyr Leu Asn Phe Leu
100 105 110
Gly Ser Arg Val Pro Glu Glu Val Trp Asn Gln Phe Arg Ala
115 120 125

<210> 473
<211> 339
<212> DNA
<213> Homo sapiens

<400> 473
accggttggg gggggaaggg acccatccca tgccacctgt cctagaaaat gtttcccctt
60
gttgagcagc tgctggatct agggctgctg ggtctaagtc caaaaaggga aaaaggaaaa
120
aggcaccaag taaaagaagg gggaagctgc caaaaccccc cctgccaaaa ctctcccacc
180
ctgcttccat ttccctctcc aggggaacagg tgtacctccc ctctccctg tcctcctcag
240
atgccccagg ggctctctac ttcatctctg ccgacctgc caggagtggc ctcaggggta
300
gaggctccta gttggagaat ttgcttgacg gaaggtgaa
339

<210> 474

<211> 97
 <212> PRT
 <213> Homo sapiens

<400> 474
 Met Phe Pro Leu Val Glu Gln Leu Leu Asp Leu Gly Leu Leu Gly Leu
 1 5 10 15
 Ser Pro Lys Arg Glu Lys Gly Lys Arg His Gln Val Lys Glu Gly Gly
 20 25 30
 Ser Cys Gln Asn Pro Pro Cys Gln Asn Ser Pro Thr Leu Leu Pro Phe
 35 40 45
 Pro Ser Pro Gly Asn Arg Cys Thr Ser Pro Pro Pro Cys Pro Pro Gln
 50 55 60
 Met Pro Gln Gly Leu Ser Thr Ser Phe Leu Pro Thr Leu Pro Gly Val
 65 70 75 80
 Ala Ser Gly Val Glu Ala Pro Ser Trp Arg Ile Cys Leu Gln Glu Gly
 85 90 95
 Glu

<210> 475
 <211> 345
 <212> DNA
 <213> Homo sapiens

<400> 475
 acgcgtgaag ggtccctcc aaactctgag cctccttcca agccttgctg ggagctcccc
 60
 agcgcttgcc ggagaggcct ctctccagg cgggcttccc gcgccgatgt gaaggagagg
 120
 ctgccccaga ggggtctgga tcgtaatcca gaaagggaca gtccacacagc cataatcccg
 180
 aatgctggga ctcttcagta aaggaagaga tggctttttc gttcatctgc ctttctgaaa
 240
 ggtaaaatat ctccagatcc gggctctctg ggcgactgcg tatgtggggg tccctgaagc
 300
 ctttgatgga tcttggttaga agtgggttgt tcatcttggg gtttt
 345

<210> 476
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 476
 Met Asn Asn Pro Leu Leu Thr Arg Ser Ile Lys Gly Phe Arg Asp Pro
 1 5 10 15
 His Ile Arg Ser Arg Pro Glu Ser Pro Asp Leu Glu Ile Phe Tyr Leu
 20 25 30
 Ser Glu Arg Gln Met Asn Glu Lys Ala Ile Ser Ser Phe Thr Glu Glu
 35 40 45
 Ser Gln His Ser Gly Leu Trp Leu Trp Asp Cys Pro Phe Leu Asp Tyr
 50 55 60
 Asp Pro Asp Pro Ser Gly Ala Ala Ser Pro Ser His Arg Arg Gly Lys

65		70		75		80									
Pro	Ala	Trp	Arg	Arg	Gly	Leu	Ser	Gly	Arg	Arg	Trp	Gly	Ala	Pro	Ser
		85		90		95									
Lys	Ala	Trp	Lys	Glu	Ala	Gln	Ser	Leu	Glu	Gly	Thr	Leu	His	Ala	
		100		105		110									

<210> 477
 <211> 422
 <212> DNA
 <213> Homo sapiens

<400> 477
 acgcgtggcc gagccagcgt gctcaaggaa atgggtcaacg gcactcttat taacggctgg
 60
 gactctcccg aggtggaacg ggcactggac ctgtgcatgg cgtgcaaagg gtgcgcccga
 120
 gattgccccca ccggaatcga catggccagc taccgcagca cggttcttga cgaaaaatac
 180
 cgtcacccgc tccgccctcg ctcccacctg acgatggggc tgctgcccac gtgggaacgt
 240
 ttgctcaatc ggaccccagg agcgccgctc ctggctaacg cagtgccttc gatgccggtc
 300
 ttgcgacgctc ttgctagatg gacagccggg gtggatcagc gtcgtccctt ccccgattc
 360
 cagccctcgg ccagattggc cagtccgcag gccgccccgg ttaaggagat tgtggcggat
 420
 cc
 422

<210> 478
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 478
 Thr Arg Gly Arg Ala Ser Val Leu Lys Glu Met Val Asn Gly Thr Leu
 1 5 10 15
 Ile Asn Gly Trp Asp Ser Pro Glu Val Glu Arg Ala Leu Asp Leu Cys
 20 25 30
 Met Ala Cys Lys Gly Cys Ala Arg Asp Cys Pro Thr Gly Ile Asp Met
 35 40 45
 Ala Ser Tyr Arg Ser Thr Val Leu Asp Glu Lys Tyr Arg His Arg Leu
 50 55 60
 Arg Pro Arg Ser His Leu Thr Met Gly Leu Leu Pro Met Trp Glu Arg
 65 70 75 80
 Leu Leu Asn Arg Thr Pro Gly Ala Pro Ser Leu Ala Asn Ala Val Leu
 85 90 95
 Ser Met Pro Val Phe Ala Arg Leu Ala Arg Trp Thr Ala Gly Val Asp
 100 105 110
 Gln Arg Arg Pro Leu Pro Arg Phe Gln Pro Ser Ala Arg Leu Ala Ser
 115 120 125
 Pro Gln Ala Ala Pro Val Lys Glu Ile Val Ala Asp
 130 135 140

<210> 479
 <211> 348
 <212> DNA
 <213> Homo sapiens

<400> 479
 cgcgtggcca ttggccgggc gctggtgcgg caccgcgac tggtgattgc cgatgagccg
 60
 atctcggcgt tggacatgac catccagaag cagattcttg agctgttcga gcgcctgcag
 120
 gcgcagtacg gctttgcctg cctgttcac tcccacgacc tggcagcggg ggaacgcac
 180
 gccacccggg tggcggatgat gagcgagggc aggggtggtg aaatgggtgc ccgcgacgag
 240
 atcttcgacc gcccgagca cccctacacc cgcaagctgc tggccgccgc cagccccttg
 300
 gagaaacttg aaaacgggtg ctaccgcac cgccagggcc ccgtaccg
 348

<210> 480
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 480
 Arg Val Ala Ile Gly Arg Ala Leu Val Arg His Pro Arg Leu Val Ile
 1 5 10 15
 Ala Asp Glu Pro Ile Ser Ala Leu Asp Met Thr Ile Gln Lys Gln Ile
 20 25 30
 Leu Glu Leu Phe Glu Arg Leu Gln Ala Gln Tyr Gly Phe Ala Cys Leu
 35 40 45
 Phe Ile Ser His Asp Leu Ala Ala Val Glu Arg Ile Ala His Arg Val
 50 55 60
 Ala Val Met Ser Glu Gly Arg Val Val Glu Met Gly Ala Arg Asp Glu
 65 70 75 80
 Ile Phe Asp Arg Pro Gln His Pro Tyr Thr Arg Lys Leu Leu Ala Ala
 85 90 95
 Ala Ser Pro Leu Glu Lys Leu Glu Asn Gly Gly Tyr Arg Ile Arg Gln
 100 105 110
 Gly Pro Val Pro
 115

<210> 481
 <211> 441
 <212> DNA
 <213> Homo sapiens

<400> 481
 aagcttctga ctgtggcatt ctccctgctt aatatgtcct caatatcccc tacttactgg
 60
 gcaaaatcct gcttatgctt tgggactagc tcaaagacca ctcccttgga tggcgccttc
 120
 cctgccctgc cggcttgccg tggcttcctc agtgtagga ttaccatcac attgcatcat
 180

gagagcagaa gaccatctcc atgtgactgc tgccctgtct cccagcaggg cccacaanca
 240
 cccagtccag gacctggctc acgctgggtg gcggatgccc aggaatgggg ctctggatct
 300
 gcctcttctc ctgcaggacc aggaaaccgc tgccctgtcc ctgccccagg aaaccctcag
 360
 taaatcccca gtcatttgag tttccctca gcgccagaga ccaataacac atctccacca
 420
 acctgaaaaa ccttcacgcg t
 441

<210> 482
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 482
 Lys Leu Leu Thr Val Ala Phe Ser Leu Leu Asn Met Ser Ser Ile Ser
 1 5 10 15
 Pro Thr Tyr Trp Ala Lys Ser Cys Leu Cys Phe Gly Thr Ser Ser Lys
 20 25 30
 Thr Thr Pro Leu Asp Gly Ala Phe Pro Ala Leu Pro Ala Cys Ala Gly
 35 40 45
 Phe Leu Ser Val Arg Ile Thr Ile Thr Leu His His Glu Ser Arg Arg
 50 55 60
 Pro Ser Pro Cys Asp Cys Cys Pro Cys Ser Gln Gln Gly Pro Gln Xaa
 65 70 75 80
 Pro Ser Pro Gly Pro Gly Ser Arg Trp Val Ala Asp Ala Gln Glu Trp
 85 90 95
 Gly Ser Gly Ser Ala Ser Ser Pro Ala Gly Pro Gly Asn Arg Cys Pro
 100 105 110
 Val Pro Ala Pro Gly Asn Pro Gln
 115 120

<210> 483
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 483
 acgcgttcat tccctgatgg ccacgcacga gctaacggag ggatggggcg aagggaaggc
 60
 caagggtgcc tcgaagacca aggagtgtgc agggcaggac ctcgttttaa aggaatatcc
 120
 tctcaccaga gacacgcggc ggccaggcag ggccggagcg gggcctgtgc ccaggctccg
 180
 agcgtctgcc cagcccagca tccctgtccc cagccaggaa tatgtcttcg tggcatagag
 240
 ggagctcttg gagccacacc tgcgtgtgca catgtgtcac cccactgctg ggaggggctc
 300
 tcccgggacc ctgcagcgtg ggctggggccc
 330

<210> 484

<211> 96
 <212> PRT
 <213> Homo sapiens

<400> 484
 Met Gly Arg Arg Glu Gly Gln Gly Cys Leu Glu Asp Gln Gly Val Cys
 1 5 10 15
 Arg Ala Gly Pro Arg Phe Lys Gly Ile Ser Ser His Gln Arg His Ala
 20 25 30
 Ala Ala Arg Gln Gly Arg Ser Gly Ala Cys Ala Gln Ala Pro Ser Val
 35 40 45
 Cys Pro Ala Gln His Pro Cys Pro Gln Pro Gly Ile Cys Leu Arg Gly
 50 55 60
 Ile Glu Gly Ala Leu Gly Ala Thr Pro Ala Cys Ala His Val Ser Pro
 65 70 75 80
 His Cys Trp Glu Gly Leu Ser Arg Asp Pro Ala Ala Trp Ala Gly Pro
 85 90 95

<210> 485
 <211> 377
 <212> DNA
 <213> Homo sapiens

<400> 485
 acgcgtgctc gcgcggacga agtcggcgct gatcgcccag tcatgcgccc tgcccgtgcc
 60
 gcccagttcg gcgatcgccg cattcggccg gccggaatcg agaaggaatg cgtggacgta
 120
 cgggggatac caaaggaatc ttgtcgaggg cttcgcggcc ctcgacgtgg atcacctgta
 180
 cccgacggac gtggggaagc cgtcccgcaa gctcacggga ctccgcgaca tcgatgtgcg
 240
 atacgatttg caccgtcgtc ggctgcgtgc gcgacacatg ctccgcgatc gcctcagcgg
 300
 tggtttccga cgtcagcagg aacgtggcga cgggtggcat ggcggtcgcc gttatgtcgg
 360
 cattcccatt cctcggg
 377

<210> 486
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 486
 Met Arg Pro Ala Arg Ala Ala Gln Phe Gly Asp Arg Arg Ile Arg Pro
 1 5 10 15
 Ala Gly Ile Glu Lys Glu Cys Val Asp Val Arg Gly Ile Pro Lys Glu
 20 25 30
 Ser Cys Arg Gly Leu Arg Gly Pro Arg Arg Gly Ser Pro Val Pro Asp
 35 40 45
 Gly Arg Gly Glu Ala Val Pro Gln Ala His Gly Thr Pro Arg His Arg
 50 55 60
 Cys Ala Ile Arg Phe Ala Pro Ser Ser Ala Ala Cys Ala Thr His Ala

65					70					75				80	
Pro	Arg	Ser	Pro	Gln	Arg	Trp	Phe	Pro	Thr	Ser	Ala	Gly	Thr	Trp	Arg
				85					90					95	
Arg	Val	Ala	Trp	Arg	Ser	Pro	Leu	Cys	Arg	His	Ser	His	Ser	Ser	
			100					105					110		

<210> 487
 <211> 459
 <212> DNA
 <213> Homo sapiens

<400> 487
 nnacgcgtaa gatcgattgt ggatcagcac cgatgctggt cccccgacg ttgttggtgg
 60
 cgggtgttgt tgtaaggagt gtgtgtgatg cgtgttggtg ttcctactga ggtaagaat
 120
 agtgagtttc gtgtggctgt gacgccggcg ggtgttcattg cggttggttg tcgtgggtcat
 180
 gaggtgttgg ttcaggctgg tgctggtgtg ggttcgggta ttccggattc ggattttgtg
 240
 ggtgctggtg cgcggttgtt gggatgatgt gagtcggtgt ggggtgatgc tgatttggtg
 300
 ttgaaggtga aggagcctgt tgcggaggag tatgggcggt tgcattgagg tttggttctt
 360
 ttacgtatc ttcatttggc tgctgatgag gcgttgactc gtgagctttt ggggcgtggg
 420
 gtgacgtcga ttgcgtatga gacggtggag ttggccgat
 459

<210> 488
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 488
 Met Arg Val Gly Val Pro Thr Glu Val Lys Asn Ser Glu Phe Arg Val
 1 5 10 15
 Ala Val Thr Pro Ala Gly Val His Ala Leu Val Gly Arg Gly His Glu
 20 25 30
 Val Leu Val Gln Ala Gly Ala Gly Val Gly Ser Gly Ile Pro Asp Ser
 35 40 45
 Asp Phe Val Gly Ala Gly Ala Arg Val Val Gly Asp Val Glu Ser Val
 50 55 60
 Trp Gly Asp Ala Asp Leu Val Leu Lys Val Lys Glu Pro Val Ala Glu
 65 70 75 80
 Glu Tyr Gly Arg Leu His Glu Gly Leu Val Leu Phe Thr Tyr Leu His
 85 90 95
 Leu Ala Ala Asp Glu Ala Leu Thr Arg Glu Leu Leu Gly Arg Gly Val
 100 105 110
 Thr Ser Ile Ala Tyr Glu Thr Val Glu Leu Ala Asp
 115 120

<210> 489
 <211> 542

<212> DNA

<213> Homo sapiens

<400> 489

nacgcgtttg gcgtactgag tgcggtggtg gatggcgacg acagtggcaa gccgctgctc
 60
 aaccagcacg gttgctacaa agtgcgcttt ccatttacct gcgatcaaaa gccagcact
 120
 cgggggttcgg catggctgcg caggggtgtcg ttgtctgccg gttccagcca tggcatgcac
 180
 tttccgctgc tcaaaggcag tgaagtgttg gtgtcatttc tggggggcga ccccgaccgg
 240
 ccgattatcg ttggctgcgt accaaactcg gaaaccccga gcatggtcgt tgagcgtaac
 300
 gccacccaga gcggcttctc cacggccgga gggcacttcc tggcgatgga agaccacccc
 360
 ggggctgccc atctgaagct ggggtgcgct ggcggaaca gcgtcttcac actgggcaat
 420
 ggcaaagtcg ccggcgcgca actgcgcacc aacgccccac atgcaattga catcgtcttc
 480
 gctcaaacac gaagtgcccg gcgtgtactc attgtcgatg ggcaccgggg acccggcggc
 540
 cg
 542

<210> 490

<211> 180

<212> PRT

<213> Homo sapiens

<400> 490

Xaa	Ala	Phe	Gly	Val	Leu	Ser	Ala	Val	Val	Asp	Gly	Asp	Asp	Ser	Gly	1	5	10	15
Lys	Pro	Leu	Leu	Asn	Gln	His	Gly	Cys	Tyr	Lys	Val	Arg	Phe	Pro	Phe	20	25	30	
Thr	Arg	Asp	Gln	Lys	Pro	Ser	Thr	Arg	Gly	Ser	Ala	Trp	Leu	Arg	Arg	35	40	45	
Val	Ser	Leu	Ser	Ala	Gly	Ser	Ser	His	Gly	Met	His	Phe	Pro	Leu	Leu	50	55	60	
Lys	Gly	Ser	Glu	Val	Leu	Val	Ser	Phe	Leu	Gly	Gly	Asp	Pro	Asp	Arg	65	70	75	80
Pro	Ile	Ile	Val	Gly	Cys	Val	Pro	Asn	Ser	Glu	Thr	Pro	Ser	Met	Val	85	90	95	
Val	Glu	Arg	Asn	Ala	Thr	Gln	Ser	Gly	Phe	Ser	Thr	Ala	Gly	Gly	His	100	105	110	
Phe	Leu	Ala	Met	Glu	Asp	His	Pro	Gly	Ala	Ala	His	Leu	Lys	Leu	Gly	115	120	125	
Ala	Pro	Gly	Gly	Asn	Ser	Val	Phe	Thr	Leu	Gly	Asn	Gly	Lys	Val	Ala	130	135	140	
Gly	Ala	Gln	Leu	Arg	Thr	Asn	Ala	Pro	His	Ala	Ile	Asp	Ile	Val	Phe	145	150	155	160
Ala	Gln	Thr	Arg	Ser	Ala	Arg	Arg	Val	Leu	Ile	Val	Asp	Gly	His	Arg	165	170	175	
Gly	Pro	Gly	Gly																

180

<210> 491
 <211> 825
 <212> DNA
 <213> Homo sapiens

<400> 491
 nacgcgtcga ggcgacggtc ggcgccgtca tggcgactgt tctcgagggc acatgggaac
 60
 gcatcgggtgc cggattccgg actgccttaa ccacagcctt ggaacgcacc gatgaatggg
 120
 tgggcgggccc tgacagcaag cccctcaacg aagtcgagac actgcgccgg tgcgccgatg
 180
 aactcatcgg cgggcccgtc ggcgcggttg ccgcgatgca cggaggggtca atcgaattgg
 240
 tcgacgtgtc ggtcgggtgac gaagagcgca gagtcgacgt caccatgaag ggagcatgcc
 300
 gaggttgccc ggcagccatc agaccctaca tcagcgcctg gaacatcaac tgagtctgcg
 360
 nattgcgcga gccggtcacc gtgcgggaaa tctgacacct actccgacag ctccacctcg
 420
 acgagcacct ccacgacgag gccaagccac tcgtagacgc attcctcctc ggcattccaat
 480
 tcctcccggg ccgcccgagc gacttcgtcg gcagtaacct ggtcgatgat ccctagcctg
 540
 gcggccatca tgccacgcag cgcattgaca gtacgaagcc aacgttgcg catcacaggg
 600
 ttcattggaga tacagccggt tcggtgcaac gtctccacat cagcacttaa ggactgagcg
 660
 tcttcccagc gcgccgcgac atcctcggcg tcatggtcga catggaattg cgcgtcagct
 720
 gagtcgtcgt cacgataggc gctgggcagg atcaatcgac gcacctcgtc gtcctcctgg
 780
 agtccagaaa actggctctc ccaaaaagcg aacgggtccc cctcc
 825

<210> 492
 <211> 58
 <212> PRT
 <213> Homo sapiens

<400> 492
 Met Asn Gly Trp Ala Ala Leu Thr Ala Ser Pro Ser Thr Lys Ser Arg
 1 5 10 15
 His Cys Ala Gly Ala Pro Met Asn Ser Ser Ala Gly Pro Ser Ala Arg
 20 25 30
 Leu Pro Arg Cys Thr Glu Gly Gln Ser Asn Trp Ser Thr Cys Arg Ser
 35 40 45
 Val Thr Lys Ser Ala Glu Ser Thr Ser Pro
 50 55

<210> 493
 <211> 863

<212> DNA

<213> Homo sapiens

<400> 493

nacgcgttcc aacctcgtca aaacggctat cgcaggaaat gaccccaact ggggtcgcac
 60
 cctcgcggcg atcggatgtg ttctgagaa tatagctccc ttcgatcccc accaggtgga
 120
 tgtgtccatc aatgacattc agatctgtaa ggccgggggt atcggggagg accgcaacct
 180
 cgtcgatatg aggccacgag aggttcacat cgatattgag ctgcatgcgg gtgatgccga
 240
 agctgcggta tggactaatg atctgaccca ccaatacgtc gaagagaata gcgcgtatac
 300
 atcatgaccc ttgctcttga catccccctc aacgactccc agttctcggc tcagcggaaa
 360
 tctgaggtcc tggtagaagc gctgccttgg atcaggcggt ttcagggccg cactgtcgtc
 420
 gtgaaatatg gcggcaacgc gatggttgat cccggtctgc agcaggcctt cgccgacgac
 480
 attgtgttta tggcctctgt ggggattcgc cctattgtcg tccacgggtg tggccctcag
 540
 atcaatgcca tgcttgctga atccgctacc ccggtggagt tccgtaatgg tttgcgggtg
 600
 acatctccgg aggtcatgga ggttgcctcg atggtgctcg tcgggcaggt gggccgtcag
 660
 ctcgttaacc gaatcaacgc ctatgcgccg ctagcagctg gcatgtcagg cgaggacttt
 720
 ggcctttttt cggcccggaa gtcgcgggta attgttgatg gcgagcaa at agacatgggt
 780
 ttagtgggag acatcgttga cgtcaacatc gatctcgta tctctatgct tgatcgcggt
 840
 cagattccgg tcattgcacc ggt
 863

<210> 494

<211> 186

<212> PRT

<213> Homo sapiens

<400> 494

Met	Thr	Leu	Ala	Leu	Asp	Ile	Pro	Leu	Asn	Asp	Ser	Gln	Phe	Ser	Ala
1				5					10					15	
Gln	Arg	Lys	Ser	Glu	Val	Leu	Val	Glu	Ala	Leu	Pro	Trp	Ile	Arg	Arg
			20					25					30		
Phe	Gln	Gly	Arg	Thr	Val	Val	Val	Lys	Tyr	Gly	Gly	Asn	Ala	Met	Val
		35					40					45			
Asp	Pro	Gly	Leu	Gln	Gln	Ala	Phe	Ala	Asp	Asp	Ile	Val	Phe	Met	Ala
		50				55					60				
Ser	Val	Gly	Ile	Arg	Pro	Ile	Val	Val	His	Gly	Gly	Gly	Pro	Gln	Ile
65					70					75				80	
Asn	Ala	Met	Leu	Ala	Glu	Ser	Ala	Thr	Pro	Val	Glu	Phe	Arg	Asn	Gly
			85					90					95		
Leu	Arg	Val	Thr	Ser	Pro	Glu	Val	Met	Glu	Val	Val	Arg	Met	Val	Leu

	100		105		110
Val Gly Gln Val Gly Arg Gln Leu Val Asn Arg Ile Asn Ala Tyr Ala					
	115		120		125
Pro Leu Ala Ala Gly Met Ser Gly Glu Asp Phe Gly Leu Phe Ser Ala					
	130		135		140
Arg Lys Ser Arg Val Ile Val Asp Gly Glu Gln Ile Asp Met Gly Leu					
145		150		155	160
Val Gly Asp Ile Val Asp Val Asn Ile Asp Leu Val Ile Ser Met Leu					
	165		170		175
Asp Arg Gly Gln Ile Pro Val Ile Ala Pro					
	180		185		

<210> 495
 <211> 514
 <212> DNA
 <213> Homo sapiens

<400> 495
 gcgcgcgaca ccggtgcccc gattagcgtg ccagtgggtg acgtcactaa gggtcacgtc
 60
 tggaatgtga caggtgacgt tcttaacgcc ngatccctcc acaatcgagg tgacnntgag
 120
 cgttggccga tccaccggga tccccggcc ttcgatgacc ttgagcccga gaccgagatg
 180
 ctggagaccg gtattaaggt ccttgacttg ctgactcctt acgtcaaggg cggcaagatt
 240
 ggcctctttg gcggcgctgg tgtgggtaag acggtgctca ttcaggagat gatttaccgt
 300
 atcgcccaca acttcggcgg tacttcgggtt ttcgccggtg tcggtgagcg taccgcgag
 360
 ggtaacgacc tcatcaacga gatggacgag gccggtgtgc tcaaagacac cgccctggta
 420
 ttcggccaga tggacgagcc cccgggcacg cggtacgagc tgtcgcgctg gcagccctgc
 480
 ggcccatgcc tggtaactg ctgtgggacc ttgg
 514

<210> 496
 <211> 171
 <212> PRT
 <213> Homo sapiens

<400> 496
 Ala Arg Asp Thr Gly Ala Pro Ile Ser Val Pro Val Gly Asp Val Thr
 1 5 10 15
 Lys Gly His Val Trp Asn Val Thr Gly Asp Val Leu Asn Ala Xaa Ser
 20 25 30
 Leu His Asn Arg Gly Asp Xaa Glu Arg Trp Pro Ile His Arg Asp Pro
 35 40 45
 Pro Ala Phe Asp Asp Leu Glu Pro Glu Thr Glu Met Leu Glu Thr Gly
 50 55 60
 Ile Lys Val Leu Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile
 65 70 75 80
 Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu

				85						90					95				
Met	Ile	Tyr	Arg	Ile	Ala	His	Asn	Phe	Gly	Gly	Thr	Ser	Val	Phe	Ala				
				100						105					110				
Gly	Val	Gly	Glu	Arg	Thr	Arg	Glu	Gly	Asn	Asp	Leu	Ile	Asn	Glu	Met				
		115						120					125						
Asp	Glu	Ala	Gly	Val	Leu	Lys	Asp	Thr	Ala	Leu	Val	Phe	Gly	Gln	Met				
		130					135						140						
Asp	Glu	Pro	Pro	Gly	Thr	Arg	Tyr	Glu	Leu	Ser	Arg	Trp	Gln	Pro	Cys				
145						150				155					160				
Gly	Pro	Cys	Leu	Val	Asn	Cys	Cys	Gly	Thr	Leu									
				165						170									

<210> 497

<211> 662

<212> DNA

<213> Homo sapiens

<400> 497

acgcgtcctg ggatctcaac cccagcagtc tggcttggtt ctcattccca caatttcctg
60
ggttccacca agcagcgaaa actgccagga tgaatgagga aaaaacccag cccacaaaac
120
gagacacacg ctggcgggga gagacgcagc agagctcctt cctgtctgtg gactcggagc
180
aaagacgtgg ggccccatct tttgtgtttt cctcaagcgg ggaaagaatg gactgtttgc
240
atgcttcgtg ccacacgccc gcggtgatcc cagccagggc cccgagcgca gaggcggagc
300
tgtgctcagc acaggcctgg gacctccccg ggcaggcacc tgtgggggggt gcagcccccg
360
ggaaggaggc aactgcctca cttaacatcc tccgctgcaa ggtggtggcg ccgagaggcg
420
tgtctgtgaa gacaggtacc aggatggcag gaccgcacg cctcttccca cacctgtcag
480
cttcggaagc atctctcgag gactctggtc ccaggatgtc tcccaggaca agccagtctg
540
cctcttcctc ctacttctgc tgtagcctgg gaccagacct ggccaaggtc agccagcggg
600
gagggccgag gtctgagctc tcgtcctgcc gtggcccccg cgatggcttg gggtgcaagc
660
tt
662

<210> 498

<211> 191

<212> PRT

<213> Homo sapiens

<400> 498

Met	Asn	Glu	Glu	Lys	Thr	Gln	Pro	His	Lys	Arg	Asp	Thr	Arg	Trp	Arg				
1				5					10					15					
Gly	Glu	Thr	Gln	Gln	Ser	Ser	Phe	Leu	Ser	Val	Asp	Ser	Glu	Gln	Arg				
			20					25					30						
Arg	Gly	Ala	Pro	Ser	Phe	Val	Phe	Ser	Ser	Ser	Gly	Glu	Arg	Met	Asp				


```

<400> 500
Met Thr Val Thr Ala Leu Leu Cys Gln Ala Phe Pro Pro Ser Ile Asp
 1             5             10             15
Glu Glu Gly Leu Leu Leu Pro His Phe Ala Asp Lys Glu Ile Glu Val
      20             25             30
Leu Arg Ser Glu Val Thr Ser Ser Asn Pro Pro Val Glu Asp Leu Asn

```

35	40	45
Pro Glu Arg Phe Gln Leu Gln Cys Ser Arg Ser Glu Leu Arg Ser Phe		
50	55	60
His Leu Lys Lys Gly Leu Leu Thr Tyr Arg Leu Leu Arg Lys Pro Glu		
65	70	75
Gly Gln Ala Glu Gly Arg Ala Pro Ala Leu Gln Gly Gly Gly Leu Thr		80
85	90	95
Gln Leu Asn Thr Ala His Pro Ser Arg		
100	105	

<210> 501
 <211> 800
 <212> DNA
 <213> Homo sapiens

<400> 501
 agatctgata cgagaagtgg ctgctcaggg aaatgactac tccatggctt tcttaactca
 60
 ggtactcctt attcaatgag aggcttgagg tgagaccgcg catgcggcgc gtggatcgca
 120
 tgggtgtagt gcacactagc aaggggctta ggtctccagc tgaggtcaga tgcacacttg
 180
 gaccttgtagc tggggagtaa cacacatctc tgtgttcagc gaaccatcca ggagctgttt
 240
 gaagtttatt ctcccatgga tgatgctggc ttcccgggtca aagctgagga gtttgtgggt
 300
 ctttctcagg aaccttctgt cacggaaacc attgcaccca aaattgcaag acctttcata
 360
 gaggccctca agagtattga gtatctggag gaggatgccc agaagtccgc acaggagggg
 420
 gtgctgggac cacacactga tgctctgtca tcagactctg agaacatgcc gtgtgatgaa
 480
 gaaccatccc aattagagga gctagctgac ttcattggagc agcttacacc aattgaaaaa
 540
 tatgctttaa attacctgga atcttgaggc agggcctgag agagcacgct gcgccgtact
 600
 tccagcagct gcggcagacc acggctccac gcctgctgca gttccctgag ctgaggctgg
 660
 tgcagttcga ctcaggtatg cggcagttgg gggcgtggcc cgtgcgggag ctgcactggc
 720
 cctggatgat gaggcgctct tgatgtgatt cgtttcccag ggaagttgga agctttagct
 780
 atcttgcttc agaaactgaa
 800

<210> 502
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 502
 Met Asp Asp Ala Gly Phe Pro Val Lys Ala Glu Glu Phe Val Val Leu
 1 5 10 15
 Ser Gln Glu Pro Ser Val Thr Glu Thr Ile Ala Pro Lys Ile Ala Arg

```

      20      25      30
Pro Phe Ile Glu Ala Leu Lys Ser Ile Glu Tyr Leu Glu Glu Asp Ala
      35      40      45
Gln Lys Ser Ala Gln Glu Gly Val Leu Gly Pro His Thr Asp Ala Leu
      50      55      60
Ser Ser Asp Ser Glu Asn Met Pro Cys Asp Glu Glu Pro Ser Gln Leu
65      70      75      80
Glu Glu Leu Ala Asp Phe Met Glu Gln Leu Thr Pro Ile Glu Lys Tyr
      85      90      95
Ala Leu Asn Tyr Leu Glu Ser
      100

```

<210> 503
 <211> 538
 <212> DNA
 <213> Homo sapiens

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<400> 503
nnacgcgttg tcgtctctcc gatcattgat tttgttgat tctgcaatga tgtaaaggaa
60
gatgatgaca cggagaagtt taaagaagcc attgtgaaat ttcattaggct gtttgggatg
120
ccagaggaag agaaactcgt caactattac tcttgacagct attggaaggg gaaggcccc
180
cgtcagggtt ggatgtacct cagcattaac cacctttgct tttattcttt tcttatggga
240
aggggaagcga aactgggtcat ccggtgggta gacatcactc agcttgagaa gaatgcccc
300
ctgcttctgc ctgatgtgat caaagtgagc acacgggtcca gtgagcattt cttctctgta
360
ttcctcaaca tcaacgagac cttcaagtta atggagcagc ttgccaacat agccatgagg
420
caactcttag acaatgaggg atttgaacaa gatcgatccc tgcccaaact caaaaggaaa
480
tctcctaaaa aagtgtctgc tctaaaacgt gatcttgatg cctgggcccct tcacgcgt
538

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<210> 504
 <211> 179
 <212> PRT
 <213> Homo sapiens

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<400> 504
Xaa Arg Val Val Val Ser Pro Ile Ile Asp Phe Val Val Phe Cys Asn
1      5      10      15
Asp Val Lys Glu Asp Asp Asp Thr Glu Lys Phe Lys Glu Ala Ile Val
      20      25      30
Lys Phe His Arg Leu Phe Gly Met Pro Glu Glu Glu Lys Leu Val Asn
      35      40      45
Tyr Tyr Ser Cys Ser Tyr Trp Lys Gly Lys Val Pro Arg Gln Gly Trp
      50      55      60
Met Tyr Leu Ser Ile Asn His Leu Cys Phe Tyr Ser Phe Leu Met Gly
65      70      75      80
Arg Glu Ala Lys Leu Val Ile Arg Trp Val Asp Ile Thr Gln Leu Glu

```

```

<400> 506
Val His Asp Thr Glu Arg Tyr Glu Arg Ile Ser Gln Ala Arg Arg Glu
 1                5                10                15
Glu Gln Gln Ala Met Leu Gly Tyr Asp Xaa Ser Arg Thr Cys Arg Met
      20                25                30
Thr Leu Leu Thr Gly Gln Leu Asp Asp Pro Ser Thr Thr Pro Cys Gly
      35                40                45
Arg Cys Asp Val Cys Ala Gly Pro Trp Tyr Ser Val Glu Val Asp Gln
      50                55                60
Ser Ala Ala Val Arg Ala Val Gln Ser Leu Asn Arg Val Gly Val Pro
65                70                75                80
Val Glu Pro Arg Ala Ala Trp Pro Ala Gly Met Asp Ala Leu Gln Val
      85                90                95
Ala Leu Lys Gly Arg Ile Ser Ala Glu Glu Ile Ala Ala Glu Gly Arg

```

	100		105		110									
Val	Ile	Ala	Arg	Leu	Ser	Asp	Leu	Gly	Trp	Gly	Gly	Ala	Leu	Arg
	115		120										125	

<210> 507
 <211> 499
 <212> DNA
 <213> Homo sapiens

<400> 507
 gccggcgtgt tcaacctcat ggtgtgggcc ttcattaccg acgtcatcga tgcccaggag
 60
 gtcattgtccg gggagcgtga agacggtgtc atctatggcg tgaactcctt cgcccgcaaa
 120
 cttgcccagg ccattgccgg tggaatcggc ggagccatgc tgacgatgat cggctaccag
 180
 tcctcctccc aaggtggtgc cgttcagtcg gagtccgtcg tcaatcacct gtacacgctc
 240
 gccaccgcca tcccgaacgat ctgctgcctc ggcgctgccc tgctcatgct gggctaccg
 300
 ctcacccgcg acaaggtggt cgccaacgcc gacgagttgg ctgctcgcca cgcagtacag
 360
 gccgagcaaa actcctgacc cataacggag gcacatcatg gacacgctca tgcggatcac
 420
 cgaccacttg acaacctcgc cgggtatcca attgaaaatt gacaagcgat ggggtgcctc
 480
 cgtcacattt gtgacgcgt
 499

<210> 508
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 508
 Ala Gly Val Phe Asn Leu Met Val Trp Ala Phe Ile Thr Asp Val Ile
 1 5 10 15
 Asp Ala Gln Glu Val Met Ser Gly Glu Arg Glu Asp Gly Val Ile Tyr
 20 25 30
 Gly Val Asn Ser Phe Ala Arg Lys Leu Ala Gln Ala Ile Ala Gly Gly
 35 40 45
 Ile Gly Gly Ala Met Leu Thr Met Ile Gly Tyr Gln Ser Ser Ser Gln
 50 55 60
 Gly Gly Ala Val Gln Ser Glu Ser Val Val Asn His Leu Tyr Thr Leu
 65 70 75 80
 Ala Thr Ala Ile Pro Thr Ile Cys Cys Leu Gly Ala Ala Leu Leu Met
 85 90 95
 Leu Gly Tyr Pro Leu Thr Arg Asp Lys Val Val Ala Asn Ala Asp Glu
 100 105 110
 Leu Ala Arg Arg His Ala Val Gln Ala Glu Gln Asn Ser
 115 120 125

<210> 509
 <211> 360

<212> DNA

<213> Homo sapiens

<400> 509

ttggccatgg atttggtcgc caagttcagt cccaaagatg tcacgctcta tctaattggac
 60
 ttcgggacca atggtgtggc accactaggc caattaccac aggtggccga caccttgctt
 120
 ttggatcata cggagaagat tgccaagttt gtacgcatca tggagcggga gctcaaccgg
 180
 cgtaagaagc tcttggtccga ctacggtggt ggtacactag agctctaccg tcaggctagc
 240
 ggtcagcaag agccggccat cgtcatcctg ctggacagtt atgagtcctat gaaggaagag
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<210> 510

<211> 120

<212> PRT

<213> Homo sapiens

<400> 510

Leu	Ala	Met	Asp	Leu	Ala	Arg	Lys	Phe	Ser	Pro	Lys	Asp	Val	Thr	Leu
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Tyr	Leu	Met	Asp	Phe	Gly	Thr	Asn	Gly	Val	Ala	Pro	Leu	Gly	Gln	Leu
			20					25					30		
Pro	Gln	Val	Ala	Asp	Thr	Leu	Leu	Leu	Asp	His	Thr	Glu	Lys	Ile	Ala
		35					40					45			
Lys	Phe	Val	Arg	Ile	Met	Glu	Arg	Glu	Leu	Asn	Arg	Arg	Lys	Lys	Leu
	50				55					60					
Leu	Ser	Asp	Tyr	Gly	Val	Gly	Thr	Leu	Glu	Leu	Tyr	Arg	Gln	Ala	Ser
65				70					75				80		
Gly	Gln	Gln	Glu	Pro	Ala	Ile	Val	Ile	Leu	Leu	Asp	Ser	Tyr	Glu	Ser
			85					90					95		
Met	Lys	Glu	Glu	Ala	Tyr	Glu	Ala	Glu	Leu	Phe	Thr	Leu	Leu	Val	Arg
			100					105					110		
Ile	Ser	Arg	Glu	Gly	Leu	Ser	Ile								
		115				120									

<210> 511

<211> 361

<212> DNA

<213> Homo sapiens

<400> 511

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 120
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 <211> 91
 <212> PRT
 <213> Homo sapiens

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 20 25 30
 Arg Lys Met Gln Asp Asp Leu Asp Asp Gly Met Asp Trp Leu Val Lys
 35 40 45
 Glu Gly Ile Val Asp Lys Gly Arg Val Cys Ile Val Gly Ala Ser Tyr
 50 55 60
 Gly Gly Tyr Ala Ala Met Trp Gly Ala Ile Arg Asn Pro Glu Arg Tyr
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 Arg Cys Ala Ala Ser Leu Ala Gly Val Ala Asp
 85 90

<210> 513
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 513
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 aataactgtg gtgtagatgg ttttggttta ggggttttgc tagaagataa gcaagtacgc
 180
 aaaatggtgt cttcttatgt gggtgaaaat gcactgtttg agaagcaatt attacaaggt
 240
 gagttggaag tcgagctcac tcctcaaggc actcttgccg aaaaactacg cgctggcggc
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 360
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 369

<210> 514
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 514
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Leu Cys Gly Ile Pro Glu Asn Leu Ile Gln Glu Ile Lys Arg Arg Gln
20           25           30
Thr Cys Asp Leu Thr Ile Val Ser Asn Asn Cys Gly Val Asp Gly Phe
35           40           45
Gly Leu Gly Val Leu Leu Glu Asp Lys Gln Val Arg Lys Met Val Ser
50           55           60
Ser Tyr Val Gly Glu Asn Ala Leu Phe Glu Lys Gln Leu Leu Gln Gly
65           70           75           80
Glu Leu Glu Val Glu Leu Thr Pro Gln Gly Thr Leu Ala Glu Lys Leu
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Arg Ala Gly Gly Ala Gly Ile Pro Ala Phe Phe Thr Ala Thr Gly Val
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Gly Thr Pro Ile Gly Glu Gly Lys Asp Thr Arg
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<210> 515
 <211> 387
 <212> DNA
 <213> Homo sapiens

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gccgacctga ccggtgcgcc gttgtac
387

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<210> 516
 <211> 129
 <212> PRT
 <213> Homo sapiens

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20           25           30
Glu Leu Ile Thr Glu Gly Val Thr Ser Phe Lys Leu Phe Val Ala Tyr
35           40           45
Lys Gly Val Phe Leu Ser Asp Asp Gly Gln Ile Leu Arg Ala Phe Gln
50           55           60
Lys Gly Ala Asp Asn Gly Ala Met Met Met Met His Ala Glu Asn Gly
65           70           75           80
Ala Ile Ile Asp Val Leu Val Gln Gln Ala Leu Glu Ala Gly Lys Thr

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85 90 95
 Thr Pro Tyr Tyr His Gly Ile Ser Arg Pro Trp Gln Ala Glu Glu Glu
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 115 120 125
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<210> 517
 <211> 377
 <212> DNA
 <213> Homo sapiens

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 240
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 <211> 118
 <212> PRT
 <213> Homo sapiens

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 20 25 30
 Ser Pro Gly Glu Ala Gln Gly Pro Leu Leu Pro Ser Pro Ala Arg Gly
 35 40 45
 Leu Lys Phe Leu Lys Leu Pro Pro Thr Ser Glu Lys Ser Pro Ser Pro
 50 55 60
 Gly Gly Pro Gln Leu Ser Pro Gln Leu Pro Arg Asn Ser Arg Ile Pro
 65 70 75 80
 Cys Arg Asn Ser Gly Ser Asp Gly Ser Pro Ser Pro Leu Leu Ala Arg
 85 90 95
 Arg Gly Leu Gly Gly Gly Glu Leu Ser Pro Glu Gly Ala Gln Gly Leu
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 Pro Thr Ser Pro Ser Arg
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<210> 519
 <211> 311

<212> DNA

<213> Homo sapiens

<400> 519

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120
aagaaattga taatttttcta ggaaaacatg acttaccaaa attaactcta gaaaagaatc
180
gatacacatc agtaacaaca gaagttgaga aagtagttaa catattgcca aacctggaat
240
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300
cagaacttaa g
311

<210> 520

<211> 92

<212> PRT

<213> Homo sapiens

<400> 520

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Thr	Phe	Ser	Ala	Thr	Leu	Lys	Asn	Val	Arg	Ile	Ser	Lys	Glu	Ile	Asp
			20					25					30		
Asn	Phe	Leu	Gly	Lys	His	Asp	Leu	Pro	Lys	Leu	Thr	Leu	Glu	Lys	Asn
		35					40				45				
Arg	Tyr	Thr	Ser	Val	Thr	Thr	Glu	Val	Glu	Lys	Val	Val	Asn	Ile	Leu
	50					55				60					
Pro	Asn	Leu	Glu	Phe	Met	Ile	Glu	Phe	Phe	Glu	Ile	Tyr	Cys	Glu	Tyr
65					70				75					80	
Ile	Leu	Cys	Leu	Cys	Ser	Ala	Val	Pro	Glu	Leu	Lys				
			85					90							

<210> 521

<211> 352

<212> DNA

<213> Homo sapiens

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352

<210> 522
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 522
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 20 25 30
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 35 40 45
 Val Ile Arg Ala Leu Met Leu Leu Arg Leu Ser Thr Leu Cys Thr Gly
 50 55 60
 Arg Thr Gly Val Arg Pro Val Val Val Glu Thr Tyr Ala Lys Ala Leu
 65 70 75 80
 Asn Ala Gly Ile Val Pro Gly Val Arg Glu Tyr Gly Ser Leu Gly Cys
 85 90 95
 Ser Gly Asp Leu Ala Pro Leu Ala His Cys Ala Leu Ala Leu Leu Gly
 100 105 110
 Glu Gly Glu Val Arg
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<210> 523
 <211> 693
 <212> DNA
 <213> Homo sapiens

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 360
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<210> 524
 <211> 193
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Phe Pro Leu Asp Phe Gln Val Ile Leu Ala Gly Ser Gln Arg Phe Arg
 50 55 60
 Glu Lys Phe Pro Pro Val Phe Phe Ser Ser Phe Arg Asn Thr Val Gln
 65 70 75 80
 Ser Ser Asn Asn Lys Phe Arg Arg Asn Phe Thr Met Thr Tyr His Leu
 85 90 95
 Ser Pro Gly Asn Tyr Val Val Val Ala Gln Thr Arg Arg Lys Ser Ala
 100 105 110
 Glu Phe Leu Leu Arg Ile Phe Leu Lys Met Pro Asp Ser Asp Arg His
 115 120 125
 Leu Ser Ser His Phe Asn Leu Arg Met Lys Gly Ser Pro Ser Glu His
 130 135 140
 Gly Ser Gln Gln Ser Ile Phe Asn Arg Tyr Ala Gln Gln Arg Leu Asp
 145 150 155 160
 Ile Asp Ala Thr Gln Leu Gln Gly Leu Leu Asn Gln Glu Leu Leu Thr
 165 170 175
 Gly Pro Pro Gly Asp Met Phe Ser Leu Asp Gly Ala Ala Ala Trp Trp
 180 185 190
 Leu

<210> 525
 <211> 1101
 <212> DNA
 <213> Homo sapiens

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<211> 290

<212> PRT

<213> Homo sapiens

<400> 526

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			20					25					30		
Gly	Asp	Gln	Ile	Leu	Asp	Trp	Gln	Tyr	Gly	Val	Thr	Gln	Ala	Phe	Pro
		35					40					45			
His	Thr	Glu	Glu	Glu	Val	Glu	Val	Asp	Ser	His	Ala	Tyr	Ser	His	Arg
	50					55					60				
Trp	Lys	Arg	Asn	Leu	Asp	Phe	Leu	Lys	Ala	Val	Asp	Thr	Asn	Arg	Ala
65				70					75					80	
Ser	Val	Gly	Gln	Asp	Ser	Leu	Glu	Pro	Arg	Ser	Phe	Thr	Asp	Leu	Leu
			85					90						95	
Leu	Asp	Asp	Gly	Gln	Asp	Asn	Asn	Thr	Gln	Ile	Glu	Glu	Asp	Thr	Asp
			100					105					110		
His	Asn	Tyr	Tyr	Ile	Ser	Arg	Ile	Tyr	Gly	Pro	Ser	Asp	Ser	Ala	Ser
	115					120						125			
Arg	Asp	Leu	Trp	Val	Asn	Ile	Asp	Gln	Met	Glu	Lys	Asp	Lys	Val	Lys
	130				135						140				
Ile	His	Gly	Ile	Leu	Ser	Asn	Thr	His	Arg	Gln	Ala	Ala	Arg	Val	Asn
145				150					155					160	
Leu	Ser	Phe	Asp	Phe	Pro	Phe	Tyr	Gly	His	Phe	Leu	Arg	Glu	Ile	Thr
			165					170						175	
Val	Ala	Thr	Gly	Gly	Phe	Ile	Tyr	Thr	Gly	Glu	Val	Val	His	Arg	Met

	180		185		190
Leu Thr Ala Thr Gln Tyr Ile Ala Pro Leu Met Ala Asn Phe Asp Pro					
	195		200		205
Ser Val Ser Arg Asn Ser Thr Val Arg Tyr Phe Asp Asn Gly Thr Ala					
	210		215		220
Leu Val Val Gln Trp Asp His Val His Leu Gln Asp Asn Tyr Asn Leu					
225		230		235	240
Gly Ser Phe Thr Phe Gln Ala Thr Leu Leu Met Asp Gly Arg Ile Ile					
	245		250		255
Phe Gly Tyr Lys Glu Ile Pro Val Leu Val Thr Gln Ile Ser Ser Thr					
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<210> 527

<211> 5343

<212> DNA

<213> Homo sapiens

<400> 527

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960

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<211> 886

<212> PRT

<213> Homo sapiens

<400> 528

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Leu	Glu	Ala	Cys	Asp	Glu	Ser	Pro	Ala	Ser	Arg	Glu	Leu	Asp	Ile	Pro
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Gly Glu Thr Pro Ala	Pro Pro Glu Glu Cys	Arg Asp Glu Lys Pro His
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420	425	430
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435	440	445
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<211> 4566

<212> DNA

<213> Homo sapiens

<400> 529

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<210> 530

<211> 802

<212> PRT

<213> Homo sapiens

<400> 530

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 Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly Ala Arg Gly Asp
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 Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser Asp Pro Asp Gly Gly
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 Pro Arg Asp Arg Asn Phe Leu Phe Val Gly Val Met Thr Ala Gln Lys
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 Tyr Leu Gln Thr Arg Ala Val Ala Ala Tyr Arg Thr Trp Ser Lys Thr
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 180 185 190
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 195 200 205
 Lys Leu Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly
 210 215 220
 Val Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly
 225 230 235 240
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 Arg Cys Val Arg Arg Phe Ala Gly Val Gln Cys Val Trp Ser Tyr Glu
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 Pro Asn Lys Asn Pro Pro Tyr Gln Tyr Arg Leu His Ser Tyr Met Leu
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 Gln Arg Glu Ala Leu Asp Asp Ile Val Met Gln Val Met Glu Met Ile

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	450		455		460
Val Pro Val Arg Arg His Ala Tyr Leu Gln Gln Thr Phe Ser Lys Ile					
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Ile Asn Gln Glu Ser Gly Ser Leu Ser Phe Leu Ser Asn Ser Leu Lys					
	500		505		510
Lys Leu Val Pro Phe Gln Leu Pro Gly Ser Lys Ser Glu His Lys Glu					
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	530		535		540
Asp Met Phe Val Arg Phe Met Gly Asn Phe Glu Lys Thr Cys Leu Ile					
	545		550		555
Pro Asn Gln Asn Val Lys Leu Val Val Leu Leu Phe Asn Ser Asp Ser					
	565		570		575
Asn Pro Asp Lys Ala Lys Gln Val Glu Leu Met Thr Asp Tyr Arg Ile					
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Lys Tyr Pro Lys Ala Asp Met Gln Ile Leu Pro Val Ser Gly Glu Phe					
	595		600		605
Ser Arg Ala Leu Ala Leu Glu Val Gly Ser Ser Gln Phe Asn Asn Glu					
	610		615		620
Ser Leu Leu Phe Phe Cys Asp Val Asp Leu Val Phe Thr Thr Glu Phe					
	625		630		635
Leu Gln Arg Cys Arg Ala Asn Thr Val Leu Gly Gln Gln Ile Tyr Phe					
	645		650		655
Pro Ile Ile Phe Ser Gln Tyr Asp Pro Lys Ile Val Tyr Ser Gly Lys					
	660		665		670
Val Pro Ser Asp Asn His Phe Ala Phe Thr Gln Lys Thr Gly Phe Trp					
	675		680		685
Arg Asn Tyr Gly Phe Gly Ile Thr Cys Ile Tyr Lys Gly Asp Leu Val					
	690		695		700
Arg Val Gly Gly Phe Asp Val Ser Ile Gln Gly Trp Gly Leu Glu Asp					
	705		710		715
Val Asp Leu Phe Asn Lys Val Val Gln Ala Gly Leu Lys Thr Phe Arg					
	725		730		735
Ser Gln Glu Val Gly Val Val His Val His His Pro Val Phe Cys Asp					
	740		745		750
Pro Asn Leu Asp Pro Lys Gln Tyr Lys Met Cys Leu Gly Ser Lys Ala					
	755		760		765
Ser Thr Tyr Gly Ser Thr Gln Gln Leu Ala Glu Met Trp Leu Glu Lys					
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<211> 321

<212> DNA

<213> Homo sapiens

<400> 531

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<210> 532

<211> 96

<212> PRT

<213> Homo sapiens

<400> 532

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			20					25					30		
Ser	Val	Lys	Arg	Cys	Arg	Thr	Ser	Val	Ser	Asn	Ala	Pro	Glu	Val	Asn
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Pro	Arg	Gly	Arg	Leu	Asn	Gln	Ala	Ser	Trp	Ala	Trp	Asp	Asp	Ser	Gly
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Cys	Ser	Gly	Ser	Asn	Gly	Ala	Cys	Gly	Ser	Ala	Leu	Ile	Asp	Ser	Arg
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<211> 335

<212> DNA

<213> Homo sapiens

<400> 533

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 35 40 45
 Lys Val Thr Leu Thr Asn Ile Asp Asn Val Leu Asn Lys Asp His Leu
 50 55 60
 Arg Trp Leu His Phe Leu Leu Glu Gly Arg Leu Glu Pro Asn Val Arg
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 <211> 402
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 <213> Homo sapiens

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 taccacaat gcaggaacaa ggctgatagc tagggctgac cacagagcca ggccgcctgc
 240
 cgaggaaacg cccccacct ggtgactgcc agtatcagca ccgcgcagct caacgacgtc
 300
 aacagtctcg ggattgacca accgccacgt atgcagggcc atgtggggga gaatcacccc
 360
 caacgccaat gctgtcaccg agcctcgggc taggccgccg gc
 402

<210> 536
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 536
 Met Ala Leu His Thr Trp Arg Leu Val Asn Pro Glu Thr Val Asp Val
 1 5 10 15
 Val Glu Leu Arg Gly Ala Asp Thr Gly Ser His Gln Val Gly Gly Val
 20 25 30
 Ser Ser Ala Gly Gly Leu Ala Leu Trp Ser Ala Leu Ala Ile Ser Leu

```

      35              40              45
Val Pro Ala Leu Trp Val Tyr Pro Val Ala Val Ala Val Gly Ile Leu
      50              55              60
Met Thr Arg Pro Arg Arg Leu Leu Leu Gly Ser Ile Val Val Leu Gly
65              70              75              80
Pro Leu Leu Val Ile Ser Pro Trp Ile Pro Arg Leu Ile Thr Glu Pro
      85              90              95
Gly Arg Met Ala Thr Gly Ala Glu Pro Val Leu Ser Pro Ala Val Glu
      100              105              110
Thr Arg

```

<210> 537
 <211> 404
 <212> DNA
 <213> Homo sapiens

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<400> 537
gtgcacatcg gcggcaccga cttcgacaaa caactctcgc tggctggcat gatgccgctg
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ttcggctacg gcagccgcat gaagagcggc gcctacatgc ccaccagcca ccacatgaac
120
ctggcgacct ggcacaccat caactcgggtg tactcgcaaa aatcccagct ggccctgggc
180
agcatgcgct acgacatcga agacaccggc ggcacgcacc gcctgttcaa gctgatcgaa
240
cagcgtgctg ggcactggct tgccatggaa gtggaagaaa ccaagatcca gctcacccat
300
caagacagcc gccacgtgcc gctggaccgc atcgaagcgg gcctgagcgt agacctgagc
360
cgggcgctgt tcgaatcgtc catcgacaac ctgctcgaac gcgt
404

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<210> 538
 <211> 118
 <212> PRT
 <213> Homo sapiens

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<400> 538
Met Met Pro Leu Phe Gly Tyr Gly Ser Arg Met Lys Ser Gly Ala Tyr
  1              5              10              15
Met Pro Thr Ser His His Met Asn Leu Ala Thr Trp His Thr Ile Asn
      20              25              30
Ser Val Tyr Ser Gln Lys Ser Gln Leu Ala Leu Gly Ser Met Arg Tyr
      35              40              45
Asp Ile Glu Asp Thr Gly Gly Ile Asp Arg Leu Phe Lys Leu Ile Glu
      50              55              60
Gln Arg Ala Gly His Trp Leu Ala Met Glu Val Glu Glu Thr Lys Ile
65              70              75              80
Gln Leu Thr His Gln Asp Ser Arg His Val Pro Leu Asp Arg Ile Glu
      85              90              95
Ala Gly Leu Ser Val Asp Leu Ser Arg Ala Leu Phe Glu Ser Ser Ile
      100              105              110
Asp Asn Leu Leu Glu Arg

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115

<210> 539
<211> 534
<212> DNA
<213> Homo sapiens

<400> 539
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ccaattttca taaaagaaag attgaagctt tttgaaatac tgaagaaaga ccatcagctc
120
ttacttgcca tttatggaaa aaagggggat acaagcaaca tcatcacagt aagagtggct
180
gatgggcaaa cagtgcagg ggaagtctgg aaaacaacgc cttaccaagt ggctgctgaa
240
attagtcagg aactggctga aagcacggta atagccaaag tcaatgggtga actgtgggac
300
ctggaccgcc cattggaagg ggactcttct ctagagctgc ttacatttga taatgaggaa
360
gctcaagctg tgagtatttt aaaaccagac agccaaactt tgggtagtta tgttgtaaac
420
tacattatat aagaggccac atattgaatt cacgaatgtt gagttttttg ggggtttcta
480
agatttaaaa tttgattatt gatgtttaat aaatatttgc ctcatgaatg ttaa
534

<210> 540
<211> 143
<212> PRT
<213> Homo sapiens

<400> 540
Xaa Arg Val Lys Lys Lys Lys Met Lys Glu Ser Glu Ala Asp Ser Glu
1 5 10 15
Val Lys His Gln Pro Ile Phe Ile Lys Glu Arg Leu Lys Leu Phe Glu
20 25 30
Ile Leu Lys Lys Asp His Gln Leu Leu Ala Ile Tyr Gly Lys Lys
35 40 45
Gly Asp Thr Ser Asn Ile Ile Thr Val Arg Val Ala Asp Gly Gln Thr
50 55 60
Val Gln Gly Glu Val Trp Lys Thr Thr Pro Tyr Gln Val Ala Ala Glu
65 70 75 80
Ile Ser Gln Glu Leu Ala Glu Ser Thr Val Ile Ala Lys Val Asn Gly
85 90 95
Glu Leu Trp Asp Leu Asp Arg Pro Leu Glu Gly Asp Ser Ser Leu Glu
100 105 110
Leu Leu Thr Phe Asp Asn Glu Glu Ala Gln Ala Val Ser Ile Leu Lys
115 120 125
Pro Asp Ser Gln Thr Leu Gly Ser Tyr Val Val Asn Tyr Ile Ile
130 135 140

<210> 541
<211> 551

<212> DNA

<213> Homo sapiens

<400> 541

ggtaccgagc tgcgcgtgtg gtatgcggcc ttctatgcca agaagatgga caagcccatg
 60
 ctgaagcagg ccggctctgg cgtccacgct gcaggcacc cagaaaacag cgtccccgtg
 120
 gagtcggagc ccagccagtg ggcgtgtaaa gtgtgttctg ccaccttcct ggagctgcag
 180
 ctctcaatg gtaaggagga cgtgtgggga gcccagttg taaaactcct gtgtcgattt
 240
 ctctctgact tacgctgtca cctgtctgcg gctgtcgggg gtgtcccaga ctttgcctg
 300
 tctgccccat tgccccacaa tgtagtcgcc agaaccaagg ctttctcagg gtttaaagct
 360
 tctgggcagt cccgcttccc acccccgacc cctgcaggcc tcaactctca ctctcctgg
 420
 ttgggaagtt gcatttcagc tgggcgcctt gactctggag cactggcagg ggccaggggc
 480
 caggagccag ccgtggcatg tgttgtgcac tcttgccctt gttgtcteta cttgacagcc
 540
 ccctcacgcg t
 551

<210> 542

<211> 168

<212> PRT

<213> Homo sapiens

<400> 542

Met	Asp	Lys	Pro	Met	Leu	Lys	Gln	Ala	Gly	Ser	Gly	Val	His	Ala	Ala	1	5	10	15
Gly	Thr	Pro	Glu	Asn	Ser	Ala	Pro	Val	Glu	Ser	Glu	Pro	Ser	Gln	Trp	20	25	30	
Ala	Cys	Lys	Val	Cys	Ser	Ala	Thr	Phe	Leu	Glu	Leu	Gln	Leu	Leu	Asn	35	40	45	
Gly	Lys	Glu	Asp	Val	Trp	Gly	Ala	Pro	Val	Val	Lys	Leu	Leu	Cys	Arg	50	55	60	
Phe	Leu	Ser	Asp	Leu	Arg	Cys	His	Leu	Ser	Ala	Ala	Val	Gly	Gly	Val	65	70	75	80
Pro	Asp	Phe	Val	Leu	Ser	Ala	Pro	Leu	Pro	His	Asn	Val	Val	Ala	Arg	85	90	95	
Thr	Lys	Ala	Phe	Ser	Gly	Phe	Lys	Ala	Ser	Gly	Gln	Ser	Arg	Phe	Pro	100	105	110	
Pro	Pro	Thr	Pro	Ala	Gly	Leu	Thr	Pro	His	Ser	Ser	Trp	Leu	Gly	Ser	115	120	125	
Cys	Ile	Ser	Ala	Gly	Arg	Leu	Asp	Ser	Gly	Ala	Leu	Ala	Gly	Ala	Arg	130	135	140	
Gly	Gln	Glu	Pro	Ala	Val	Ala	Cys	Val	Val	His	Ser	Cys	Leu	Cys	Cys	145	150	155	160
Leu	Tyr	Leu	Thr	Ala	Pro	Ser	Arg									165			

<210> 543
 <211> 349
 <212> DNA
 <213> Homo sapiens

<400> 543
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 gggggcaaag gcagccgcct ggccccgatg accgatcagg tggccaaacc agccgtgccg
 120
 tttatgggga cgtaccgcct gattgacttt tcgctgtcca acattgtcca cagcggcttg
 180
 caggacgtct ggatcattga gcaaaacctg ccccatagct taaacgagca cctggctggg
 240
 gggcgctcct gggatctgga ccgcacccgc ggtggcctga aggtcatgcc gcccttttcc
 300
 ggccctgccg atgaggacgg tggcttttcc gaaggcaacg cacacgcgt
 349

<210> 544
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 544
 Xaa Lys Pro Asp Met Asn Thr Arg Ile Ala Gly Lys Thr Val Leu Thr
 1 5 10 15
 Ile Ile Leu Ala Gly Gly Lys Gly Ser Arg Leu Ala Pro Met Thr Asp
 20 25 30
 Gln Val Ala Lys Pro Ala Val Pro Phe Met Gly Thr Tyr Arg Leu Ile
 35 40 45
 Asp Phe Ser Leu Ser Asn Ile Val His Ser Gly Leu Gln Asp Val Trp
 50 55 60
 Ile Ile Glu Gln Asn Leu Pro His Ser Leu Asn Glu His Leu Ala Gly
 65 70 75 80
 Gly Arg Ser Trp Asp Leu Asp Arg Thr Arg Gly Gly Leu Lys Val Met
 85 90 95
 Pro Pro Phe Ser Gly Pro Ala Asp Glu Asp Gly Gly Phe Ser Glu Gly
 100 105 110
 Asn Ala His Ala
 115

<210> 545
 <211> 390
 <212> DNA
 <213> Homo sapiens

<400> 545
 catgatgcaa aaacagacat gcttatttca aaatataaaa gtgaaaaaga tcgttttagca
 60
 caagaaattg ttggtgtcat cacaggttct gcaatgccgg gtggttcagc aaaccgtatc
 120
 ccaaataaag caggctcaaa tccagaaggt tctattgcaa cgcgttttat tgcagaaaca
 180

atgtataacg aactcaaaac agtggattta actattcaaa atgctggcgg tgtacgcgca
 240
 gatattttac cggggaatgt aacctttaac gatgcttata ctttcttacc tttcgggaat
 300
 acgttatata cctataaaat ggaaagttca ttagtgaaac aagtgcctga agatgcaatg
 360
 ctatttgctt tgggtcccc ccccccccc
 390

<210> 546
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 546
 His Asp Ala Lys Thr Asp Met Leu Ile Ser Lys Tyr Lys Ser Glu Lys
 1 5 10 15
 Asp Arg Leu Ala Gln Glu Ile Val Gly Val Ile Thr Gly Ser Ala Met
 20 25 30
 Pro Gly Gly Ser Ala Asn Arg Ile Pro Asn Lys Ala Gly Ser Asn Pro
 35 40 45
 Glu Gly Ser Ile Ala Thr Arg Phe Ile Ala Glu Thr Met Tyr Asn Glu
 50 55 60
 Leu Lys Thr Val Asp Leu Thr Ile Gln Asn Ala Gly Gly Val Arg Ala
 65 70 75 80
 Asp Ile Leu Pro Gly Asn Val Thr Phe Asn Asp Ala Tyr Thr Phe Leu
 85 90 95
 Pro Phe Gly Asn Thr Leu Tyr Thr Tyr Lys Met Glu Ser Ser Leu Val
 100 105 110
 Lys Gln Val Leu Glu Asp Ala Met Leu Phe Ala Leu Gly Pro Pro Pro
 115 120 125
 Pro Pro
 130

<210> 547
 <211> 306
 <212> DNA
 <213> Homo sapiens

<400> 547
 aagcttggtt ttctgatttt tattcaaate tctatcatgg atgaagcatg cagtttcaga
 60
 atcagttcag tgttgacaac atatcaagat attctgcagt caatctcaat gtatgttcat
 120
 gaagcctcca acatattttg tgggatacca tctttgtcag gcattgtgct aggcactgtc
 180
 cctgcagtga ataagaaaga caggatttct gtatttatgg ggcttagtac caagttgttc
 240
 tcaaactttc atgtttgtgt atacaaatca gctgaggcct tcactaaact cnnnnnccnn
 300
 nnnccnn
 306

<210> 548

<211> 90
 <212> PRT
 <213> Homo sapiens

<400> 548
 Met Asp Glu Ala Cys Ser Phe Arg Ile Ser Ser Val Leu Thr Thr Tyr
 1 5 10 15
 Gln Asp Ile Leu Gln Ser Ile Ser Met Tyr Val His Glu Ala Ser Asn
 20 25 30
 Ile Phe Cys Gly Ile Pro Ser Leu Ser Gly Ile Val Leu Gly Thr Val
 35 40 45
 Pro Ala Val Asn Lys Lys Asp Arg Ile Ser Val Phe Met Gly Leu Ser
 50 55 60
 Thr Lys Leu Phe Ser Asn Phe His Val Cys Val Tyr Lys Ser Ala Glu
 65 70 75 80
 Ala Phe Thr Lys Leu Xaa Xaa Xaa Xaa Xaa
 85 90

<210> 549
 <211> 780
 <212> DNA
 <213> Homo sapiens

<400> 549
 nnacgcgtac ttccaacacc tatgctccag tatggaggac gggtaaagtc tcttggttaat
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 gttttaatca tacacatatt gtctgtaagt atgaagagaa aggcatatca gaaatatttc
 120
 aattcagcga ttgaaatgt ttactttctg tttattgaaa atttttgttc tttttcacca
 180
 tggtattttt ttctcctcgt gtagaatcgg acagtagcaa caccgagcca tggagtatgg
 240
 gacatgcgag ggaaacaatt ccacacagga gttgaaatca aaatgtgggc tatcgcttgt
 300
 tttgccacac agaggcagtg cagagaagaa atattgaagg gtttcacaga ccagctgcgt
 360
 aagatttcta aggatgcagg gatgcccatc cagggccagc catgcttctg caaatatgca
 420
 caggggggcag acagcgtaga gcccatgttc cggcatctca agaacacata ttctggccta
 480
 cagcttatta tcgtcatcct gccggggaag acaccagtgt atgcggaagt gaaacgtgta
 540
 ggagacacac ttttgggtat ggctacacaa tgtgttcaag tcaagaatgt aataaaaaca
 600
 tctcctcaaa ctctgtcaaa cttgtgccta aagataaatg ttaaactcgg agggatcaat
 660
 aatattcttg tacctcatca aagaccttct gtgttccagc aaccagtgat ctttttggga
 720
 gccgatgtca ctcatccacc tgctgggtgat ggaaagaagc cttctattgc tgctgttgta
 780

<210> 550
 <211> 192
 <212> PRT

<213> Homo sapiens

<400> 550

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Asn Arg Thr Val Ala Thr Pro Ser His Gly Val Trp Asp Met Arg Gly
 1           5           10           15
Lys Gln Phe His Thr Gly Val Glu Ile Lys Met Trp Ala Ile Ala Cys
           20           25           30
Phe Ala Thr Gln Arg Gln Cys Arg Glu Glu Ile Leu Lys Gly Phe Thr
           35           40           45
Asp Gln Leu Arg Lys Ile Ser Lys Asp Ala Gly Met Pro Ile Gln Gly
 50           55           60
Gln Pro Cys Phe Cys Lys Tyr Ala Gln Gly Ala Asp Ser Val Glu Pro
65           70           75           80
Met Phe Arg His Leu Lys Asn Thr Tyr Ser Gly Leu Gln Leu Ile Ile
           85           90           95
Val Ile Leu Pro Gly Lys Thr Pro Val Tyr Ala Glu Val Lys Arg Val
           100          105          110
Gly Asp Thr Leu Leu Gly Met Ala Thr Gln Cys Val Gln Val Lys Asn
           115          120          125
Val Ile Lys Thr Ser Pro Gln Thr Leu Ser Asn Leu Cys Leu Lys Ile
           130          135          140
Asn Val Lys Leu Gly Gly Ile Asn Asn Ile Leu Val Pro His Gln Arg
145          150          155          160
Pro Ser Val Phe Gln Gln Pro Val Ile Phe Leu Gly Ala Asp Val Thr
           165          170          175
His Pro Pro Ala Gly Asp Gly Lys Lys Pro Ser Ile Ala Ala Val Val
           180          185          190

```

<210> 551

<211> 291

<212> DNA

<213> Homo sapiens

<400> 551

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nnggatccgg attatggggc tattgctaac aggtcaacgg ccatcaaggt gctcgttgcc
60
gtggcaccgc cagccccgga gcctactcgc gagccaccga cgaactccgc tccttccgag
120
gaaccgtcct cgtcgtcaat cgcaccgggtc ccgccggccc cgacgactgc agtaccacg
180
actagttcgt cgtcggggccg ctgaccgatg cgcccatcgg cgggctcatc tggctggcgc
240
tagcgggggc ttcgatgtcc ccataccaca gcgtccgcta aattgccnc c
291

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<210> 552

<211> 67

<212> PRT

<213> Homo sapiens

<400> 552

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Xaa Asp Pro Asp Tyr Gly Ala Ile Ala Asn Arg Ser Thr Ala Ile Lys
 1           5           10           15
Val Leu Val Ala Val Ala Pro Pro Ala Pro Glu Pro Thr Arg Glu Pro

```

```

          20          25          30
Pro Thr Asn Ser Ala Pro Ser Glu Glu Pro Ser Ser Ser Ile Ala
          35          40          45
Pro Val Pro Pro Ala Pro Thr Thr Ala Val Pro Thr Thr Ser Ser Ser
          50          55          60
Ser Gly Arg
65

```

<210> 553
 <211> 471
 <212> DNA
 <213> Homo sapiens

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<400> 553
ctagccgatg taggattagt aggttttccg agcgtgggta aatctacctt actctcaata
60
gtatctaaag ccaaaccgaa aattggtgca tatcatttca ctacaattaa acctaactta
120
ggtggtgttt ccacaaaaga tcaacgtagt tttgttatgg cagatttacc aggtttaatt
180
gaaggtgcat ctgatggcgt tggattagga catcaatttt taagacatgt agagagaaca
240
aaagttattg ttcacatgat tgatatgagc ggttctgaag gtagagaacc tattgaagat
300
tataaagtca ttaatcaaga attagctgcg tacgagcaac gtttagaaga tagacctcaa
360
atcgtagtag ctaacaagat ggattttacct gaatcacaag ataatttaaa cttgttttaa
420
gaagaaattg gcgaagatgt gccagttatt ccagtttcaa caataacgcg t
471

```

<210> 554
 <211> 157
 <212> PRT
 <213> Homo sapiens

```

<400> 554
Leu Ala Asp Val Gly Leu Val Gly Phe Pro Ser Val Gly Lys Ser Thr
1          5          10          15
Leu Leu Ser Ile Val Ser Lys Ala Lys Pro Lys Ile Gly Ala Tyr His
          20          25          30
Phe Thr Thr Ile Lys Pro Asn Leu Gly Val Val Ser Thr Lys Asp Gln
          35          40          45
Arg Ser Phe Val Met Ala Asp Leu Pro Gly Leu Ile Glu Gly Ala Ser
          50          55          60
Asp Gly Val Gly Leu Gly His Gln Phe Leu Arg His Val Glu Arg Thr
65          70          75          80
Lys Val Ile Val His Met Ile Asp Met Ser Gly Ser Glu Gly Arg Glu
          85          90          95
Pro Ile Glu Asp Tyr Lys Val Ile Asn Gln Glu Leu Ala Ala Tyr Glu
          100          105          110
Gln Arg Leu Glu Asp Arg Pro Gln Ile Val Val Ala Asn Lys Met Asp
          115          120          125
Leu Pro Glu Ser Gln Asp Asn Leu Asn Leu Phe Lys Glu Glu Ile Gly

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130 135 140
 Glu Asp Val Pro Val Ile Pro Val Ser Thr Ile Thr Arg
 145 150 155

<210> 555
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 555
 tctagagatt gagaacaatt atggatacag aaatggttga ttccgtcaaa tatattcgag
 60
 attcgggaatc atgtgaggct cgcgtgctgg agatcttagc cagaaggccg tccatgatgg
 120
 tgcagatctt gcgtggcgac ggcttaatta acgaagacca gagattagtc agattatggc
 180
 ttaataaagt acctagaatt gttcgcctgc ttctccggct tagtgtgttc gtcgctgcgg
 240
 caataggtgc ccgtgcggta tgggcggcgg cttccggtaa tcccgatctt gttcacgcgt
 300

<210> 556
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 556
 Met Asp Thr Glu Met Val Asp Ser Val Lys Tyr Ile Arg Asp Ser Glu
 1 5 10 15
 Ser Cys Glu Ala Arg Val Leu Glu Ile Leu Ala Arg Arg Pro Ser Met
 20 25 30
 Met Val Gln Ile Leu Arg Gly Asp Gly Leu Ile Asn Glu Asp Gln Arg
 35 40 45
 Leu Val Arg Leu Trp Leu Asn Lys Val Pro Arg Ile Val Arg Leu Leu
 50 55 60
 Leu Arg Leu Ser Val Phe Val Ala Ala Ala Ile Gly Ala Arg Ala Val
 65 70 75 80
 Trp Ala Ala Ala Ser Gly Asn Pro Asp Leu Val His Ala
 85 90

<210> 557
 <211> 678
 <212> DNA
 <213> Homo sapiens

<400> 557
 atcttcccgg tttatgagga gaatgcgctg cgtgtcgagt ttttcggcga cgaaattgag
 60
 gccctcacga cgatgcaccc gctcaccggg gaggtcatca gcgaggacga gcaggtctac
 120
 gtgttcccgg ctaccacta tgtcgccggc ccggaacgta tggagcgggc catagcgtcc
 180
 atccagcagg agctcgagga gcgcctggcc gttctagagc gtgatgggaa actgttgagg
 240

gcccaacggt tacgtatgcg tactacctac gatatcgaga tgatgcagca ggtcgggtgcc
 300
 tgtgctggca tcgaaaacta ttcgeggac atcgacggac gcgctcccgg ctcagccccg
 360
 aactgtctgc ttgactactt tccggaagat tttgtgctcg tcattgatga atcccacgtg
 420
 accgtcccgc agattggcgg gatgtatgag ggggacatga gccgcaagcg gacattggta
 480
 gaacatggtt tccgactgcc cagcgcgatg gacaaccgtc ctctcaaatt cgacgagttc
 540
 acccagcgga tcggccagac tgtctacctg tccgccacgc ccggttcgta cgagaccgaa
 600
 cgagctcacg gcgtcgtcga acaaatcatt cgtccgacag gtctggtgga tccggagatt
 660
 atcgtcaagc ctacgcgt
 678

<210> 558

<211> 226

<212> PRT

<213> Homo sapiens

<400> 558

Ile	Phe	Pro	Val	Tyr	Glu	Glu	Asn	Ala	Leu	Arg	Val	Glu	Phe	Phe	Gly
1				5					10					15	
Asp	Glu	Ile	Glu	Ala	Leu	Thr	Thr	Met	His	Pro	Leu	Thr	Gly	Glu	Val
			20					25					30		
Ile	Ser	Glu	Asp	Glu	Gln	Val	Tyr	Val	Phe	Pro	Ala	Thr	His	Tyr	Val
	35					40					45				
Ala	Gly	Pro	Glu	Arg	Met	Glu	Arg	Ala	Ile	Ala	Ser	Ile	Gln	Gln	Glu
	50					55					60				
Leu	Glu	Glu	Arg	Leu	Ala	Val	Leu	Glu	Arg	Asp	Gly	Lys	Leu	Leu	Glu
65				70					75					80	
Ala	Gln	Arg	Leu	Arg	Met	Arg	Thr	Thr	Tyr	Asp	Ile	Glu	Met	Met	Gln
			85						90					95	
Gln	Val	Gly	Ala	Cys	Ala	Gly	Ile	Glu	Asn	Tyr	Ser	Arg	His	Ile	Asp
			100						105				110		
Gly	Arg	Ala	Pro	Gly	Ser	Ala	Pro	Asn	Cys	Leu	Leu	Asp	Tyr	Phe	Pro
	115					120						125			
Glu	Asp	Phe	Val	Leu	Val	Ile	Asp	Glu	Ser	His	Val	Thr	Val	Pro	Gln
	130					135						140			
Ile	Gly	Gly	Met	Tyr	Glu	Gly	Asp	Met	Ser	Arg	Lys	Arg	Thr	Leu	Val
145				150						155				160	
Glu	His	Gly	Phe	Arg	Leu	Pro	Ser	Ala	Met	Asp	Asn	Arg	Pro	Leu	Lys
			165						170					175	
Phe	Asp	Glu	Phe	Thr	Gln	Arg	Ile	Gly	Gln	Thr	Val	Tyr	Leu	Ser	Ala
			180						185					190	
Thr	Pro	Gly	Ser	Tyr	Glu	Thr	Glu	Arg	Ala	His	Gly	Val	Val	Glu	Gln
		195				200						205			
Ile	Ile	Arg	Pro	Thr	Gly	Leu	Val	Asp	Pro	Glu	Ile	Ile	Val	Lys	Pro
	210					215					220				
Thr	Arg														
225															

<210> 559
 <211> 335
 <212> DNA
 <213> Homo sapiens

<400> 559
 ggatcctatg gagctcaagt tcaagaaaag aaactgtaaa catggagggt ttgtgataaa
 60
 tggaatgcag tcagagggaa ggaactgccn gcttaaagtg tcctatgctg cgctttccag
 120
 agcaatacag tacacagtgg agggcgctac catggagtct ctgggtgaaa gttaggatgg
 180
 tatggtggca ccagccaaac ttctcagggt tcataggcag acagcagctc tggagtggaa
 240
 ctaaagtgtg tccaggagct gaagccctta atcagctagg gctcacacag agtcaaggta
 300
 ggggtcaaaaa cattcagtct gggaccatat ctaga
 335

<210> 560
 <211> 92
 <212> PRT
 <213> Homo sapiens

<400> 560
 Met Glu Cys Ser Gln Arg Glu Gly Thr Ala Xaa Leu Lys Cys Pro Met
 1 5 10 15
 Leu Arg Phe Pro Glu Gln Tyr Ser Thr Gln Trp Arg Ala Leu Pro Trp
 20 25 30
 Ser Leu Trp Val Lys Val Arg Met Val Trp Trp His Gln Pro Asn Phe
 35 40 45
 Ser Gly Phe Ile Gly Arg Gln Gln Leu Trp Ser Gly Thr Lys Val Tyr
 50 55 60
 Pro Gly Ala Glu Ala Leu Asn Gln Leu Gly Leu Thr Gln Ser Gln Gly
 65 70 75 80
 Arg Val Lys Asn Ile Gln Ser Gly Thr Ile Ser Arg
 85 90

<210> 561
 <211> 477
 <212> DNA
 <213> Homo sapiens

<400> 561
 ngcgcgcccc ctctccgat ggcggcggag atccagccca agcctctgac ccgcaagccg
 60
 atcctgctgc agcggatgga ggggtcccag gaggtggtga atatggccgt gatcgtgccc
 120
 aaagaggagg gcgtcatcag cgtctccgag gacaggacag ttcgtgtttg gttaaagaga
 180
 gacagtggac agtattggcc aagcgtatac catgcaatgc cttgagttta tattgtcaga
 240
 agattataac aagatgactc ctgtgaaaaa ctatcaagcg catcagagca gagtgacgat
 300

gacccctgttt gtcctggagc tggagtgggt gctgagcaca ggacaggaca agcaatttgc
 360
 ctggcactgc tctgagagtg ggcagcgcct gggaggttat cggaccagtg ctgtggcctc
 420
 aggcctgcaa tttgatgttg aaacccggca tgtgtttatc ggtgaccact caggcca
 477

<210> 562
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 562
 Xaa Ala Pro Pro Pro Pro Met Ala Ala Glu Ile Gln Pro Lys Pro Leu
 1 5 10 15
 Thr Arg Lys Pro Ile Leu Leu Gln Arg Met Glu Gly Ser Gln Glu Val
 20 25 30
 Val Asn Met Ala Val Ile Val Pro Lys Glu Glu Gly Val Ile Ser Val
 35 40 45
 Ser Glu Asp Arg Thr Val Arg Val Trp Leu Lys Arg Asp Ser Gly Gln
 50 55 60
 Tyr Trp Pro Ser Val Tyr His Ala Met Pro
 65 70

<210> 563
 <211> 403
 <212> DNA
 <213> Homo sapiens

<400> 563
 ccatggcaga cagggagctg agcggcctgc ggaccaggt gcaccagagc atggtgcccc
 60
 tgctcctaca cctgaaggac caatgcccaa ctgtcgccac gggcaatgcc caccccaaga
 120
 aaaggaaggg aaaaggcctc aaccttggcc agggctggaa cccacaggag gccaggggtac
 180
 ggggcagacg gatggcagca gcactgcctg agagtgggg gagctccac ggggcagcaa
 240
 gtggcgggca gagggctctg ccatctgcac tggtttctgt gaccacagtt ggcctgcccc
 300
 ctccccact gcaccactga cgaagcgaga ccctgcctca aaaaaaaaaa caaaaacaaa
 360
 aacaaaaaca aaactcaaac ttcacactgg agatctgtgc aat
 403

<210> 564
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 564
 Met Ala Asp Arg Glu Leu Ser Gly Leu Arg Thr Gln Val His Gln Ser
 1 5 10 15
 Met Val Pro Leu Leu Leu His Leu Lys Asp Gln Cys Pro Thr Val Ala

	20		25		30										
Thr	Gly	Asn	Ala	His	Pro	Lys	Lys	Arg	Lys	Gly	Lys	Gly	Leu	Asn	Leu
	35		40		45										
Gly	Gln	Gly	Trp	Asn	Pro	Gln	Glu	Ala	Arg	Val	Arg	Gly	Arg	Arg	Met
	50		55		60										
Ala	Ala	Ala	Leu	Pro	Glu	Ser	Trp	Gly	Ser	Ser	His	Gly	Ala	Ala	Ser
65			70		75									80	
Gly	Gly	Gln	Arg	Val	Trp	Pro	Ser	Ala	Leu	Val	Ser	Val	Thr	Thr	Val
			85		90									95	
Gly	Leu	Pro	Ala	Pro	Pro	Leu	His	His							
	100				105										

<210> 565
 <211> 311
 <212> DNA
 <213> Homo sapiens

<400> 565
 ncctctccat ggagcagccc catcttcact cttcacctgg ggccaggcct tccacagcag
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 ccaccaccca gcgaccacag agaggctgcg cggaggacac aggagagagg gagcccacgg
 120
 gcacgatctc caccggcttt cccagctccc tgggtcagcc ccacgggacc tctctctctc
 180
 tctcccatat ctccaagcca gccttgcata tagtaagagc tgtgatcagg atggaaagag
 240
 gcttgggccc cacagacctg gacaatgtcc cagtgagggc tggaggtgct agaagggcac
 300
 aggaggcccc n
 311

<210> 566
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 566
 Met Glu Gln Pro His Leu His Ser Ser Pro Gly Ala Arg Pro Ser Thr
 1 5 10 15
 Ala Ala Thr Thr Gln Arg Pro Gln Arg Gly Cys Ala Glu Asp Thr Gly
 20 25 30
 Glu Arg Glu Pro Thr Gly Thr Ile Ser Thr Gly Phe Pro Ser Ser Leu
 35 40 45
 Gly Gln Pro His Gly Thr Ser Pro Pro Leu Ser His Ile Ser Lys Pro
 50 55 60
 Ala Leu His Ile Val Arg Ala Val Ile Arg Met Glu Arg Gly Leu Gly
 65 70 75 80
 Arg Thr Asp Leu Asp Asn Val Pro Val Arg Ala Gly Gly Ala Arg Arg
 85 90 95
 Ala Gln Glu Ala Pro
 100

<210> 567
 <211> 929

<212> DNA

<213> Homo sapiens

<400> 567

atcacatcgg tcgctgaacc ccgacgagcc tcaccttgct gaaatattca tccttgagat
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 cagcccacgt gccgtcgacc tctacctcgg tgagggctgc gggcgggtac caacagccga
 120
 cctcgtcctc ggctccactc atggcgga caa gttccgctgc cagtccgggg atcgtcgggg
 180
 catgggcat gatgagcagg ttatccacat cgtcgtcgat ttctccgatg cgcgcagca
 240
 cggatcagt gccgcagtaa tagagggctc gcatgaattc gaccggacaa tccagttgga
 300
 ggcagtccca ggtctggcgg gtgcgtaggg catcggagac cagagcatgt ccaacattgc
 360
 gcagtcctaa acgcgtgccg acctcacggg cctgacggcg cccacgtcg gtgagcggac
 420
 gctcccgatc cccgcccga gcatgggatg cgggctgtgc atgtctcatg aggaacagag
 480
 tgtgcatgga tccatcggtg cacttcgcgg tcgccgcggt tctacgatgt tggcatgccg
 540
 ttgacggatt tgggcattga tgaggcgcgt acctaccgcc cgaacgtccc tgaacccgat
 600
 ggtttcgact ctttttgggc cgagaccctc gatgagtatt ccggcggtcc ccaagatctg
 660
 acggcgggtgc ctttcgataa ccgtcaggct ctgatagata cctgggattt gtcgtgggtg
 720
 gggatcacca actctcgggt gagcgggtga ttacatgccc cagccgctgt gaacggccca
 780
 ttcccccttg tcatcgagta cctcgggtac tcgagttcgc gtggtgtgcc gattggatca
 840
 gtcttcgctg ctgctggcta tgcacatata gtcgtcgatc cacgtgggtca ggggtggggc
 900
 caccacacct tgacggaaaa ctgtccgga
 929

<210> 568

<211> 71

<212> PRT

<213> Homo sapiens

<400> 568

Met	Pro	Leu	Thr	Asp	Leu	Gly	Ile	Asp	Glu	Ala	Arg	Thr	Tyr	Arg	Pro
1				5					10					15	
Asn	Val	Pro	Glu	Pro	Asp	Gly	Phe	Asp	Ser	Phe	Trp	Ala	Glu	Thr	Leu
			20					25					30		
Asp	Glu	Tyr	Ser	Gly	Val	Pro	Gln	Asp	Leu	Thr	Ala	Val	Pro	Phe	Asp
		35					40					45			
Asn	Arg	Gln	Ala	Leu	Ile	Asp	Thr	Trp	Asp	Leu	Ser	Trp	Val	Gly	Tyr
	50					55					60				
His	Asn	Ser	Arg	Val	Ser	Gly									
65						70									

<210> 569
 <211> 371
 <212> DNA
 <213> Homo sapiens

<400> 569
 ncgcaaactt caacggtgcc atctgccata ttccagggat gccagatttg gatggaaaat
 60
 accatatcac tctcgattca gaattcgtag ttgatttagt ggcctttaac aaaacgctac
 120
 ctgtcgatta cttaatgggtc gaaggaacgg aacttggtga ttcaaactg gaagaactac
 180
 ctgaatgccc atattatcca aaagatcaaa agccaatcgt gattgggaaa aacacaaaac
 240
 tcaaggaaca accaacagcc gttgctctct tctcggatgt tgataaacgg ccagagatta
 300
 aatcaaaaat cttagaccgc tatgataatg atattgaaat ccgtacttgg ggcggtactt
 360
 cccatgtcta n
 371

<210> 570
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 570
 Met Pro Asp Leu Asp Gly Lys Tyr His Ile Thr Leu Asp Ser Glu Phe
 1 5 10 15
 Val Leu Asp Leu Val Ala Phe Asn Lys Thr Leu Pro Val Asp Tyr Leu
 20 25 30
 Met Val Glu Gly Thr Glu Leu Val Tyr Ser Asn Met Glu Glu Leu Pro
 35 40 45
 Glu Cys Pro Tyr Tyr Pro Lys Asp Gln Lys Pro Ile Val Ile Gly Lys
 50 55 60
 Asn Thr Lys Leu Lys Glu Gln Pro Thr Ala Val Ala Leu Phe Ser Asp
 65 70 75 80
 Val Asp Lys Arg Pro Glu Ile Lys Ser Lys Ile Leu Asp Arg Tyr Asp
 85 90 95
 Asn Asp Ile Glu Ile Arg Thr Trp Gly Gly Thr Ser His Val Xaa
 100 105 110

<210> 571
 <211> 407
 <212> DNA
 <213> Homo sapiens

<400> 571
 nacgcgtatc ttcgctgggtc cacaccagac gtggcattaa acgacgtcac aagaacgaca
 60
 ccgggccttg acgggcccac gcacgaagag gccaaagacac tgaccgagac tactgtttcc
 120
 gttccacact ccttcgccga cctcggcggtc cgagaagata tctgccaggc gctggaaggg
 180

gtgggaattg tctccccgtt cccgatccag gccatgtcga tcccgattgc cgtcgagggc
 240
 acggatctta ttgggcaggg gcgtactggc actggcaaaa cactcgctt cggeatcacc
 300
 atcttgagc gcatcaccct gcccggtgac gaagggtggg aagaactcac caccaaaggc
 360
 aagcccccaa gcactcgtga tgtgcccta cccgggagct aggtcgg
 407

<210> 572
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 572
 Leu Thr Glu Thr Thr Val Ser Val Pro Thr Ser Phe Ala Asp Leu Gly
 1 5 10 15
 Val Arg Glu Asp Ile Cys Gln Ala Leu Glu Gly Val Gly Ile Val Ser
 20 25 30
 Pro Phe Pro Ile Gln Ala Met Ser Ile Pro Ile Ala Val Glu Gly Thr
 35 40 45
 Asp Leu Ile Gly Gln Ala Arg Thr Gly Thr Gly Lys Thr Leu Ala Phe
 50 55 60
 Gly Ile Thr Ile Leu Gln Arg Ile Thr Leu Pro Gly Asp Glu Gly Trp
 65 70 75 80
 Glu Glu Leu Thr Thr Lys Gly Lys Pro Pro Ser Thr Arg Asp Val Pro
 85 90 95
 Leu Pro Gly Ser
 100

<210> 573
 <211> 393
 <212> DNA
 <213> Homo sapiens

<400> 573
 acgcgtctac cgtaggatcc atgaccttcc gcaagaccga ccaccacaag aacgccattg
 60
 actacgaggt cgccggacta atgtggctcg ctgctgcccg gccagatggg gccggcatcg
 120
 tcgaggtgct cgaccacggc aagggatggc tcaccgaacc cgaattgtcc actgggcacc
 180
 ccaccgcga ggcagccgag gactttggcc gccgactggc tcacacccac gcagccgggg
 240
 cctcacacct gggggctgca cctgacgggt ttgttcccga cgatgggtat atcggccgtg
 300
 ctcccctgcc actgccgtcc gaaccaatct cctcctgggg agagttttac gctcagtgc
 360
 gcatcgaacc atatatggac agtctcgacg ctg
 393

<210> 574
 <211> 124
 <212> PRT

<213> Homo sapiens

<400> 574

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Met Thr Phe Arg Lys Thr Asp His His Lys Asn Ala Ile Asp Tyr Glu
 1           5           10           15
Val Ala Gly Leu Met Trp Leu Ala Ala Ala Arg Pro Asp Gly Ala Gly
          20           25           30
Ile Val Glu Val Leu Asp His Gly Lys Gly Trp Leu Thr Glu Pro Glu
          35           40           45
Leu Ser Thr Gly His Pro Thr Arg Glu Ala Ala Glu Asp Phe Gly Arg
          50           55           60
Arg Leu Ala His Thr His Ala Ala Gly Ala Ser His Leu Gly Ala Ala
65           70           75           80
Pro Asp Gly Phe Val Pro Asp Asp Gly Tyr Ile Gly Arg Ala Pro Leu
          85           90           95
Pro Leu Pro Ser Glu Pro Ile Ser Ser Trp Gly Glu Phe Tyr Ala Gln
          100          105          110
Cys Arg Ile Glu Pro Tyr Met Asp Ser Leu Asp Ala
          115          120

```

<210> 575

<211> 372

<212> DNA

<213> Homo sapiens

<400> 575

```

nntatccatg cagacatggg accaggggtct ctgagggcag gaagcaaagt gggtgagggg
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gatgggacaa gatgccctgg tgctaaggcc tctggagctg gagctgggta tagggatgat
120
accaggcacc ctgagtcact cgcacctcac aatggggccg cttctgggag ccagtgggct
180
tatggggctg gcaatgtgct gggttatgag gatggatcag aacttccagg gcctcagga
240
actgggggtca gaacagccta tggagaaagg tcaaggggcc ttgggcctag gagtacaggg
300
ccaggggggtg aggcaggctt tagagatggt tcaggaggcc tccaaggaat gggatcagca
360
gatgggccccg gt
372

```

<210> 576

<211> 124

<212> PRT

<213> Homo sapiens

<400> 576

```

Xaa Ile His Ala Asp Met Gly Pro Gly Ser Leu Arg Ala Gly Ser Lys
 1           5           10           15
Val Gly Glu Gly Asp Gly Thr Arg Cys Pro Gly Ala Lys Ala Ser Gly
          20           25           30
Ala Gly Ala Gly Tyr Arg Asp Asp Thr Arg His Pro Glu Ser Leu Ala
          35           40           45
Pro His Asn Gly Ala Ala Ser Gly Ser Gln Trp Ala Tyr Gly Ala Gly

```

```

      50      55      60
Asn Val Leu Gly Tyr Glu Asp Gly Ser Glu Leu Pro Gly Pro Gln Gly
65      70      75      80
Thr Gly Val Arg Thr Ala Tyr Gly Glu Arg Ser Arg Gly Leu Gly Pro
      85      90      95
Arg Ser Thr Gly Pro Gly Gly Glu Ala Gly Phe Arg Asp Gly Ser Gly
      100      105      110
Gly Leu Gln Gly Met Gly Ser Ala Asp Gly Pro Gly
      115      120

```

<210> 577
 <211> 432
 <212> DNA
 <213> Homo sapiens

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<400> 577
nagcgcaatg tcatgatgtc ggatttgtca atgtcggatt tctcatccca gccatcaccc
60
ccgcagcgcc gggcgcggat gaccagcggc cagcgccgtg aacagctcat cagcgtggcc
120
cgtcgcctct tcgcagacaa tggcatggca gggacctccg tcgaggagat cgccgctacc
180
gcgggagtct ccaaaccggt catctacgag catttcgggt ccaaggatgg gctgtacgcc
240
gtcgtcgtag accgcgaggt acgccaccta caagattccc tcaacgccgc catgaccgcg
300
ccaaagcaag gcccgaaacg caccctggag tcagcggtag tggccctgct ggactacatc
360
gacgaccgtc cagacggttt tcggatcatc tcgcgagact cctcggtcgg ttcagccacc
420
ggttcgtacg cg
432

```

<210> 578
 <211> 118
 <212> PRT
 <213> Homo sapiens

```

<400> 578
Met Thr Ser Gly Gln Arg Arg Glu Gln Leu Ile Ser Val Ala Arg Arg
1      5      10      15
Leu Phe Ala Asp Asn Gly Met Ala Gly Thr Ser Val Glu Glu Ile Ala
      20      25      30
Ala Thr Ala Gly Val Ser Lys Pro Val Ile Tyr Glu His Phe Gly Ser
      35      40      45
Lys Asp Gly Leu Tyr Ala Val Val Val Asp Arg Glu Val Arg His Leu
      50      55      60
Gln Asp Ser Leu Asn Ala Ala Met Thr Arg Pro Lys Gln Gly Pro Lys
65      70      75      80
Arg Thr Leu Glu Ser Ala Val Leu Ala Leu Leu Asp Tyr Ile Asp Asp
      85      90      95
Arg Pro Asp Gly Phe Arg Ile Ile Ser Arg Asp Ser Ser Val Gly Ser
      100      105      110
Ala Thr Gly Ser Tyr Ala

```

115

<210> 579
<211> 320
<212> DNA
<213> Homo sapiens

<400> 579
ggccccaac actccgacct cagctgggtcc agcatgctgg gcaccgtgct gctgctggcc
60
ctgctcccag ggatcaccac cttaccacagc gggccacctg ctcccccggt ccccgcggcg
120
cccggcccct ggctgcgagc acccctcttc agcctgaagc tgtccgacac agaggacgtc
180
tttcctcgcc gcgcggggcc gctcgaggtc ccggccgaca gccgcgtggt cgtgcaggcg
240
gccttggtcc gtccctcccc gcgctggggc ctggccctgc accgctgctc agtgacgccg
300
tcctcagcc cggccccggg
320

<210> 580
<211> 95
<212> PRT
<213> Homo sapiens

<400> 580
Met Leu Gly Thr Val Leu Leu Leu Ala Leu Leu Pro Gly Ile Thr Thr
1 5 10 15
Leu Pro Ser Gly Pro Pro Ala Pro Pro Phe Pro Ala Ala Pro Gly Pro
20 25 30
Trp Leu Arg Arg Pro Leu Phe Ser Leu Lys Leu Ser Asp Thr Glu Asp
35 40 45
Val Phe Pro Arg Arg Ala Gly Pro Leu Glu Val Pro Ala Asp Ser Arg
50 55 60
Val Phe Val Gln Ala Ala Leu Ala Arg Pro Ser Pro Arg Trp Gly Leu
65 70 75 80
Ala Leu His Arg Cys Ser Val Thr Pro Ser Ser Arg Pro Ala Pro
85 90 95

<210> 581
<211> 419
<212> DNA
<213> Homo sapiens

<400> 581
nacgacggca accattcgct gtggaaggag ctgaacggcc agctcgacgt gcagtttttc
60
cacgtcggca tgggcttcaa gacgccagta cgcattgcaca gcgtcgaccc caagaccgcg
120
gaagcccgcg aggtgcattt ccgcccgtcg ctgttcaact atgccaagac cacggtggac
180
accaagcagc tgaccggcga cctgggtttc tccggtttca agctgttcaa ggcgccggaa
240

ctggatcgcc atgacgtgct gtcgtttctc ggcgccagtt acttccgtgc ggtggacgca
 300
 acccgccagt acggcctctc cgcacgcggc ctggcgattg atacctacgc gaaaaaacgc
 360
 gaggaattcc ccgacttcac gcagttctgg ttcgaaaccc cgagcaagga cccacgcgt
 419

<210> 582
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 582
 Xaa Asp Gly Asn His Ser Leu Trp Lys Glu Leu Asn Gly Gln Leu Asp
 1 5 10 15
 Val Gln Phe Phe His Val Gly Met Gly Phe Lys Thr Pro Val Arg Met
 20 25 30
 His Ser Val Asp Pro Lys Thr Arg Glu Ala Arg Glu Val His Phe Arg
 35 40 45
 Pro Ser Leu Phe Asn Tyr Ala Lys Thr Thr Val Asp Thr Lys Gln Leu
 50 55 60
 Thr Gly Asp Leu Gly Phe Ser Gly Phe Lys Leu Phe Lys Ala Pro Glu
 65 70 75 80
 Leu Asp Arg His Asp Val Leu Ser Phe Leu Gly Ala Ser Tyr Phe Arg
 85 90 95
 Ala Val Asp Ala Thr Arg Gln Tyr Gly Leu Ser Ala Arg Gly Leu Ala
 100 105 110
 Ile Asp Thr Tyr Ala Lys Lys Arg Glu Glu Phe Pro Asp Phe Thr Gln
 115 120 125
 Phe Trp Phe Glu Thr Pro Ser Lys Asp Pro Arg
 130 135

<210> 583
 <211> 407
 <212> DNA
 <213> Homo sapiens

<400> 583
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 60
 gattatatgg agcagggatg ggagccggag acgctggtga acctagttgc cctcacgggc
 120
 tatagctatg cgaatttgga gcatgctgat catgatgtca agacgatgaa cgaactcatc
 180
 cgtgactttg agcttactcg tatctcccat acgcgagcca cactcccat ggacaagctt
 240
 gtgtttttga acaagcatca cttgacaaat aagctggcgc tcgccacgac gtgtgagcag
 300
 accaaacaag acctattgtc gcgtatccgg ccgatcacta cctcgtggta cggcgattat
 360
 tcagatgatt atatcctgcg cgtcgtaaca ctgggacccc aacgcgt
 407

<210> 584

<211> 135
 <212> PRT
 <213> Homo sapiens

<400> 584
 Leu Leu Ile Asn Ala Asp Gly Thr Lys Leu Ser Lys Arg Ser Gly Asp
 1 5 10 15
 Val Arg Val Ala Asp Tyr Met Glu Gln Gly Trp Glu Pro Glu Thr Leu
 20 25 30
 Val Asn Leu Val Ala Leu Thr Gly Tyr Ser Tyr Ala Asn Leu Glu His
 35 40 45
 Ala Asp His Asp Val Lys Thr Met Asn Glu Leu Ile Arg Asp Phe Glu
 50 55 60
 Leu Thr Arg Ile Ser His Thr Arg Ala Thr Leu Pro Met Asp Lys Leu
 65 70 75 80
 Val Phe Leu Asn Lys His His Leu Thr Asn Lys Leu Ala Leu Ala Thr
 85 90 95
 Thr Cys Glu Gln Thr Lys Gln Asp Leu Leu Ser Arg Ile Arg Pro Ile
 100 105 110
 Thr Thr Ser Trp Tyr Gly Asp Tyr Ser Asp Asp Tyr Ile Leu Arg Val
 115 120 125
 Val Thr Leu Gly Pro Gln Arg
 130 135

<210> 585
 <211> 502
 <212> DNA
 <213> Homo sapiens

<400> 585
 nnacgcgtcc tcgctggata tgaggctgtg aagaggggaac gctgcgtcat tgatctggac
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 gatattttgt tgtgcgcggt gggattgttg gttcagcacc gtgacatcac tgaggagatt
 120
 cgggctcggt accgacattt cggtgtcgac gaataccagg acgtttctcc gctgcagcat
 180
 aggttgcttg aactgtgggt tggcgatcga aatgatgtat gcgtcgtggg agatccgcac
 240
 caggccattc actcttatgc aggcgacga gctgactacc tcctcgactt cggtgccgat
 300
 catcctggcg ctaaacgcat cgatttggtt cgcaactacc gctccactcc cgagatcggt
 360
 cagttggcca atgaagttct tgtcaaccgt atgactccag aggaggcttt ggaacatggc
 420
 aggggagtca cattgggtttc gcggggtcga tccgggtccc agcccatcta tcaggctctc
 480
 ggggacgatg cctccgaagc tt
 502

<210> 586
 <211> 167
 <212> PRT
 <213> Homo sapiens

<400> 586

Xaa Arg Val Leu Ala Gly Tyr Glu Ala Val Lys Arg Glu Arg Cys Val
 1 5 10 15
 Ile Asp Leu Asp Asp Ile Leu Leu Cys Ala Val Gly Leu Leu Val Gln
 20 25 30
 His Arg Asp Ile Thr Glu Glu Ile Arg Ala Arg Tyr Arg His Phe Val
 35 40 45
 Val Asp Glu Tyr Gln Asp Val Ser Pro Leu Gln His Arg Leu Leu Glu
 50 55 60
 Leu Trp Phe Gly Asp Arg Asn Asp Val Cys Val Val Gly Asp Pro His
 65 70 75 80
 Gln Ala Ile His Ser Tyr Ala Gly Ala Arg Ala Asp Tyr Leu Leu Asp
 85 90 95
 Phe Val Ala Asp His Pro Gly Ala Lys Arg Ile Asp Leu Val Arg Asn
 100 105 110
 Tyr Arg Ser Thr Pro Glu Ile Val Gln Leu Ala Asn Glu Val Leu Val
 115 120 125
 Asn Arg Met Thr Pro Glu Glu Ala Leu Glu His Gly Arg Gly Val Thr
 130 135 140
 Leu Val Ser Arg Gly Arg Ser Gly Pro Glu Pro Ile Tyr Gln Ala Leu
 145 150 155 160
 Gly Asp Asp Ala Ser Glu Ala
 165

<210> 587

<211> 746

<212> DNA

<213> Homo sapiens

<400> 587

gcgtcctgcc tcgagggcct cgggagcttc cgctgcctct gttggccagg ctacagcggc
 60
 gagctgtgcg aggtggacga ggacgagtgt gcatcgagcc cctgccagca tgggggcccga
 120
 tgctgcagc gctctgaccc ggccctctac gggggtgtcc aggccgcctt ccctggcgcc
 180
 ttcagcttcc gccatgctgc gggtttctctg tgccactgcc ctcttggtt tgaggagacc
 240
 gactgcggtg tggaggtgga cgagtgtgcc tcacggccat gcctcaatgg aggccactgc
 300
 caggacctgc ccaatggctt ccagtgtcac tgcccagatg gctacgcagg gccgacatgt
 360
 gaggaagatg tggatgaatg cctgtccgat ccctgcctgc acggcggaac ctgcagtgc
 420
 actgtggcag gctatatctg caggtgcccga gagacctggg gtgggcccga ctgttctgtg
 480
 cagctcactg gctgccaggg ccacacctgc ccgctggctg ccacctgcat ccctatcttc
 540
 gagtctgggg tccacagtta cgtctgccac tgcccacctg gtacctatgg accgttctgt
 600
 ggccagaata ccaccttctc tgtgatggct gggagcccga ttcaggcatc agtgccagct
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 ggtggccccc tgggtctggc actgaggttt cgcaccacac tgcccgtgg gaccttgcc
 720

actcgcaatg acaccaagga aagctt
746

<210> 588
<211> 248
<212> PRT
<213> Homo sapiens

<400> 588
Ala Ser Cys Leu Glu Gly Leu Gly Ser Phe Arg Cys Leu Cys Trp Pro
1 5 10 15
Gly Tyr Ser Gly Glu Leu Cys Glu Val Asp Glu Asp Glu Cys Ala Ser
20 25 30
Ser Pro Cys Gln His Gly Gly Arg Cys Leu Gln Arg Ser Asp Pro Ala
35 40 45
Leu Tyr Gly Gly Val Gln Ala Ala Phe Pro Gly Ala Phe Ser Phe Arg
50 55 60
His Ala Ala Gly Phe Leu Cys His Cys Pro Pro Gly Phe Glu Gly Ala
65 70 75 80
Asp Cys Gly Val Glu Val Asp Glu Cys Ala Ser Arg Pro Cys Leu Asn
85 90 95
Gly Gly His Cys Gln Asp Leu Pro Asn Gly Phe Gln Cys His Cys Pro
100 105 110
Asp Gly Tyr Ala Gly Pro Thr Cys Glu Glu Asp Val Asp Glu Cys Leu
115 120 125
Ser Asp Pro Cys Leu His Gly Gly Thr Cys Ser Asp Thr Val Ala Gly
130 135 140
Tyr Ile Cys Arg Cys Pro Glu Thr Trp Gly Gly Arg Asp Cys Ser Val
145 150 155 160
Gln Leu Thr Gly Cys Gln Gly His Thr Cys Pro Leu Ala Ala Thr Cys
165 170 175
Ile Pro Ile Phe Glu Ser Gly Val His Ser Tyr Val Cys His Cys Pro
180 185 190
Pro Gly Thr His Gly Pro Phe Cys Gly Gln Asn Thr Thr Phe Ser Val
195 200 205
Met Ala Gly Ser Pro Ile Gln Ala Ser Val Pro Ala Gly Gly Pro Leu
210 215 220
Gly Leu Ala Leu Arg Phe Arg Thr Thr Leu Pro Ala Gly Thr Leu Ala
225 230 235 240
Thr Arg Asn Asp Thr Lys Glu Ser
245

<210> 589
<211> 381
<212> DNA
<213> Homo sapiens

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120
gtgggttggtg taacttcagc tttaggtcag cagccttcca tttccagttt ggctcaaccc
180

cagctacat attctcaggc ggctcctcca gtgcaaactc cccttccagg ggcaccacca
 240
 ccccaacagt tacagtatgg acaacagcaa ccaatgggtt ctacacagat ggccccaggc
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 catgtcaaat cagtgactca aaatcctgct tcagagtatg tacaacagca gccaatctt
 360
 caaacagcaa tgcctccgg a
 381

<210> 590
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 590
 Ile Ser Gln Val Gln Leu Gln Ser Gln Glu Leu Ser Tyr Gln Gln Lys
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 Gln Gly Leu Gln Pro Val Pro Leu Gln Ala Thr Met Ser Ala Ala Thr
 20 25 30
 Gly Ile Gln Pro Ser Pro Val Asn Val Val Gly Val Thr Ser Ala Leu
 35 40 45
 Gly Gln Gln Pro Ser Ile Ser Ser Leu Ala Gln Pro Gln Leu Pro Tyr
 50 55 60
 Ser Gln Ala Ala Pro Pro Val Gln Thr Pro Leu Pro Gly Ala Pro Pro
 65 70 75 80
 Pro Gln Gln Leu Gln Tyr Gly Gln Gln Gln Pro Met Val Ser Thr Gln
 85 90 95
 Met Ala Pro Gly His Val Lys Ser Val Thr Gln Asn Pro Ala Ser Glu
 100 105 110
 Tyr Val Gln Gln Gln Pro Ile Leu Gln Thr Ala Met Ser Ser Gly
 115 120 125

<210> 591
 <211> 684
 <212> DNA
 <213> Homo sapiens

<400> 591
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 gccaccgcgc cggtacgcaa cgagcagaag ctggggccgta acgaactgtg ctactgcggt
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 480

cttgtgacgg cagtgcagat atcacattaa aaggagggca ttcattgggtg ttggttctgg
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<210> 592
 <211> 133
 <212> PRT
 <213> Homo sapiens

<400> 592
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 20 25 30
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 35 40 45
 His Val Gln Gly Pro Gly Glu Lys Ser Val Ser Lys Xaa Lys Ala Arg
 50 55 60
 Leu Arg Gln Glu Ala Glu Ala Leu Ala Gln Arg Met Gln Phe Glu His
 65 70 75 80
 Ala Glu Ala Pro Gly Leu Asp Ala Pro Glu Ile Leu Gly Glu Glu Val
 85 90 95
 Asp Val Ala Leu Ala Thr Ala Pro Val Arg Asn Glu Gln Lys Leu Gly
 100 105 110
 Arg Asn Glu Leu Cys Tyr Cys Gly Ser Gly Lys Lys Tyr Lys His Cys
 115 120 125
 His Gly Gln Ile Ser
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<210> 593
 <211> 615
 <212> DNA
 <213> Homo sapiens

<400> 593
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 180
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 480
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<210> 594
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 594
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 Pro Leu Arg Ala Ala Arg Phe Thr Asp Thr Ile Pro Ala Pro Leu Gly
 35 40 45
 Gln Pro Arg Trp Ser Thr Ala Thr Ile Gln Thr Pro Val Ile Pro Thr
 50 55 60
 Thr Arg Gly Arg Phe Val Ile Gly Pro Val Met Met Arg Thr Ile Asp
 65 70 75 80
 Pro Phe Gly Met Ala Arg His His Thr Asp Leu Gly Gln Val Ala Glu
 85 90 95
 Val Ile Val Thr Pro Arg Ile Val Asp Leu Gly Ala Ser Gly Glu Leu
 100 105 110
 Gly Gly Gln Gly Phe Asp Thr Arg Ser Ser Ala Ile His Ala Gly Arg
 115 120 125
 Arg Gly Pro Asp Asp Ala Met Val Arg Asp Trp His Thr Gly Asp Ser
 130 135 140
 Val Arg Arg Ile His Trp Arg Ser Thr Ala His Arg Gly Asp Leu Met
 145 150 155 160
 Val Arg Cys Glu Glu Gln Ala Trp Asn Pro Ser Val Val Ile Val Leu
 165 170 175
 Asp Ser Arg Ala Arg Arg His Ala Gly Thr Gly Pro Asp Ala Ser Phe
 180 185 190
 Glu Trp Ala Val Asn Ala Val Ala Ser Ile Ser Thr Arg
 195 200 205

<210> 595
 <211> 303
 <212> DNA
 <213> Homo sapiens

<400> 595
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<210> 596
 <211> 88
 <212> PRT
 <213> Homo sapiens

<400> 596
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 20 25 30
 Ala Arg Leu Cys Pro Gln Pro Pro Arg Asn Ser Leu Pro Gly Thr Val
 35 40 45
 Ser Ala Leu Arg Ser Pro Glu Gln Gly Ser Glu Lys Cys Pro Ser Gln
 50 55 60
 Lys His Gly Thr Cys Leu Ser Ser Gly Lys Ser Ser Lys Ser Gly Trp
 65 70 75 80
 Asp Gln Gly Pro Arg Asp Leu Val
 85

<210> 597
 <211> 2709
 <212> DNA
 <213> Homo sapiens

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 660

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 2700
 aaaaaaaaaa
 2709

<210> 598

<211> 240

<212> PRT

<213> Homo sapiens

<400> 598

Xaa	Ala	Cys	Thr	Gln	Cys	Gly	Lys	Ala	Phe	Arg	Trp	Lys	Ser	Asn	Phe	1	5	10	15
Asn	Leu	His	Lys	Lys	Asn	His	Met	Val	Glu	Lys	Thr	Tyr	Glu	Cys	Lys	20	25	30	
Glu	Cys	Gly	Lys	Ser	Phe	Gly	Asp	Leu	Val	Ser	Arg	Arg	Lys	His	Met	35	40	45	
Arg	Ile	His	Ile	Val	Lys	Lys	Pro	Val	Glu	Cys	Arg	Gln	Cys	Gly	Lys	50	55	60	
Thr	Phe	Arg	Asn	Gln	Ser	Ile	Leu	Lys	Thr	His	Met	Asn	Ser	His	Thr	65	70	75	80
Gly	Glu	Lys	Pro	Tyr	Gly	Cys	Asp	Leu	Cys	Gly	Lys	Ala	Phe	Ser	Ala	85	90	95	
Ser	Ser	Asn	Leu	Thr	Ala	His	Arg	Lys	Ile	His	Thr	Gln	Glu	Arg	Arg	100	105	110	
Tyr	Glu	Cys	Ala	Ala	Cys	Gly	Lys	Val	Phe	Gly	Asp	Tyr	Leu	Ser	Arg	115	120	125	
Arg	Arg	His	Met	Ser	Val	His	Leu	Val	Lys	Lys	Arg	Val	Glu	Cys	Arg	130	135	140	
His	Cys	Gly	Lys	Ala	Phe	Arg	Asn	Gln	Ser	Thr	Leu	Lys	Thr	His	Met	145	150	155	160
Arg	Ser	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Asp	His	Cys	Gly	Lys	165	170	175	
Ala	Phe	Ser	Ile	Gly	Ser	Asn	Leu	Asn	Val	His	Arg	Arg	Ile	His	Thr	180	185	190	
Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Leu	Val	Cys	Gly	Lys	Ala	Phe	Ser	Asp	195	200	205	
His	Ser	Ser	Leu	Arg	Ser	His	Val	Lys	Thr	His	Arg	Gly	Glu	Lys	Leu	210	215	220	
Phe	Xaa	Cys	His	Pro	Cys	Gly	Lys	Gly	Ser	Ser	Glu	Arg	Ala	Xaa	Leu	225	230	235	240

<210> 599
 <211> 340
 <212> DNA
 <213> Homo sapiens

<400> 599
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 240
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 cacccggcga tgggtgctcca gatcgtccag ggcgatgatca
 340

<210> 600
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 600
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 Arg Ala Lys Pro Ser Pro Leu Thr Ser Ser Ser Ser Asp Glu Pro His
 20 25 30
 Ser Leu Pro Thr Arg Ser Ser Arg Gly Thr Pro Thr His Gly Ser Asn
 35 40 45
 Cys Arg Pro Ala Pro Arg Pro Ile Gly His Gly Leu Gln Val Gln Gly
 50 55 60
 Met Arg Pro Gly Lys His Ala Trp Ala Lys Arg Cys Arg Leu Arg Cys
 65 70 75 80
 Thr Ala Thr Pro Ser Thr Cys Ala Met Thr Pro Asn Lys Arg Ser Asp
 85 90 95
 Thr Thr Glu Arg Ser His His Asp Val Lys Ser Arg Glu Ala Arg
 100 105 110

<210> 601
 <211> 421
 <212> DNA
 <213> Homo sapiens

<400> 601
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 ccgcgctcca ccattttgat ggacggcgtc ccgctggcgg tcgcgcctta cggccagccg
 120
 cagctgtcga tggccccgct gtctatcggt aatctgcaat cgggtggacgt ggtgcgcggc
 180
 ggcggcgcgg tgcgctacgg gccgcagaac gtcggcggcg tgatcaactt cgttacccga
 240

gacattccca aaacgttttg cggtgccgcc agcgtacaaa ccaggggtgc cagccacggc
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ggcctgaaga ccctgaccag cgcctccgtg ggcggcaccg cagacaacgg cctcggcgcc
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gagctgctct actccggcct gcacggccag ggctaccgcg acaacaacga caacaccgac
420
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421

<210> 602
<211> 140
<212> PRT
<213> Homo sapiens

<400> 602
Ala Gly Gly Ser Asp Ile Ser Leu Asn Val Gly Val Arg Gly Leu Thr
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Ser Arg Leu Ser Pro Arg Ser Thr Ile Leu Met Asp Gly Val Pro Leu
20 25 30
Ala Val Ala Pro Tyr Gly Gln Pro Gln Leu Ser Met Ala Pro Leu Ser
35 40 45
Ile Gly Asn Leu Gln Ser Val Asp Val Val Arg Gly Gly Gly Ala Val
50 55 60
Arg Tyr Gly Pro Gln Asn Val Gly Gly Val Ile Asn Phe Val Thr Arg
65 70 75 80
Asp Ile Pro Lys Thr Phe Gly Gly Ala Ala Ser Val Gln Thr Gln Gly
85 90 95
Ala Ser His Gly Gly Leu Lys Thr Leu Thr Ser Ala Ser Val Gly Gly
100 105 110
Thr Ala Asp Asn Gly Leu Gly Ala Glu Leu Leu Tyr Ser Gly Leu His
115 120 125
Gly Gln Gly Tyr Arg Asp Asn Asn Asp Asn Thr Asp
130 135 140

<210> 603
<211> 309
<212> DNA
<213> Homo sapiens

<400> 603
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180
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240
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cgtaacgcg
309

<210> 604

<211> 103
 <212> PRT
 <213> Homo sapiens

<400> 604
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 Asp Lys Ile Gly Phe Asp Gly Leu Ala Ile Gly Gly Leu Ser Val Gly
 20 25 30
 Glu Pro Lys His Glu Met Ile Lys Val Leu Asp Tyr Leu Pro Gly Leu
 35 40 45
 Met Pro Ala Asp Lys Pro Arg Tyr Leu Met Gly Val Gly Lys Pro Glu
 50 55 60
 Asp Leu Val Glu Gly Val Arg Arg Gly Val Asp Met Phe Asp Cys Val
 65 70 75 80
 Met Pro Thr Arg Asn Ala Arg Asn Gly His Leu Phe Ile Asp Thr Gly
 85 90 95
 Val Leu Lys Ile Arg Asn Ala
 100

<210> 605
 <211> 428
 <212> DNA
 <213> Homo sapiens

<400> 605
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 180
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<210> 606
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 606
 Met Asp Glu Leu Thr Asn Tyr Thr Tyr Leu Ala Gln Ala Tyr Thr Ile
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 20 25 30
 Ser Glu Ala Ile Asn Val Leu Thr Ala Ser Leu Ser Gln Asp Val Ala

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      35              40              45
Trp Gly Pro Leu His Trp Glu Ser Val Ile Thr Phe Gln Asn Ser Ser
      50              55              60
Ser Gln Thr Ala Leu Pro Leu Pro Lys Leu Asn Ile Tyr Ser Asn Leu
65              70              75              80
Phe Phe Arg Leu Lys Ile Ala Lys Val Leu Lys Cys Asp Val Gly Ala
      85              90              95
Asp Val Arg Tyr Phe Thr Lys Tyr Tyr Ala Pro Asp Tyr Ser Pro Ala
      100             105             110
Leu Gly Gln Phe Val Val Gln Glu Asn Thr Asp Arg Val Glu Ile Gly
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Asn Tyr Pro Ile Val Asn Ala
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<210> 607
 <211> 366
 <212> DNA
 <213> Homo sapiens

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<400> 607
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gttttcaacg gcaaacatta tcaaattgta aagaaagagg atgacctatt caaattgacc
180
aaaagcaatt gttacaagtt gagcaacata aaatttaaca attggaaata cttgtacttg
240
acaacgcacg gtgtgtacaa cgtgttcacc aacagctttc attcgagctg tccatttttg
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366

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<210> 608
 <211> 122
 <212> PRT
 <213> Homo sapiens

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<400> 608
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Asn Val Val Thr Gly Val Asn Leu Val Phe Asn Gly Lys His Tyr Gln
      35              40              45
Ile Val Lys Lys Glu Asp Asp Leu Phe Lys Leu Thr Lys Ser Asn Cys
      50              55              60
Tyr Lys Leu Ser Asn Ile Lys Phe Asn Asn Trp Lys Tyr Leu Tyr Leu
65              70              75              80
Thr Thr His Gly Val Tyr Asn Val Phe Thr Asn Ser Phe His Ser Ser
      85              90              95
Cys Pro Phe Leu Leu Gly Thr Thr Leu Pro Gln Thr Phe Lys Lys Pro

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<210> 609
 <211> 291
 <212> DNA
 <213> Homo sapiens

<400> 609
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 291

<210> 610
 <211> 69
 <212> PRT
 <213> Homo sapiens

<400> 610
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 20 25 30
 Pro Lys Pro Gln Thr Ser Pro Ala Pro Tyr Ala Gly Pro Ala Pro Lys
 35 40 45
 Thr Pro Ala Thr Pro Gly Pro Ser Gly Ala Gly Ala Pro Pro Trp Trp
 50 55 60
 Trp Arg Val Glu Pro
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<210> 611
 <211> 393
 <212> DNA
 <213> Homo sapiens

<400> 611
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<210> 612

<211> 119

<212> PRT

<213> Homo sapiens

<400> 612

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			20					25					30		
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			35				40					45			
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			50			55					60				
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Met	Ala	Thr	Val	Leu	Glu	Ser	Tyr	Leu	Arg	Glu	Glu	Phe	Pro	Ser	Ser
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Glu	Ile	Arg	Ser	Asp	Ser	Gln	Asn	Lys	Ser	Ile	Asp	Glu	Thr	Ile	Ser
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<211> 567

<212> DNA

<213> Homo sapiens

<400> 613

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 <211> 187
 <212> PRT
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 35 40 45
 Ser Glu Phe Ala Val Ser Asn Ala Phe Phe Thr Arg Asn Ser Asp Leu
 50 55 60
 Pro Arg Ser Pro Trp Gly Gln Ile Thr Asp Leu Lys Thr Ser Glu Gln
 65 70 75 80
 Ile Glu Asp His Asp Glu Ile Tyr Ala Glu Ala Gln Glu Leu Val Asn
 85 90 95
 Asp Trp Leu Asp Thr Lys Leu Lys Gln Glu Leu Ala Ser Glu Glu Glu
 100 105 110
 Gly Asp Ala Lys Asn Thr Val Ser Ser Val Thr Ile Met Pro Glu Ala
 115 120 125
 Asn Gly His Leu Lys Tyr Asp Lys Phe Asp Asp Leu Cys Gly Tyr Leu
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 <212> DNA
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 <211> 213
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 35 40 45
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 50 55 60
 Ala Ala Lys Arg Glu Ala Leu Phe Asn Val Ile Met Asp Lys Ala Leu
 65 70 75 80
 Ala Val Ser Trp Val Arg Val Glu Ala Asp Glu Cys Asp Arg Leu Gly
 85 90 95
 Met Gln Glu Ala Asp Ile Ser Gly Leu Arg Arg Ala Val Val Arg Leu
 100 105 110
 Gly Val Glu Pro Gly Tyr Val Leu Ser Asp Gly Phe Pro Val Asp Gly
 115 120 125
 Leu Thr Val Pro Asp Leu Gly Met Trp Lys Gly Asp Ser Val Cys Ala
 130 135 140
 Cys Val Ala Ala Ala Ser Ile Val Ala Lys Val Ala Arg Asp Arg Ile
 145 150 155 160
 Met Ile Ala Met Asp Ala Glu Ile Pro Gly Tyr Asp Phe Ala Val His
 165 170 175
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 <211> 337
 <212> DNA
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<210> 618
<211> 112
<212> PRT
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Arg Cys Arg Ser Thr Thr Ser Ser Ser Ala Pro Thr Ala Ser Ala Arg
35 40 45
Pro Cys Ser Ser Lys Thr Phe Pro Ala Phe Pro Glu Arg Ile Leu Arg
50 55 60
Asn Phe Asp Leu Ser Gln Gln Asp Ser Ala Leu Val Ile Ser Ser Ser
65 70 75 80
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Ala Ser Ala Ser Ser Arg Ser Ser Arg Trp Arg Thr Arg Arg Arg Arg
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 35 40 45
 Ser Ile Lys Val Met Ile His Ser Lys Ser Gly Ser Gly Lys His Gly
 50 55 60
 His Asn Leu Asp Asp Leu Ile Glu His Leu Ser Lys Phe Glu Ser Gly
 65 70 75 80
 Ile Asp Ser Ser Gly Leu Ala Gly Leu Pro Ser Asp Lys Asp Ala Ile
 85 90 95
 Lys Leu Arg Tyr Ala Glu Met Ile Lys Thr Pro Ile Asp Ala Phe Glu
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 <211> 453
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<210> 622
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      35           40           45
Pro Val Glu Cys Val Val Arg Gly Tyr Leu Thr Gly Ser Gly Trp Ala
      50           55           60
Glu Tyr Gln Arg Asn Gln Ala Val Cys Gly Ile Arg Leu Pro Glu Gly
      65           70           75           80
Leu Gln Asn Gly Ser Arg Leu Glu Glu Pro Ile Phe Thr Pro Ala Ile
      85           90           95
Lys Ala Pro Gln Gly Glu His Asp Glu Asn Ile Asp Tyr Leu Arg Leu
      100          105          110
Val Glu Leu Val Gly Pro Xaa Xaa Ser Ala Gln Leu His Asp Leu Ser
      115          120          125
Leu Arg Val Tyr Gln Arg Ala Glu Glu Ile Ala Arg Lys Arg Gly Ile
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240
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345

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<210> 624
 <211> 111
 <212> PRT
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      20           25           30
Gly Thr Ile Ala Gln Ala Glu Asp Leu Pro Pro Asp Asp Thr His Thr
      35           40           45
Gly Ala Glu Leu Val Lys Ser Val Val Asn Ser Ile Thr Cys Val Ser
      50           55           60
Pro Leu Tyr Ile Glu Asp Phe Thr Thr Ile Glu Ile Gln Gly Leu Gly

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65		70		75		80									
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 <211> 339
 <212> DNA
 <213> Homo sapiens

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<400> 626
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35 40 45
Ala Gln Cys Lys Gly Arg Gln Thr Cys Trp Ser Leu Gly Tyr Asp Pro
50 55 60
Glu Gln Ser Gly Gly Ala Glu Ser Ser Cys Leu Trp Ala Ser Ile Ala
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<211> 1294

<212> PRT

<213> Homo sapiens

<400> 628

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Ser Ser Asp Ser Gly Asp Leu Gly Lys Trp Gln Asp Lys Ile Thr Val						
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Cys Lys Phe Cys Ser Phe Ser Cys Glu Ser Ser Ser Ser Leu Lys Leu						
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Val Leu Leu Phe His Tyr Glu Ser Val His Glu Ser Gln Ala Ser Asp						
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Val Lys Gln Glu Ala Asn His Leu Gln Gly Ser Asp Gly Gln Gln Ser						

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Cys Gly Ile Val Phe Leu Asp Glu Val Met Tyr Ala Leu His Met Ser		1230
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Cys His Gly Asp Ser Gly Pro Phe Gln Cys Ser Ile Cys Gln His Leu		1245
	1250	1255
Cys Thr Asp Lys Tyr Asp Phe Thr Thr His Ile Gln Arg Gly Leu His		1260
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Thr Leu Pro Gly Arg Asn Trp Ile Asn Leu Gly Leu Leu Val Val Ile			
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Ile Ala Cys Gly Ile Trp Phe Ser Asn Val Ser Gly Gly Ile Ala Trp			
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Leu Pro Leu Ala Leu Leu Thr Leu Ala Ser Leu Phe Leu Gly Phe His			
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Phe Val Ala Ala Ile Gly Gly Ala Asp Met Pro Val Val Ile Ser Met			
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<211> 275

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<210> 636

<211> 619

<212> PRT

<213> Homo sapiens

<400> 636

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			20					25					30		
Tyr	Leu	Leu	Asp	Val	Val	Asp	Ser	Glu	Glu	Gln	Asp	Met	Ala	Leu	Asn
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Ile	His	Ala	Phe	Ser	Ala	Gly	Leu	Gly	Gly	Ala	Ile	Gly	Tyr	Val	Leu
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Gly	Gly	Leu	Asp	Trp	Thr	Gln	Thr	Phe	Leu	Gly	Ser	Trp	Phe	Arg	Thr
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Gln	Asn	Gln	Val	Leu	Phe	Phe	Phe	Ala	Ala	Ile	Ile	Phe	Thr	Val	Ser
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Val	Ala	Leu	His	Leu	Phe	Ser	Ile	Asp	Glu	Glu	Gln	Tyr	Ser	Pro	Gln
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Gln	Glu	Arg	Ser	Ala	Glu	Glu	Pro	Gly	Ala	Leu	Asp	Gly	Gly	Glu	Pro
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His	Gly	Val	Pro	Ala	Phe	Pro	Asp	Glu	Val	Gln	Ser	Glu	His	Glu	Leu
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Ala	Leu	Asp	Tyr	Pro	Asp	Val	Asp	Ile	Met	Arg	Ser	Lys	Ser	Asp	Ser
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Ala	Leu	His	Val	Pro	Asp	Thr	Ala	Leu	Asp	Leu	Glu	Pro	Glu	Leu	Leu
			165					170					175		
Phe	Leu	His	Asp	Ile	Glu	Pro	Ser	Ile	Phe	His	Asp	Ala	Ser	Tyr	Pro
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Ala	Thr	Pro	Arg	Ser	Thr	Ser	Gln	Glu	Leu	Ala	Lys	Thr	Lys	Leu	Pro
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Pro	Thr	Lys	Asp	Ala	Leu	Gly	Gly	Tyr	Thr	Arg	Val	Asp	Thr	Lys	Pro
			245					250					255		
Ser	Ala	Thr	Ser	Ser	Ser	Met	Arg	Arg	Arg	Arg	His	Ala	Phe	Arg	Arg
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Gln	Ala	Ser	Ser	Thr	Phe	Ser	Tyr	Tyr	Gly	Lys	Leu	Gly	Ser	His	Cys
	275					280					285				
Tyr	Arg	Tyr	Arg	Arg	Ala	Asn	Ala	Val	Val	Leu	Ile	Lys	Pro	Ser	Arg

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Ser Met Ser Asp Leu Tyr Asp Met Gln Lys Arg Gln Arg Gln His Arg				
305		310		315
His Arg Asn Gln Ser Gly Ala Thr Thr Ser Ser Gly Asp Thr Glu Ser				
	325		330	335
Glu Glu Gly Glu Gly Glu Thr Thr Val Arg Leu Leu Trp Leu Ser Met				
	340		345	350
Leu Lys Met Pro Arg Glu Leu Met Arg Leu Cys Leu Cys His Leu Leu				
	355		360	365
Thr Trp Phe Ser Val Ile Ala Glu Ala Val Phe Tyr Thr Asp Phe Met				
	370		375	380
Gly Gln Val Ile Phe Glu Gly Asp Pro Lys Ala Pro Ser Asn Ser Thr				
385		390		395
Ala Trp Gln Ala Tyr Asn Ala Gly Val Lys Met Gly Cys Trp Gly Leu				
	405		410	415
Val Ile Tyr Ala Ala Thr Gly Ala Ile Cys Ser Ala Leu Leu Gln Lys				
	420		425	430
Tyr Leu Asp Asn Tyr Asp Leu Ser Val Arg Val Ile Tyr Val Leu Gly				
	435		440	445
Thr Leu Gly Phe Ser Val Gly Thr Ala Val Met Ala Met Phe Pro Asn				
	450		455	460
Val Tyr Val Ala Met Val Thr Ile Ser Thr Met Gly Ile Val Ser Met				
465		470		475
Ser Ile Ser Tyr Cys Pro Tyr Ala Leu Leu Gly Gln Tyr His Asp Ile				
	485		490	495
Lys Gln Tyr Ile His His Ser Pro Gly Asn Ser Lys Arg Gly Phe Gly				
	500		505	510
Ile Asp Cys Ala Ile Leu Ser Cys Gln Val Tyr Ile Ser Gln Ile Leu				
	515		520	525
Val Ala Ser Ala Leu Gly Gly Val Val Asp Ala Val Gly Thr Val Arg				
	530		535	540
Val Ile Pro Met Val Ala Ser Val Gly Ser Phe Leu Gly Phe Leu Thr				
545		550		555
Ala Thr Phe Leu Val Ile Tyr Pro Asp Val Ser Glu Glu Ala Lys Glu				
	565		570	575
Glu Gln Lys Gly Leu Ser Ser Pro Leu Ala Gly Glu Gly Arg Ala Gly				
	580		585	590
Gly Asn Ser Glu Lys Pro Thr Val Leu Lys Leu Thr Arg Lys Glu Gly				
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Leu Gln Gly Pro Val Glu Thr Glu Ser Val Val				
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<210> 637

<211> 370

<212> DNA

<213> Homo sapiens

<400> 637

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<210> 638
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 638
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 35 40 45
 Ile Ala Ile Pro Val Phe Leu Thr Val Pro Asn Ile Ile Asn Ile Gly
 50 55 60
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 Ser Ala Met

<210> 639
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 639
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<210> 640
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 640

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 Ala Leu Phe Ala Asp Ser Gln Ser Ala Glu Ser Arg His Asp Met Gly
 20 25 30
 Gly Asp Ile Ile Pro Arg Phe Val Glu Ala Gly Asp Ala Gln Val Tyr
 35 40 45
 Asp Phe Cys Asp Asn Gln Val Pro Gly Thr Thr Glu Lys Asp Arg Asp
 50 55 60
 Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala Tyr His Asp Ala His Met
 65 70 75 80
 Asp Leu Val Ser Val Glu Pro Glu Phe Asn Leu Tyr Asn Pro Asp Trp
 85 90 95
 Pro Ile Trp Ser Ile Gln Glu Gln Ala Pro Gly Ala Lys Phe
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<210> 641

<211> 491

<212> DNA

<213> Homo sapiens

<400> 641

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<210> 642

<211> 163

<212> PRT

<213> Homo sapiens

<400> 642

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 20 25 30
 Pro Asn Thr Val Ser Asn Ser Ile Gly Asp Ile His Arg Asn Lys Arg
 35 40 45
 Lys Val Phe Ser Lys Ile Phe Ser His Glu Ala Leu Glu Ser Tyr Leu

50	55	60
Pro Lys Ile Gln Leu Val	Ile Gln Asp Thr Leu Arg Ala Trp Ser Ser	
65	70	75
His Pro Glu Ala Ile Asn Val	Tyr Gln Glu Ala Gln Lys Leu Thr Phe	80
	85	90
Arg Met Ala Ile Arg Val Leu Leu Gly Phe Ser Ile Pro Glu Glu Asp		95
	100	105
Leu Gly His Leu Phe Glu Val Tyr Gln Gln Phe Val Asp Asn Val Phe		110
	115	120
Ser Leu Pro Val Asp Leu Pro Phe Ser Gly Tyr Arg Arg Gly Ile Gln		125
	130	135
Ala Arg Gln Ile Leu Gln Lys Gly Leu Glu Lys Ala Ile Arg Glu Lys		140
145	150	155
Leu Gln Cys		160

<210> 643
 <211> 628
 <212> DNA
 <213> Homo sapiens

<400> 643
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 628

<210> 644
 <211> 209
 <212> PRT
 <213> Homo sapiens

<400> 644
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 Ala Glu Gln Asp Ala Ile Thr Leu Arg Glu Gly Gln Tyr Val Glu Val

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Leu	Asp	Ala	Ala	His	Pro	Leu	Arg	Trp	Leu	Val	Arg	Thr	Lys	Pro	Thr
	35		40		45										
Lys	Ser	Ser	Pro	Ser	Arg	Gln	Gly	Trp	Val	Ser	Pro	Ala	Tyr	Leu	Asp
	50		55		60										
Arg	Arg	Leu	Lys	Leu	Ser	Pro	Glu	Trp	Gly	Ala	Ala	Glu	Ala	Pro	Glu
65			70		75									80	
Phe	Pro	Gly	Glu	Ala	Val	Ser	Glu	Asp	Glu	Tyr	Lys	Ala	Arg	Leu	Ser
		85		90		95									
Ser	Val	Ile	Gln	Glu	Leu	Leu	Ser	Ser	Glu	Gln	Ala	Phe	Val	Glu	Glu
	100		105		110										
Leu	Gln	Phe	Leu	Gln	Ser	His	His	Leu	Gln	His	Leu	Glu	Arg	Cys	Pro
	115		120		125										
His	Val	Pro	Ile	Ala	Val	Ala	Gly	Gln	Lys	Ala	Val	Ile	Phe	Arg	Asn
	130		135		140										
Val	Arg	Asp	Ile	Gly	Arg	Phe	His	Ser	Ser	Phe	Leu	Gln	Glu	Leu	Gln
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Gln	Cys	Asp	Thr	Asp	Asp	Asp	Val	Ala	Met	Cys	Phe	Ile	Lys	Asn	Gln
		165		170		175									
Ala	Ala	Phe	Glu	Gln	Tyr	Leu	Glu	Phe	Leu	Val	Gly	Arg	Val	Gln	Ala
	180		185		190										
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<210> 645

<211> 417

<212> DNA

<213> Homo sapiens

<400> 645

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417

<210> 646

<211> 95

<212> PRT

<213> Homo sapiens

<400> 646

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	20	25	30
Gly Ser Val Leu Phe Arg Arg Tyr Trp Arg His Trp Leu Asp Ile Leu			
	35	40	45
Gln Pro Ser Gln Glu Ala Gln Lys Val Asp Val Ile Thr Thr Pro Ile			
	50	55	60
Phe Gln Met Lys Lys Leu Ser Leu Trp Asp Leu Arg Lys Leu Pro Glu			
65	70	75	80
Leu Glu Gln Leu Val Pro Gly Pro Tyr Thr His Ser Thr Val Ser			
	85	90	95

<210> 647

<211> 421

<212> DNA

<213> Homo sapiens

<400> 647

acgcgttttcg gttcttgagc gcttccacca attcagcggg ggtgagcggc ccctgtgcat
60cgcgagcag ggtgatcaga taggcgatat ccgcctcgtt cagttgcacg gtgtcggttat
120cggtagccat gcgtggcgaa ctcccttggc atgggaaaat cgggtgaggg caacggggcac
180agcaacagga cgtgtccctt gcggcacgtg gcaacacgtc agtatagcgc gtttccgccc
240ggatttccgt tgaatgaagg caagaagtcg ggcacgcac cactgctac cgctcggtgg
300tacgatagcc gcggcgccac caggttggtt acattccaaa cgcaacgcag gaaccgcgat
360gaacagcgtt tttcgcaaca aacccttat gacgctgggt ctggggcatt tcagtgtcga
420

c

421

<210> 648

<211> 90

<212> PRT

<213> Homo sapiens

<400> 648

Met Gly Lys Ser Gly Glu Ala Asn Gly His Ser Asn Arg Thr Cys Pro
1 5 10 15Leu Arg His Val Ala Thr Arg Gln Tyr Ser Ala Phe Pro Pro Gly Phe
20 25 30Pro Leu Asn Glu Gly Lys Lys Ser Gly Thr His Pro Pro Ala Thr Ala
35 40 45Arg Trp Tyr Asp Ser Arg Gly Ala Thr Arg Leu Ala Thr Phe Gln Thr
50 55 60Gln Arg Arg Asn Pro His Glu Gln Arg Phe Ser Gln Gln Thr Pro Tyr
65 70 75 80Asp Ala Gly Ser Arg Ala Phe Gln Cys Arg
85 90

<210> 649
 <211> 563
 <212> DNA
 <213> Homo sapiens

<400> 649
 cgcaacatgc ataaacacat gtgctcctcc gagactcagc tacttccttt gccctctctg
 60
 gacctcagtg tccaggcttg tgcatttagg ggctcagggt tgggctctgt gcctatgagc
 120
 cagtctatgt gtgcactgtc tgtctgtctg tccgtctgcc agcaaccttc aaggccccag
 180
 gagggaagg caccaatgga aggtgggggc agggaaggag gtagcgttga caagttccaa
 240
 tgtctggctt tccctcctgg aaaccccgag ctggggctgg ccccccttc ccttcctgtc
 300
 tctctcgtc aagcacgtcc cttctaagag cccctctctg cagacgcccc cagtggaacc
 360
 aagcctagat tcgctgccaa gaaggccgac attttttaga cttgccacgt taaaggggac
 420
 tgcacaggca cgcactcaaa tccccccctc catgtcctcc gcctgtgcac attcaggcaa
 480
 cccgaaacac acaaagacac ggttggacac agcggccacc tgtgcacaca ggaggtagca
 540
 catggagcgc atctgacccc ggg
 563

<210> 650
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 650
 Met His Lys His Met Cys Ser Ser Glu Thr Gln Leu Leu Pro Leu Pro
 1 5 10 15
 Ser Leu Asp Leu Ser Val Gln Ala Cys Ala Phe Arg Gly Ser Gly Leu
 20 25 30
 Gly Ser Val Pro Met Ser Gln Ser Met Cys Ala Leu Ser Val Cys Leu
 35 40 45
 Ser Val Cys Gln Gln Pro Ser Arg Pro Gln Glu Gly Lys Ala Pro Met
 50 55 60
 Glu Gly Gly Gly Arg Glu Gly Gly Ser Val Asp Lys Phe Gln Cys Leu
 65 70 75 80
 Ala Phe Pro Pro Gly Asn Pro Glu Leu Gly Leu Ala Pro Pro Ser Leu
 85 90 95
 Pro Val Ser Leu Ala Gln Ala Arg Pro Phe
 100 105

<210> 651
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 651

gaattcttca acaagctctc ctgctctagg atcaaggata gacctataca aggtccaaac
60
cataatggag tccatgggggt caaagttatc tcctggagct cagcagttga tggatatggt
120
taggtgtcag cagcggaatt gtattcccat tggagagcag cttcagtcgg tgttgggcaa
180
ttctggatac aagcatatga ttggactaca atcctcatct accttaggaa ccttaaacia
240
gtcgtcctcc acaccttttc cttttagaac tggattgaca tctgggaacg tgactgaaaa
300
cttacaagcg tacattgata aaagtacaca actgcctggt ggagagaatt c
351

<210> 652

<211> 95

<212> PRT

<213> Homo sapiens

<400> 652

Met	Glu	Ser	Met	Gly	Ser	Lys	Leu	Ser	Pro	Gly	Ala	Gln	Gln	Leu	Met
1				5				10						15	
Asp	Met	Val	Arg	Cys	Gln	Gln	Arg	Asn	Cys	Ile	Pro	Ile	Gly	Glu	Gln
			20					25					30		
Leu	Gln	Ser	Val	Leu	Gly	Asn	Ser	Gly	Tyr	Lys	His	Met	Ile	Gly	Leu
			35				40					45			
Gln	Ser	Ser	Ser	Thr	Leu	Gly	Thr	Leu	Asn	Lys	Ser	Ser	Ser	Thr	Pro
			50			55					60				
Phe	Pro	Phe	Arg	Thr	Gly	Leu	Thr	Ser	Gly	Asn	Val	Thr	Glu	Asn	Leu
65					70					75				80	
Gln	Ala	Tyr	Ile	Asp	Lys	Ser	Thr	Gln	Leu	Pro	Gly	Gly	Glu	Asn	
				85					90					95	

<210> 653

<211> 399

<212> DNA

<213> Homo sapiens

<400> 653

nncccgggtg gggctgggggt ggggccagca tcagaggagg acatgaccaa gctgtgcaac
60
caccggcgga aagctgttgc tatggcaact ctgtaccgca gcatggagac cacctgctca
120
cactcttctc ctggagaggg agcgagcccc caaatgttcc acactgtgtc cccagggccc
180
ccctctgccc gccctccctg tcgagtteet cctacaactc cacttaatgg gggcctggc
240
tccttcccc cagaaccacc ctcaagtttc caggcctttc ccactctagc aggccctggg
300
gggcttttcc cccaagggt tgctgacca gtcccttctg ggggcagtag cagccccgt
360
ttcttcccaa ggggcaatgc cccctetcca gccccacct
399

<210> 654

<211> 133
 <212> PRT
 <213> Homo sapiens

<400> 654

Xaa	Pro	Gly	Gly	Ala	Gly	Val	Gly	Pro	Ala	Ser	Glu	Glu	Asp	Met	Thr
1				5					10					15	
Lys	Leu	Cys	Asn	His	Arg	Arg	Lys	Ala	Val	Ala	Met	Ala	Thr	Leu	Tyr
			20					25					30		
Arg	Ser	Met	Glu	Thr	Thr	Cys	Ser	His	Ser	Ser	Pro	Gly	Glu	Gly	Ala
		35					40					45			
Ser	Pro	Gln	Met	Phe	His	Thr	Val	Ser	Pro	Gly	Pro	Pro	Ser	Ala	Arg
	50					55					60				
Pro	Pro	Cys	Arg	Val	Pro	Pro	Thr	Thr	Pro	Leu	Asn	Gly	Gly	Pro	Gly
65					70					75				80	
Ser	Leu	Pro	Pro	Glu	Pro	Pro	Ser	Val	Ser	Gln	Ala	Phe	Pro	Thr	Leu
				85					90					95	
Ala	Gly	Pro	Gly	Gly	Leu	Phe	Pro	Pro	Arg	Leu	Ala	Asp	Pro	Val	Pro
			100					105					110		
Ser	Gly	Gly	Ser	Ser	Ser	Pro	Arg	Phe	Leu	Pro	Arg	Gly	Asn	Ala	Pro
		115					120					125			
Ser	Pro	Ala	Pro	Pro											

<210> 655
 <211> 368
 <212> DNA
 <213> Homo sapiens

<400> 655

tgaaggaaat tctctatggc ttgtgttcat catgtagaac agcccatgag gagaatagga
 60
 gatgaggtgg gaagtgcact gggatctggg ggaagaagcc cgggggttcaa gactcagcta
 120
 ctgactgcat ggtgtcaaag gattcgggca tcctctctga ggctgagtct tcagatgaca
 180
 gtgagaacag ggacacctgc cctgcccttc tcacggggcg tgtgggcacc catgagcatg
 240
 cttgacaaat gcaagggtgcc atacaaacag gaactgcaca atctcaccgc ccggcctact
 300
 cagcattggt atttttacct ttacatctat atgaagatgt agttccattc cttttaactg
 360
 ttgttttc
 368

<210> 656
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 656

Met	Ala	Cys	Val	His	His	Val	Glu	Gln	Pro	Met	Arg	Arg	Ile	Gly	Asp
1				5					10					15	
Glu	Val	Gly	Ser	Ala	Leu	Gly	Ser	Gly	Gly	Arg	Ser	Pro	Gly	Phe	Lys

		20						25						30					
Thr	Gln	Leu	Leu	Thr	Ala	Trp	Cys	Gln	Arg	Ile	Arg	Ala	Ser	Ser	Leu				
		35						40						45					
Arg	Leu	Ser	Leu	Gln	Met	Thr	Val	Arg	Thr	Gly	Thr	Pro	Ala	Leu	Pro				
		50						55						60					
Phe	Ser	Arg	Gly	Val	Trp	Ala	Pro	Met	Ser	Met	Leu	Asp	Lys	Cys	Lys				
65						70					75				80				
Val	Pro	Tyr	Lys	Gln	Glu	Leu	His	Asn	Leu	Thr	Ala	Arg	Pro	Thr	Gln				
						85					90				95				
His	Cys	Tyr	Phe	Tyr	Leu	Tyr	Ile	Tyr	Met	Lys	Met								
					100						105								

<210> 657
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 657
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 60
 aacgaggcgg gcttcaagcg cgccctcgaa gagcgtggca tggccaacgc cggtgtcgag
 120
 cgtattcagg acagcgacct ggacgtggtg ccgcaattga cccgcctga aaaacgccgg
 180
 tgccgacacc ttgctgatgg tggcaacgt cgcccttcg gcacaggtgg tcaagtcct
 240
 ggaccgcatg ggttgggacg tgcctgtggt gtctcactgg gggccggccg gnggtcgctt
 300
 tggcgagctg gcggggccta acgcttctcg
 330

<210> 658
 <211> 102
 <212> PRT
 <213> Homo sapiens

Met	Lys	Lys	Pro	Gly	Met	Ile	Leu	Ile	Asn	Asn	Pro	Trp	Gly	Glu	Ser				
1				5					10					15					
Asn	Glu	Ala	Gly	Phe	Lys	Arg	Ala	Leu	Glu	Glu	Arg	Gly	Met	Ala	Asn				
				20				25					30						
Ala	Gly	Val	Glu	Arg	Ile	Gln	Asp	Ser	Asp	Leu	Asp	Val	Val	Pro	Gln				
		35					40					45							
Leu	Thr	Pro	Pro	Glu	Lys	Arg	Arg	Cys	Arg	His	Leu	Ala	Asp	Gly	Arg				
		50				55					60								
Gln	Arg	Arg	Pro	Phe	Gly	Thr	Gly	Gly	Gln	Val	Pro	Gly	Pro	His	Gly				
65				70					75					80					
Leu	Gly	Arg	Ala	Cys	Gly	Val	Ser	Leu	Gly	Ala	Gly	Arg	Xaa	Ser	Leu				
				85					90					95					
Trp	Arg	Ala	Gly	Gly	Ala														
				100															

<210> 659
 <211> 1505

<212> DNA

<213> Homo sapiens

<400> 659

gccaggatca tgtccaccac cacatgccaa gtggtggcgt tcctcctgtc catcctgggg
60
ctggccggct gcatcgcggc caccgggatg gacatgtgga gcacccagga cctgtacgac
120
aaccctgtca cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt gaggcagagt
180
tcaggcttca ccgaatgcag gccctatttc accatcctgg gacttccage catgctgcag
240
gcagtgcgag ccctgatgat cgtaggcate gtcctgggtg ccattggcct cctggtatcc
300
atctttgccc tgaaatgcat ccgcattggc agcatggagg actctgccaa agccaacatg
360
acactgacct ccgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct
420
gtgtttgcca acatgctggg gactaacttc tggatgtcca cagctaacat gtacaccggc
480
atgggtggga tgggtgcagac tgttcagacc aggtacacat ttggtgcggc tctgttcgtg
540
ggctgggtcg ctggaggcct cacactaatt ggggggtgtga tgatgtgcat cgcctgccgg
600
ggcctggcac cagaagaaac caactacaaa gccgtttctt atcatgcctc aggccacagt
660
gttgccctaca agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac
720
aagaagatat acgatggagg tgcccgcaca gaggacgagg tacaatctta tccttccaag
780
cacgactatg tgtaatgctc taagacctct cagcacgggc ggaagaaact cccggagagc
840
tcacccaaaa aacaaggaga tcccatctag atttcttctt gcttttgact cacagctgga
900
agttagaaaa gcctcgattt catctttgga gaggccaaagt ggtcttagcc tcagtctctg
960
tctctaaata ttccaccata aaacagctga gttatttatg aattagaagc tatagctcac
1020
attttcaatc ctctatttct ttttttaaat ataactttct actctgatga gagaatgtgg
1080
ttttaatctc tctctcacat tttgatgatt tagacagact cccctcttc ctctagtca
1140
ataaaccat tgatgatcta tttccagct tatccccaag aaaacttttg aaaggaaaga
1200
gtagacccaa agatgttatt ttctgctgtt tgaattttgt ctccccaccc ccaacttggc
1260
tagtaataaa cacttactga agaagaagca ataagagaaa gatatttgta atctctccag
1320
cccatgatct cggttttctt acactgtgat cttaaaagt accaaaccaa agtcattttc
1380
agtttgaggc aaccaaacct ttctactgct gttgacatct tcttattaca gcaacaccat
1440
tctaggagtt tcctgagctc tccactggag tcctccccct ctgtcgtctt ctgcgagcgg
1500

tacc

1505

<210> 660

<211> 261

<212> PRT

<213> Homo sapiens

<400> 660

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Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile Leu
 1          5          10          15
Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr
 20          25          30
Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln Tyr Glu Gly
 35          40          45
Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe Thr Glu Cys Arg
 50          55          60
Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met Leu Gln Ala Val Arg
 65          70          75          80
Ala Leu Met Ile Val Gly Ile Val Leu Gly Ala Ile Gly Leu Leu Val
 85          90          95
Ser Ile Phe Ala Leu Lys Cys Ile Arg Ile Gly Ser Met Glu Asp Ser
100          105          110
Ala Lys Ala Asn Met Thr Leu Thr Ser Gly Ile Met Phe Ile Val Ser
115          120          125
Gly Leu Cys Ala Ile Ala Gly Val Ser Val Phe Ala Asn Met Leu Val
130          135          140
Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Thr Gly Met Gly Gly
145          150          155          160
Met Val Gln Thr Val Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe
165          170          175
Val Gly Trp Val Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met
180          185          190
Cys Ile Ala Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala
195          200          205
Val Ser Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly
210          215          220
Phe Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile
225          230          235          240
Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro Ser
245          250          255
Lys His Asp Tyr Val
260

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<210> 661

<211> 451

<212> DNA

<213> Homo sapiens

<400> 661

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nnacgcgtgt agtttgtgta tcggcgcgga actcgccgcg tctgatctcg aggagcttcc
60
cccatggacg agattttaac cttgcttgcc ggaggcgggtg acgacgagcc agagtggcat
120

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gacaaggcat tatgtgcca gactgatccg gaggcattct tccctgaaaa ggggtggatcc
 180
 acccgtgagg ccaagcgcac ctgtgagtc tgtgaggtcc gccaggagtg cttggagtag
 240
 gcccttgcca atgacgagag gtccggaatc tggggcggat tgcctgagat ggagaggcgt
 300
 cggtcgcca agcgggcgtg acctgacgtc ggagcgcgtt tattgacacg gcccggtaaa
 360
 atgccctgtc tgcccgggat ggctgtctgc acgatgcggc atatgcgatg atgcgagacg
 420
 tgggtgtgcat cccgtgtctc atgacgtcga c
 451

<210> 662

<211> 85

<212> PRT

<213> Homo sapiens

<400> 662

Met	Asp	Glu	Ile	Leu	Thr	Leu	Leu	Ala	Gly	Gly	Gly	Asp	Asp	Glu	Pro
1				5					10					15	
Glu	Trp	His	Asp	Lys	Ala	Leu	Cys	Ala	Gln	Thr	Asp	Pro	Glu	Ala	Phe
			20					25					30		
Phe	Pro	Glu	Lys	Gly	Gly	Ser	Thr	Arg	Glu	Ala	Lys	Arg	Ile	Cys	Glu
		35				40					45				
Ser	Cys	Glu	Val	Arg	Gln	Glu	Cys	Leu	Glu	Tyr	Ala	Leu	Ala	Asn	Asp
	50				55				60						
Glu	Arg	Phe	Gly	Ile	Trp	Gly	Gly	Leu	Ser	Glu	Met	Glu	Arg	Arg	Arg
65				70				75					80		
Leu	Arg	Lys	Arg	Ala											
				85											

<210> 663

<211> 552

<212> DNA

<213> Homo sapiens

<400> 663

ctcgagcgtc tcgacgccga cgccgcccag ggagccaagg aagacctctc gcagcgcgac
 60
 ccctacgacg tgctcgtcgt aggggcgggt cccgcccgtg ccgcggccgc cgtgtacgcg
 120
 gctcgtaagg gcattcgcac cgccatggtc gggctctcga tcggcggcca ggtactcgat
 180
 accgaggcca tcgacaacct catctcgggt ccgcacacca ccggtccgcg tctggccgac
 240
 gccctccgca gccacgtcaa cgactacaac attgacgtta ttgagcgtca gaccgccagc
 300
 gccatagaga ccaccggcgg tatgaccacc gtgcatctga ccgacggcga cctgcgggcg
 360
 cgctcagtca tcgtggccac cggtgcccgc tggcgcaacc ttggcgtacc tggcgaggag
 420
 gaataccgca ccaagggtgt gacctactgc ccgcactgcg atggcccgtt attcacaggc
 480

aaaaaggtgg ccgtcgtcgg aggtggaaac tccggtattg aggccgctat cgacctcgcc
 540
 ggcgtcgtcg ac
 552

<210> 664
 <211> 184
 <212> PRT
 <213> Homo sapiens

<400> 664
 Leu Glu Arg Leu Asp Ala Asp Ala Ala Gln Gly Ala Lys Glu Asp Leu
 1 5 10 15
 Ser Gln Arg Asp Pro Tyr Asp Val Leu Val Val Gly Ala Gly Pro Ala
 20 25 30
 Gly Ala Ala Ala Val Tyr Ala Ala Arg Lys Gly Ile Arg Thr Ala
 35 40 45
 Met Val Gly Ser Arg Ile Gly Gly Gln Val Leu Asp Thr Glu Ala Ile
 50 55 60
 Asp Asn Leu Ile Ser Val Pro His Thr Thr Gly Pro Arg Leu Ala Asp
 65 70 75 80
 Ala Leu Arg Ser His Val Asn Asp Tyr Asn Ile Asp Val Ile Glu Arg
 85 90 95
 Gln Thr Ala Ser Ala Ile Glu Thr Thr Gly Gly Met Thr Thr Val His
 100 105 110
 Leu Thr Asp Gly Asp Leu Arg Ala Arg Ser Val Ile Val Ala Thr Gly
 115 120 125
 Ala Arg Trp Arg Asn Leu Gly Val Pro Gly Glu Glu Glu Tyr Arg Thr
 130 135 140
 Lys Gly Val Thr Tyr Cys Pro His Cys Asp Gly Pro Leu Phe Thr Gly
 145 150 155 160
 Lys Lys Val Ala Val Val Gly Gly Gly Asn Ser Gly Ile Glu Ala Ala
 165 170 175
 Ile Asp Leu Ala Gly Val Val Asp
 180

<210> 665
 <211> 352
 <212> DNA
 <213> Homo sapiens

<400> 665
 acgcgtacag ttcgccgtcg aggttgaaca ccacgatcgg tgtaccgggtc acttcgtcga
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 acacgtcttt catttcgccc ggcagcagtt cggcgccggc gcagacaaag gtccaggcct
 120
 cgctcacgcg gtggccccgg ccagcgggctt ttccaggatc tcgaaacgca ggtcgtcgcg
 180
 cttggggatg ccgaatcggt cgtcgccata cgggaacggc ttcttgatgc cggtgcgag
 240
 gtagccgcgg cgctcgtaga agcgatcaga tcgcgcgcac gtcgatcact gtcattctgca
 300
 ttaccggcac gttccattcg cgcgcggcgt gggcttcggc ggcgtccatc aa
 352

<210> 666
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 666
 Met Glu Arg Ala Gly Asn Ala Asp Asp Ser Asp Arg Arg Ala Arg Asp
 1 5 10 15
 Leu Ile Ala Ser Thr Ser Ala Ala Ala Thr Cys Ala Pro Ala Ser Arg
 20 25 30
 Ser Arg Ser Arg Met Ala Thr Asn Asp Ser Ala Ser Pro Ser Ala Thr
 35 40 45
 Thr Cys Val Ser Arg Ser Trp Lys Ser Arg Trp Pro Gly Pro Pro Arg
 50 55 60
 Glu Arg Gly Leu Asp Leu Cys Leu Arg Arg Arg Arg Thr Ala Ala Gly
 65 70 75 80
 Arg Asn Glu Glu Arg Val Arg Arg Ser Asp Arg Tyr Thr Asp Arg Gly
 85 90 95
 Val Gln Pro Arg Arg Arg Thr Val Arg
 100 105

<210> 667
 <211> 391
 <212> DNA
 <213> Homo sapiens

<400> 667
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 60
 cgggagatct ttgaatctct cggcccgggtg ctcgacaaga atccgcagta cgtggaggca
 120
 gccgtgttgt cgcgcatctg cgaaccggaa cgccagatca ttttccgggt gccgtgggtt
 180
 gacgacgagg gcaagatccg tatcaaccgt ggcttccgcg ttgaatatcc gtcggtactg
 240
 gggccgtata aggggtggatt gcgattccac ccctcgggtg acttaggaac gattaagttc
 300
 cttggttttg agcagatctt caaaaatgct ctgactggca tgccgatcgg tggcgcaag
 360
 ggtgggtcgg actttgatcc ccatgacgcg t
 391

<210> 668
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 668
 Xaa Ala Tyr Glu Ser Val Leu Arg Arg Asn Pro Gly Glu Ala Glu Phe
 1 5 10 15
 His Gln Ala Val Arg Glu Ile Phe Glu Ser Leu Gly Pro Val Leu Asp
 20 25 30
 Lys Asn Pro Gln Tyr Val Glu Ala Ala Val Leu Ser Arg Ile Cys Glu

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      35      40      45
Pro Glu Arg Gln Ile Ile Phe Arg Val Pro Trp Val Asp Asp Glu Gly
   50      55      60
Lys Ile Arg Ile Asn Arg Gly Phe Arg Val Glu Tyr Ser Ser Val Leu
65      70      75      80
Gly Pro Tyr Lys Gly Gly Leu Arg Phe His Pro Ser Val Tyr Leu Gly
      85      90      95
Thr Ile Lys Phe Leu Gly Phe Glu Gln Ile Phe Lys Asn Ala Leu Thr
      100      105      110
Gly Met Pro Ile Gly Gly Ala Lys Gly Gly Ser Asp Phe Asp Pro His
      115      120      125
Asp Ala
      130

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<210> 669
 <211> 707
 <212> DNA
 <213> Homo sapiens

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<400> 669
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attgagaaca cccttgcctgc ctccggccac gcggtcgagg tgggatgcac ctaccttgaa
120
actgacgttc acgcgaccag cgacgggggtg ctagtggcct tccacgatcc gatactcgat
180
cgcgtcactg aatcaggcgg agtcatcgcc gccatgccgt ggcacaaggt caaacaagcc
240
aaggttggtg gcgaaccgat cccacacctt gatgagattt tcgacgcctt tcccgcgcgg
300
ttcatcaata tcgacatcaa gcatgatggc gccaccatgc cgctcatcga cgttctttcc
360
cgtcaccggg cttggagtcg ggtttgcgtc gggtcgttca gcagtaaacg catccagacc
420
ttccgtcgcc tgggttcaggg acgcactgcg actgcagtgg ggtcgggtggg agtcnnggct
480
gggctgtcat cagccctcat agcatgcaga tggcacagtc ccatgggaat gcgtaccagg
540
tgccgcaccg cttgaccggg tnatgggggtg ccccttgtga caccgacctt cattaaagct
600
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<212> PRT

<213> Homo sapiens

<400> 672

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Asn Thr Val His Leu Lys Arg Pro Gly Arg Ile Thr Trp Val Thr Leu
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Cys Asp Arg His Tyr Leu Cys Ser Arg Ser Phe Ser Ser Cys Gln Tyr
65      70      75      80
Arg Ile Phe Arg Arg Arg Leu His Gln Lys Asn Val Gly Val Thr Ala
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Pro Gln Thr Met Arg Thr Leu Ala Leu Thr Met Glu Ala Leu Lys Ser
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Tyr	Asn	Gln	Pro	Ser	Asp	Thr	Arg	Gln	Tyr	His	Glu	Asn	Ile	Lys	Ile		
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Asn	Gln	Ala	Met	Arg	Lys	Lys	Leu	Ile	Leu	Tyr	Phe	Lys	Arg	Arg	Asn		
	275						280					285					
His	Ala	Arg	Lys	Gln	Trp	Glu	Gln	Lys	Phe	Cys	Gln	Arg	Tyr	Asp	Gln		
	290				295				300								
Leu	Met	Glu	Ala	Trp	Glu	Lys	Lys	Val	Glu	Arg	Ile	Glu	Asn	Asn	Pro		
305				310					315					320			
Arg	Arg	Arg	Ala	Lys	Glu	Ser	Lys	Val	Arg	Glu	Tyr	Tyr	Glu	Lys	Gln		
			325					330					335				
Phe	Pro	Glu	Ile	Arg	Lys	Gln	Arg	Glu	Leu	Gln	Glu	Arg	Met	Gln	Gly		
		340					345					350					
Arg	Val	Gly	Gln	Arg	Gly	Ser	Gly	Leu	Ser	Met	Ser	Ala	Ala	Arg	Ser		
	355					360					365						
Glu	His	Glu	Val	Ser	Glu	Ile	Ile	Asp	Gly	Leu	Ser	Glu	Gln	Glu	Asn		
	370				375				380								
Leu	Glu	Lys	Gln	Met	Arg	Gln	Leu	Ala	Val	Ile	Pro	Pro	Met	Leu	Tyr		
385				390					395					400			
Asp	Ala	Asp	Gln	Gln	Arg	Ile	Lys	Phe	Ile	Asn	Met	Asn	Gly	Leu	Met		
			405					410				415					
Ala	Asp	Pro	Met	Lys	Val	Tyr	Lys	Asp	Arg	Gln	Val	Met	Asn	Met	Trp		
		420						425				430					
Ser	Glu	Gln	Glu	Lys	Glu	Thr	Phe	Arg	Glu	Lys	Phe	Met	Gln	His	Pro		
	435					440					445						
Lys	Asn	Phe	Gly	Leu	Ile	Ala	Ser	Phe	Leu	Glu	Arg	Lys	Thr	Val	Ala		
	450				455				460								
Glu	Cys	Val	Leu	Tyr	Tyr	Tyr	Leu	Thr	Lys	Lys	Asn	Glu	Asn	Tyr	Lys		
465				470					475					480			
Ser	Leu	Val	Arg	Arg	Ser	Tyr	Arg	Arg	Arg	Gly	Lys	Ser	Gln	Gln	Gln		
			485					490				495					
Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Pro		
		500						505				510					
Met	Pro	Arg	Ser	Ser	Gln	Glu	Glu	Lys	Asp	Glu	Lys	Glu	Lys	Glu	Lys		
	515					520						525					
Glu	Ala	Glu	Lys	Glu	Glu	Glu	Lys	Pro	Glu	Val	Glu	Asn	Asp	Lys	Glu		
	530				535						540						
Asp	Leu	Leu	Lys	Glu	Lys	Thr	Asp	Asp	Thr	Ser	Gly	Glu	Asp	Asn	Asp		
545				550				555						560			
Glu	Lys	Glu	Ala	Val	Ala	Ser	Lys	Gly	Arg	Lys	Thr	Ala	Asn	Ser	Gln		
			565					570				575					
Gly	Arg	Arg	Lys	Gly	Arg	Ile	Thr	Arg	Ser	Met	Ala	Asn	Glu	Ala	Asn		
	580						585					590					
Ser	Glu	Glu	Ala	Ile	Thr	Pro	Gln	Gln	Ser	Ala	Glu	Leu	Ala	Ser	Met		

595	600	605
Glu Leu Asn Glu Ser Ser Arg Trp Thr Glu Glu Glu Met Glu Thr Ala		
610	615	620
Lys Lys Gly Leu Leu Glu His Gly Arg Asn Trp Ser Ala Ile Ala Arg		
625	630	635
Met Val Gly Ser Lys Thr Val Ser Gln Cys Lys Asn Phe Tyr Phe Asn		
645	650	655
Tyr Lys Lys Arg Gln Asn Leu Asp Glu Ile Leu Gln Gln His Lys Leu		
660	665	670
Lys Met Glu Lys Glu Arg Asn Ala Arg Arg Lys Lys Lys Lys Ala Pro		
675	680	685
Ala Ala Ala Ser Glu Glu Ala Ala Phe Pro Pro Val Val Glu Asp Glu		
690	695	700
Glu Met Glu Ala Ser Gly Val Ser Gly Asn Glu Glu Glu Met Val Glu		
705	710	715
Glu Ala Glu Ala Leu His Ala Ser Gly Asn Glu Val Pro Arg Gly Glu		
725	730	735
Cys Ser Gly Pro Ala Thr Val Asn Asn Ser Ser Asp Thr Glu Ser Ile		
740	745	750
Pro Ser Pro His Thr Glu Ala Ala Lys Asp Thr Gly Gln Asn Gly Pro		
755	760	765
Lys Pro Pro Ala Thr Leu Gly Ala Asp Gly Pro Pro Pro Gly Pro Pro		
770	775	780
Thr Pro Pro Arg Arg Thr Ser Arg Ala Pro Ile Glu Pro Thr Pro Ala		
785	790	795
Ser Glu Ala Thr Gly Ala Pro Thr Pro Pro Pro Ala Pro Pro Ser Pro		
805	810	815
Ser Ala Pro Pro Pro Val Val Pro Lys Glu Glu Lys Glu Glu Glu Thr		
820	825	830
Ala Ala Ala Pro Pro Val Glu Glu Gly Glu Glu Gln Lys Pro Pro Ala		
835	840	845
Ala Glu Glu Leu Ala Val Asp Thr Gly Lys Ala Glu Glu Pro Val Lys		
850	855	860
Ser Glu Cys Thr Glu Glu Ala Glu Glu Gly Pro Ala Lys Gly Lys Asp		
865	870	875
Ala Glu Ala Ala Glu Ala Thr Ala Glu Gly Ala Leu Lys Ala Glu Lys		
885	890	895
Lys Glu Gly Gly Ser Gly Arg Ala Thr Thr Ala Lys Ser Ser Gly Ala		
900	905	910
Pro Gln Asp Ser Asp Ser Ser Ala Thr Cys Ser Ala Asp Glu Val Asp		
915	920	925
Glu Ala Glu Gly Gly Asp Lys Asn Arg Leu Leu Ser Pro Arg Pro Ser		
930	935	940
Leu Leu Thr Pro Thr Gly Asp Pro Arg Ala Asn Ala Ser Pro Gln Lys		
945	950	955
Pro Leu Asp Leu Lys Gln Leu Lys Gln Arg Ala Ala Ala Ile Pro Pro		
965	970	975
Ile Gln Val Thr Lys Val His Glu Pro Pro Arg Glu Asp Ala Ala Pro		
980	985	990
Thr Lys Pro Ala Pro Pro Ala Pro Pro Pro Pro Gln Asn Leu Gln Pro		
995	1000	1005
Glu Ser Asp Ala Pro Gln Gln Pro Gly Ser Ser Pro Arg Gly Lys Ser		
1010	1015	1020
Arg Ser Pro Ala Pro Pro Ala Asp Lys Glu Ala Phe Ala Ala Glu Ala		

1025		1030		1035		1040
Gln Lys Leu Pro Gly Asp Pro Pro Cys Trp Thr Ser Gly Leu Pro Phe						
	1045		1050		1055	
Pro Val Pro Pro Arg Glu Val Ile Lys Ala Ser Pro His Ala Pro Asp						
	1060		1065		1070	
Pro Ser Ala Phe Ser Tyr Ala Pro Pro Gly His Pro Leu Pro Leu Gly						
	1075		1080		1085	
Leu His Asp Thr Ala Arg Pro Val Leu Pro Arg Pro Pro Thr Ile Ser						
	1090		1095		1100	
Asn Pro Pro Pro Leu Ile Ser Ser Ala Lys His Pro Ser Val Leu Glu						
1105		1110		1115		1120
Arg Gln Ile Gly Ala Ile Ser Gln Gly Met Ser Val Gln Leu His Val						
	1125		1130		1135	
Pro Tyr Ser Glu His Ala Lys Ala Pro Val Gly Pro Val Thr Met Gly						
	1140		1145		1150	
Leu Pro Leu Pro Met Asp Pro Lys Lys Leu Ala Pro Phe Ser Gly Val						
	1155		1160		1165	
Lys Gln Glu Gln Leu Ser Pro Arg Gly Gln Ala Gly Pro Pro Glu Ser						
	1170		1175		1180	
Leu Gly Val Pro Thr Ala Gln Glu Ala Ser Val Leu Arg Gly Thr Ala						
1185		1190		1195		1200
Leu Gly Ser Val Pro Gly Gly Ser Ile Thr Lys Gly Ile Pro Ser Thr						
	1205		1210		1215	
Arg Val Pro Ser Asp Ser Ala Ile Thr Tyr Arg Gly Ser Ile Thr His						
	1220		1225		1230	
Gly Thr Pro Ala Asp Val Leu Tyr Lys Gly Thr Ile Thr Arg Ile Ile						
	1235		1240		1245	
Gly Glu Asp Ser Pro Ser Arg Leu Asp Arg Gly Arg Glu Asp Ser Leu						
	1250		1255		1260	
Pro Lys Gly His Val Ile Tyr Glu Gly Lys Lys Gly His Val Leu Ser						
1265		1270		1275		1280
Tyr Glu Gly Gly Met Ser Val Thr Gln Cys Ser Lys Glu Asp Gly Arg						
	1285		1290		1295	
Ser Ser Ser Gly Pro Pro His Glu Thr Ala Ala Pro Lys Arg Thr Tyr						
	1300		1305		1310	
Asp Met Met Glu Gly Arg Val Gly Arg Ala Ile Ser Ser Ala Ser Ile						
	1315		1320		1325	
Glu Gly Leu Met Gly Arg Ala Ile Pro Pro Glu Arg His Ser Pro His						
	1330		1335		1340	
His Leu Lys Glu Gln His His Ile Arg Gly Ser Ile Thr Gln Gly Ile						
1345		1350		1355		1360
Pro Arg Ser Tyr Val Glu Ala Gln Glu Asp Tyr Leu Arg Arg Glu Ala						
	1365		1370		1375	
Lys Leu Leu Lys Arg Glu Gly Thr Pro Pro Pro Pro Pro Pro Ser Arg						
	1380		1385		1390	
Asp Leu Thr Glu Ala Tyr Lys Thr Gln Ala Leu Gly Pro Leu Lys Leu						
	1395		1400		1405	
Lys Pro Ala His Glu Gly Leu Val Ala Thr Val Lys Glu Ala Gly Arg						
	1410		1415		1420	
Ser Ile His Glu Ile Pro Arg Glu Glu Leu Arg His Thr Pro Glu Leu						
1425		1430		1435		1440
Pro Leu Ala Pro Arg Pro Leu Lys Glu Gly Ser Ile Thr Gln Gly Thr						
	1445		1450		1455	
Pro Leu Lys Tyr Asp Thr Gly Ala Ser Thr Thr Gly Ser Lys Lys His						

1460	1465	1470
Asp Val Arg Ser Leu Ile Gly Ser Pro Gly Arg Thr Phe Pro Pro Val		
1475	1480	1485
His Pro Leu Asp Val Met Ala Asp Ala Arg Ala Leu Glu Arg Ala Cys		
1490	1495	1500
Tyr Glu Glu Ser Leu Lys Ser Arg Pro Gly Thr Ala Ser Ser Ser Gly		
1505	1510	1515
Gly Ser Ile Ala Arg Gly Ala Pro Val Ile Val Pro Glu Leu Gly Lys		
1525	1530	1535
Pro Arg Gln Ser Pro Leu Thr Tyr Glu Asp His Gly Ala Pro Phe Ala		
1540	1545	1550
Gly His Leu Pro Arg Gly Ser Pro Val Thr Thr Arg Glu Pro Thr Pro		
1555	1560	1565
Arg Leu Gln Glu Gly Ser Leu Ser Ser Ser Lys Ala Ser Gln Asp Arg		
1570	1575	1580
Lys Leu Thr Ser Thr Pro Arg Glu Ile Ala Lys Ser Pro His Ser Thr		
1585	1590	1595
Val Pro Glu His His Pro His Pro Ile Ser Pro Tyr Glu His Leu Leu		
1605	1610	1615
Arg Gly Val Ser Gly Val Asp Leu Tyr Arg Ser His Ile Pro Leu Ala		
1620	1625	1630
Phe Asp Pro Thr Ser Ile Pro Arg Gly Ile Pro Leu Asp Ala Ala Ala		
1635	1640	1645
Ala Tyr Tyr Leu Pro Arg His Leu Ala Pro Asn Pro Thr Tyr Pro His		
1650	1655	1660
Leu Tyr Pro Pro Tyr Leu Ile Arg Gly Tyr Pro Asp Thr Ala Ala Leu		
1665	1670	1675
Glu Asn Arg Gln Thr Ile Ile Asn Asp Tyr Ile Thr Ser Gln Gln Met		
1685	1690	1695
His His Asn Thr Ala Thr Ala Met Ala Gln Arg Ala Asp Met Leu Arg		
1700	1705	1710
Gly Leu Ser Pro Arg Glu Ser Ser Leu Ala Leu Asn Tyr Ala Ala Gly		
1715	1720	1725
Pro Arg Gly Ile Ile Asp Leu Ser Gln Val Pro His Leu Pro Val Leu		
1730	1735	1740
Val Pro Pro Thr Pro Gly Thr Pro Ala Thr Ala Met Asp Arg Leu Ala		
1745	1750	1755
Tyr Leu Pro Thr Ala Pro Gln Pro Phe Ser Ser Arg His Ser Ser Ser		
1765	1770	1775
Pro Leu Ser Pro Gly Gly Pro Thr His Leu Thr Lys Pro Thr Thr Thr		
1780	1785	1790
Ser Ser Ser Glu Arg Glu Arg Asp Arg Asp Arg Glu Arg Asp Arg Asp		
1795	1800	1805
Arg Glu Arg Glu Lys Ser Ile Leu Thr Ser Thr Thr Thr Val Glu His		
1810	1815	1820
Ala Pro Ile Trp Arg Pro Gly Thr Glu Gln Ser Ser Gly Ser Ser Gly		
1825	1830	1835
Ser Ser Gly Gly Gly Gly Gly Ser Ser Ser Arg Pro Ala Ser His Ser		
1845	1850	1855
His Ala His Gln His Ser Pro Ile Ser Pro Arg Thr Gln Asp Ala Leu		
1860	1865	1870
Gln Gln Arg Pro Ser Val Leu His Asn Thr Gly Met Lys Gly Ile Ile		
1875	1880	1885
Thr Ala Val Glu Pro Ser Thr Pro Thr Val Leu Arg Ser Thr Ser Thr		

1890	1895	1900	
Ser Ser Pro Val Arg	Pro Ala Ala Thr Phe	Pro Pro Ala Thr His Cys	
1905	1910	1915	1920
Pro Leu Gly Gly Thr	Leu Asp Gly Val Tyr	Pro Thr Leu Met Glu Pro	
	1925	1930	1935
Val Leu Leu Pro Lys	Glu Ala Pro Arg Val	Ala Arg Pro Glu Arg Pro	
	1940	1945	1950
Arg Ala Asp Thr Gly	His Ala Phe Leu Ala Lys	Pro Pro Ala Arg Ser	
	1955	1960	1965
Gly Leu Glu Pro Ala	Ser Ser Pro Ser Lys	Gly Ser Glu Pro Arg Pro	
1970	1975	1980	
Leu Val Pro Pro Val	Ser Gly His Ala Thr	Ile Ala Arg Thr Pro Ala	
1985	1990	1995	2000
Lys Asn Leu Ala Pro	His His Ala Ser Pro	Asp Pro Pro Ala Pro Pro	
	2005	2010	2015
Ala Ser Ala Ser Asp	Pro His Arg Glu Lys	Thr Gln Ser Lys Pro Phe	
	2020	2025	2030
Ser Ile Gln Glu Leu	Glu Leu Arg Ser Leu	Gly Tyr His Gly Ser Ser	
	2035	2040	2045
Tyr Ser Pro Glu Gly	Val Glu Pro Val Ser	Pro Val Ser Ser Pro Ser	
2050	2055	2060	
Leu Thr His Asp Lys	Gly Leu Pro Lys His	Leu Glu Glu Leu Asp Lys	
2065	2070	2075	2080
Ser His Leu Glu Gly	Glu Leu Arg Pro Lys	Gln Pro Gly Pro Val Lys	
	2085	2090	2095
Leu Gly Gly Glu Ala	Ala His Leu Pro His	Leu Arg Pro Leu Pro Glu	
	2100	2105	2110
Ser Gln Pro Ser Ser	Ser Pro Leu Leu Gln	Thr Ala Pro Gly Val Lys	
	2115	2120	2125
Gly His Gln Arg Val	Val Thr Leu Ala Gln	His Ile Ser Glu Val Ile	
2130	2135	2140	
Thr Gln Asp Tyr Thr	Arg His His Pro Gln	Gln Leu Ser Ala Pro Leu	
2145	2150	2155	2160
Pro Ala Pro Leu Tyr	Ser Phe Pro Gly Ala	Ser Cys Pro Val Leu Asp	
	2165	2170	2175
Leu Arg Arg Pro Pro	Ser Asp Leu Tyr Leu	Pro Pro Pro Asp His Gly	
	2180	2185	2190
Ala Pro Ala Arg Gly	Ser Pro His Ser Glu	Gly Gly Lys Arg Ser Pro	
	2195	2200	2205
Glu Pro Asn Lys Thr	Ser Val Leu Gly Gly	Gly Glu Asp Gly Ile Glu	
2210	2215	2220	
Pro Val Ser Pro Pro	Glu Gly Met Thr Glu	Pro Gly His Ser Arg Ser	
2225	2230	2235	2240
Ala Val Tyr Pro Leu	Leu Tyr Arg Asp Gly	Glu Gln Thr Glu Pro Ser	
	2245	2250	2255
Arg Met Gly Ser Lys	Ser Pro Gly Asn Thr	Ser Gln Pro Pro Ala Phe	
	2260	2265	2270
Phe Ser Lys Leu Thr	Glu Ser Asn Ser Ala	Met Val Lys Ser Lys Lys	
	2275	2280	2285
Gln Glu Ile Asn Lys	Lys Leu Asn Thr His	Asn Arg Asn Glu Pro Glu	
2290	2295	2300	
Tyr Asn Ile Ser Gln	Pro Gly Thr Glu Ile	Phe Asn Met Pro Ala Ile	
2305	2310	2315	2320
Thr Gly Thr Gly Leu	Met Thr Tyr Arg Ser	Gln Ala Val Gln Glu His	

2325 2330 2335
 Ala Ser Thr Asn Met Gly Leu Glu Ala Ile Ile Arg Lys Ala Leu Met
 2340 2345 2350
 Gly Lys Tyr Asp Gln Trp Glu Glu Ser Pro Pro Leu Ser Ala Asn Ala
 2355 2360 2365
 Phe Asn Pro Leu Asn Ala Ser Ala Ser Leu Pro Ala Ala Met Pro Ile
 2370 2375 2380
 Thr Ala Ala Asp Gly Arg Ser Asp His Thr Leu Thr Ser Pro Gly Gly
 2385 2390 2395 2400
 Gly Gly Lys Ala Lys Val Ser Gly Arg Pro Ser Ser Arg Lys Ala Lys
 2405 2410 2415
 Ser Pro Ala Pro Gly Leu Ala Ser Gly Asp Arg Pro Pro Ser Val Ser
 2420 2425 2430
 Ser Val His Ser Glu Gly Asp Cys Asn Arg Arg Thr Pro Leu Thr Asn
 2435 2440 2445
 Arg Val Trp Glu Asp Arg Pro Ser Ser Ala Gly Ser Thr Pro Phe Pro
 2450 2455 2460
 Tyr Asn Pro Leu Ile Met Arg Leu Gln Ala Gly Val Met Ala Ser Pro
 2465 2470 2475 2480
 Pro Pro Pro Gly Leu Pro Ala Gly Ser Gly Pro Leu Ala Gly Pro His
 2485 2490 2495
 His Ala Trp Asp Glu Glu Pro Lys Pro Leu Leu Cys Ser Gln Tyr Glu
 2500 2505 2510
 Thr Leu Ser Asp Ser Glu
 2515

<210> 677
 <211> 345
 <212> DNA
 <213> Homo sapiens

<400> 677
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 60
 gaggggtatag ctccggcacg ccgtgggtgtt ccacagattg aagttacttt cgatatcgat
 120
 gccaacggta tcttgaatgt gagcgcaaag gataaggcta ccggtaagga acagaagatt
 180
 cgcacggaag cttcaagtgg tttgagtcag gaagaaatcg acagaatgaa agctgaggca
 240
 gaacagaatg cagcagcagg caaggctgaa cgcgaaaaga ttgataagct gaaccaagct
 300
 gactcaatga tttccccccc cgaaaactcc tgaaagacaa cgatn
 345

<210> 678
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 678
 Val Met Gln Gly Glu Arg Pro Met Ala Ala Gln Asn Lys Ser Ile Gly
 1 5 10 15
 Gln Phe Thr Leu Glu Gly Ile Ala Pro Ala Arg Arg Gly Val Pro Gln


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      20      25      30
Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly Ile Leu Asn Val Ser
      35      40      45
Ala Lys Asp Lys Ala Thr Gly Lys Glu Gln Lys Ile Arg Ile Glu Ala
      50      55      60
Ser Ser Gly Leu Ser Gln Glu Glu Ile Asp Arg Met Lys Ala Glu Ala
65      70      75      80
Glu Gln Asn Ala Ala Ala Gly Lys Ala Glu Arg Glu Lys Ile Asp Lys
      85      90      95
Leu Asn Gln Ala Asp Ser Met Ile Ser Pro Pro Glu Asn Ser
      100      105      110

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<210> 679
 <211> 362
 <212> DNA
 <213> Homo sapiens

<400> 679
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 atgggaaaaa tgtacgttaa atgtgctaac gcgcagtatg atgtatctat gaatcttgag
 120
 ggtacaggcc tggatttcaa gcgtgccatt gctgacgtca cgcattgtgcc acccgaacgc
 180
 caaaaagtac tcatcaaggg aggattgcta aaagacgata cccattagg taaagtgggt
 240
 gcgcgtgcag gacagcagtt catggtgctg ggtgctgtgg gtgagctgcc caaggcccca
 300
 gaaaaacctg tgctgttcct ggaggatttg ccggaagacg agctcaacaa ggctaaggat
 360
 cc
 362

<210> 680
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 680
 Met Gly Lys Met Tyr Val Lys Cys Ala Asn Ala Gln Tyr Asp Val Ser
 1 5 10 15
 Met Asn Leu Glu Gly Thr Gly Leu Asp Phe Lys Arg Ala Ile Ala Asp
 20 25 30
 Val Thr His Val Pro Pro Glu Arg Gln Lys Val Leu Ile Lys Gly Gly
 35 40 45
 Leu Leu Lys Asp Asp Thr Pro Leu Gly Lys Val Gly Ala Arg Ala Gly
 50 55 60
 Gln Gln Phe Met Val Leu Gly Ala Val Gly Glu Leu Pro Lys Ala Pro
 65 70 75 80
 Glu Lys Pro Val Leu Phe Leu Glu Asp Leu Pro Glu Asp Glu Leu Asn
 85 90 95
 Lys Ala Lys Asp
 100

<210> 681
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 681
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 60
 gaacaattac tgatggcaga ctgttcaaca gtagaagaaa tgattcacgc tgatgaactc
 120
 ggttttgatt ttatcggaag tacttttagta ggatatacaa aacaaagtaa aggtgacaaa
 180
 atcgaagaaa atgactttga aatcttgaga acagtttttag aacgaattaa acatccacta
 240
 attgcagaag gcaatatcga tacacctgaa aaggtgaaac gtgtgcttga gttaggcgcg
 300
 tatagtgtcg ttgtagggtc agcgattact cgtccacaac tcatcacgaa aaaattt
 357

<210> 682
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 682
 Thr Arg Pro Asn Gly Gln Thr Leu Asp Asp Phe Tyr His Glu Ile Arg
 1 5 10 15
 Ala Lys Tyr Pro Glu Gln Leu Leu Met Ala Asp Cys Ser Thr Val Glu
 20 25 30
 Glu Met Ile His Ala Asp Glu Leu Gly Phe Asp Phe Ile Gly Ser Thr
 35 40 45
 Leu Val Gly Tyr Thr Lys Gln Ser Lys Gly Asp Lys Ile Glu Glu Asn
 50 55 60
 Asp Phe Glu Ile Leu Arg Thr Val Leu Glu Arg Ile Lys His Pro Leu
 65 70 75 80
 Ile Ala Glu Gly Asn Ile Asp Thr Pro Glu Lys Val Lys Arg Val Leu
 85 90 95
 Glu Leu Gly Ala Tyr Ser Val Val Val Gly Ser Ala Ile Thr Arg Pro
 100 105 110
 Gln Leu Ile Thr Lys Lys Phe
 115

<210> 683
 <211> 411
 <212> DNA
 <213> Homo sapiens

<400> 683
 ntctccgacc gcgtggtaaa actggcgacc ttaattgctg aagatgagca agctgaaatg
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 aatattgttt tgcccgcagc gtggttgcat gattgcgtca gttaccctaa aaaccatgta
 120
 ttaagagcac aaagtgcatt acatgcagca gataaagcga ttgtattttt gcgcagtatt
 180

aattacccca aacaatactt attagcaatt catcatgcaa tttcagcgca cagtgtcagt
 240
 ggtaaaatac aggcaatgag tttagaagct caaatagtgc aagatgcaga tagattggat
 300
 gcgctagggg caattggcgt ggctcggtgc attcaagtaa gtagccagtt acagcgccca
 360
 ctatattctg aagttgaccc cttcagcgag acacgatctc tagtctgcat g
 411

<210> 684
 <211> 137
 <212> PRT
 <213> Homo sapiens

<400> 684
 Xaa Ser Asp Arg Val Val Lys Leu Ala Thr Leu Ile Ala Glu Asp Glu
 1 5 10 15
 Gln Ala Glu Met Asn Ile Val Leu Pro Ala Ala Trp Leu His Asp Cys
 20 25 30
 Val Ser Tyr Pro Lys Asn His Val Leu Arg Ala Gln Ser Ala Leu His
 35 40 45
 Ala Ala Asp Lys Ala Ile Val Phe Leu Arg Ser Ile Asn Tyr Pro Lys
 50 55 60
 Gln Tyr Leu Leu Ala Ile His His Ala Ile Ser Ala His Ser Val Ser
 65 70 75 80
 Gly Lys Ile Gln Ala Met Ser Leu Glu Ala Gln Ile Val Gln Asp Ala
 85 90 95
 Asp Arg Leu Asp Ala Leu Gly Ala Ile Gly Val Ala Arg Cys Ile Gln
 100 105 110
 Val Ser Ser Gln Leu Gln Arg Pro Leu Tyr Ser Glu Val Asp Pro Phe
 115 120 125
 Ser Glu Thr Arg Ser Leu Val Cys Met
 130 135

<210> 685
 <211> 417
 <212> DNA
 <213> Homo sapiens

<400> 685
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 60
 cgccgtcact gcgatgctgg tctgctatgc catggaggac cgcagccact ggttcgtgct
 120
 gctgttcgcg gccgcttgge gctcggttcg gcctacggct tcctccaagg cgcctggccg
 180
 ttcggcttcg tcgaggcgat atgggcgctc gttgcctgcg gcgtggtgga cgatcaggcc
 240
 gcgatgaccg catcgtccgg cttagcccg gaaacgaaac cgaccagtgc gctggtttga
 300
 tgggcggcgc gtcgctggat gcacagcgtc tcgacgcgag cgtgatgatg gcctcagcgc
 360
 gtgcatgccg acgctgtcgc tcacgcgct acgctcgacc acggcgcgcg gcaatag
 417

<210> 686
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 686
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 Leu Gly Ala Arg Phe Gly Leu Arg Leu Pro Pro Arg Arg Leu Ala Val
 20 25 30
 Arg Leu Arg Arg Gly Asp Met Gly Ala Arg Cys Leu Arg Arg Gly Gly
 35 40 45
 Arg Ser Gly Arg Asp Asp Arg Ile Val Arg Leu Lys Pro Gly Asn Glu
 50 55 60
 Thr Asp Gln Cys Ala Gly Leu Met Gly Gly Ala Ser Leu Asp Ala Gln
 65 70 75 80
 Arg Leu Asp Ala Ser Val Met Met Ala Ser Ala Arg Ala Cys Arg Arg
 85 90 95
 Cys Arg Ser Ser Arg Tyr Ala Arg Pro Arg Arg Ala Ala Ile
 100 105 110

<210> 687
 <211> 412
 <212> DNA
 <213> Homo sapiens

<400> 687
 nnacgcgtga ccgaccaact gcgagccacc ctgctcgcca tggctgctat ggggttgac
 60
 gacggcatcg atattccgtc tggggcgatt attgaaagct gccgcacctt atcagccgtt
 120
 ctcgatgaaa cccacggtgg tcgcacgacg gagcttcggg taccacctgc gtgcgcggtt
 180
 caattggcgg ccattgagtc gggccccaac caccaccggg gcaactccgcc caatgtggcc
 240
 gagaccgacc ctgtcacctt cctgcagttg gcaactggct tctcacactg gccagaaatg
 300
 cgctcagcag gacgggttca ggcgtctgga tcccacgtcg acgacgttgc tggcgtgttc
 360
 ccagtcgttg atatggccgg ggttttccgc gacatttttg ccgacgacta ga
 412

<210> 688
 <211> 136
 <212> PRT
 <213> Homo sapiens

<400> 688
 Xaa Arg Val Thr Asp Gln Leu Arg Ala Thr Leu Leu Ala Met Ala Ala
 1 5 10 15
 Met Gly Leu His Asp Gly Ile Asp Ile Pro Ser Gly Ala Ile Ile Glu
 20 25 30
 Ser Cys Arg Thr Leu Ser Ala Val Leu Asp Glu Thr His Gly Gly Arg

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      35      40      45
Thr Ile Glu Leu Arg Val Pro Pro Ala Cys Ala Val Gln Leu Ala Ala
      50      55      60
Ile Glu Ser Gly Pro Asn His His Arg Gly Thr Pro Pro Asn Val Ala
65      70      75      80
Glu Thr Asp Pro Val Thr Phe Leu Gln Leu Ala Thr Gly Phe Ser His
      85      90      95
Trp Pro Glu Met Arg Ser Ala Gly Arg Val Gln Ala Ser Gly Ser His
      100      105      110
Val Asp Asp Val Ala Gly Val Phe Pro Val Val Asp Met Ala Gly Val
      115      120      125
Phe Arg Asp Ile Phe Ala Asp Asp
      130      135

```

<210> 689
 <211> 499
 <212> DNA
 <213> Homo sapiens

```

<400> 689
cgcgtcgcgg tactcgacgt cgattttcat cacggtaacg gcacccagaa cattttttac
60
ccgcgcaatg acgtgatgtt catatcgctg cacggcgagc cggccgtgtc ctatccctac
120
tattcgggggt tcagcgatga agtcggcgca ggtgttggcg aagggttcaa cctcaactac
180
ccgctgccga aaaacaccgc ctgggatacc taccgcgacg ccctgctgca tgcctgcagg
240
aaactccagc aattctcgcc gcaggtattg gtgatctcac tgggggtcga caccttcaag
300
gacgaccgca tcagtcactt cctgctggaa ggcgaggatt tcatcgggat cggcgagctg
360
atagcgagtg tgggttgccc caccctgttt gtgatggaag gcggctatat ggtcgatgaa
420
atcggaatca acgcggtgaa cgtactgcat ggcttcgaga gcaagcgcgc ttgagcatcc
480
gcccgaaagac ggcgtgata
499

```

<210> 690
 <211> 157
 <212> PRT
 <213> Homo sapiens

```

<400> 690
Arg Val Ala Val Leu Asp Val Asp Phe His His Gly Asn Gly Thr Gln
1      5      10      15
Asn Ile Phe Tyr Pro Arg Asn Asp Val Met Phe Ile Ser Leu His Gly
      20      25      30
Glu Pro Ala Val Ser Tyr Pro Tyr Tyr Ser Gly Phe Ser Asp Glu Val
      35      40      45
Gly Ala Gly Val Gly Glu Gly Phe Asn Leu Asn Tyr Pro Leu Pro Lys
      50      55      60
Asn Thr Ala Trp Asp Thr Tyr Arg Asp Ala Leu Leu His Ala Cys Arg

```

```

65          70          75          80
Lys Leu Gln Gln Phe Ser Pro Gln Val Leu Val Ile Ser Leu Gly Val
          85          90          95
Asp Thr Phe Lys Asp Asp Pro Ile Ser His Phe Leu Leu Glu Gly Glu
          100          105          110
Asp Phe Ile Gly Ile Gly Glu Leu Ile Ala Ser Val Gly Cys Pro Thr
          115          120          125
Leu Phe Val Met Glu Gly Gly Tyr Met Val Asp Glu Ile Gly Ile Asn
          130          135          140
Ala Val Asn Val Leu His Gly Phe Glu Ser Lys Arg Ala
145          150          155

```

<210> 691
 <211> 336
 <212> DNA
 <213> Homo sapiens

```

<400> 691
ntgctgctg aaaacgtgca gcgcggcgca tcagcgactg gcgagcgctt tggctggagt
60
tcgcaaaggc aaggcccctg ggagttggcc tgcgacatcg cgctgccgtg cgccaccag
120
aacgaactgg acgccgacgc cgcccgcacg ctgctgcgca acggctgcct ttgctggct
180
ggaggcgcca atatgccgcc cgcgcttgag gctgtggata tctttatcga ggcgggcatt
240
ctgttcgcgc ccggcaaggc atccaatgcc ggcggcgtgg ccgtgagtgg cctggaaatg
300
tcgcagaacg ccatgcgcct gctgtggacc gccggc
336

```

<210> 692
 <211> 112
 <212> PRT
 <213> Homo sapiens

```

<400> 692
Xaa Leu Arg Glu Asn Val Gln Arg Gly Ala Ser Ala Thr Gly Glu Arg
1          5          10          15
Phe Gly Trp Ser Ser Gln Arg Gln Gly Pro Trp Glu Leu Ala Cys Asp
          20          25          30
Ile Ala Leu Pro Cys Ala Thr Gln Asn Glu Leu Asp Ala Asp Ala Ala
          35          40          45
Arg Thr Leu Leu Arg Asn Gly Cys Leu Cys Val Ala Gly Gly Ala Asn
          50          55          60
Met Pro Pro Ala Leu Glu Ala Val Asp Ile Phe Ile Glu Ala Gly Ile
65          70          75          80
Leu Phe Ala Pro Gly Lys Ala Ser Asn Ala Gly Gly Val Ala Val Ser
          85          90          95
Gly Leu Glu Met Ser Gln Asn Ala Met Arg Leu Leu Trp Thr Ala Gly
          100          105          110

```

<210> 693
 <211> 580

<212> DNA

<213> Homo sapiens

<400> 693

ngggcaaccc ggaaggccg gcgtcccagc cgcctacctc gctgggaccc tggctcttgct
60
gtcccccgct ggcctcctgc ccaagcgact gcggccagga tgggccggaa ggtgaccgtg
120
gccacctgcg cactcaacca gtgggccctg gacttcgagg gcaatttgca aagaatttta
180
aagagtattg aaattgccaa aaacagagga gcaagatata ggcttggacc agagctggaa
240
atatgcggct gcggatgttg ggatcattat tacgagtcgg acaccctctt gcactcgttt
300
caagtcctag cggcccttgt ggagtctccc gtcactcagg acatcatctg cgacgtgggg
360
atacctgtaa tgcaccgaaa cgcccgctac aactgcagag tgatattcct caacaggaag
420
atcctgctca tcagacccaa gatggccttg gccaatgaag gcaactaccg cgagctgcgc
480
tggttcacc cgtggtcgag gagtcggtga gtcgggtgcc tgaccactcc tgggatgtgc
540
gttaagcacc tccgctgtgt gtagccttgg gtcctgatca
580

<210> 694

<211> 136

<212> PRT

<213> Homo sapiens

<400> 694

Met	Gly	Arg	Lys	Val	Thr	Val	Ala	Thr	Cys	Ala	Leu	Asn	Gln	Trp	Ala
1				5					10					15	
Leu	Asp	Phe	Glu	Gly	Asn	Leu	Gln	Arg	Ile	Leu	Lys	Ser	Ile	Glu	Ile
			20					25					30		
Ala	Lys	Asn	Arg	Gly	Ala	Arg	Tyr	Arg	Leu	Gly	Pro	Glu	Leu	Glu	Ile
		35				40					45				
Cys	Gly	Cys	Gly	Cys	Trp	Asp	His	Tyr	Tyr	Glu	Ser	Asp	Thr	Leu	Leu
	50					55					60				
His	Ser	Phe	Gln	Val	Leu	Ala	Ala	Leu	Val	Glu	Ser	Pro	Val	Thr	Gln
65				70						75				80	
Asp	Ile	Ile	Cys	Asp	Val	Gly	Ile	Pro	Val	Met	His	Arg	Asn	Val	Arg
			85						90					95	
Tyr	Asn	Cys	Arg	Val	Ile	Phe	Leu	Asn	Arg	Lys	Ile	Leu	Leu	Ile	Arg
		100						105					110		
Pro	Lys	Met	Ala	Leu	Ala	Asn	Glu	Gly	Asn	Tyr	Arg	Glu	Leu	Arg	Trp
		115				120						125			
Phe	Thr	Pro	Trp	Ser	Arg	Ser	Arg								
	130					135									

<210> 695

<211> 439

<212> DNA

<213> Homo sapiens

<400> 695

ntggtgactc aggcgtccaa tggcacgatg gctgacgtcg tcaatatgcc gtcctcgacc
60
atcatggctc tgtcgagggc tgattacctg ctcgatatcg agacttcggt gcccggtatc
120
ggcgacaagt tcgtcccga cgtctggggc aaactcaaac tcggcaagga caacgagcac
180
accgctctgc cctggtactt cggcccgttc gtcgtgacgt acaacaagga cattttcaag
240
gatgttgccc tcgatcccga aatcccgcgc aagacgatga ccgagtacct cgacttcgcc
300
aagaaaatca ccgctgccgg caagcaggcg gtctatggca acacgtcgtg gtacatgctc
360
gcggaatggc gtgccctcgg cgtcaaggtc atgaatgacg acttcaccaa gttcactttt
420
gcctcggaat ccaacgcgt
439

<210> 696

<211> 146

<212> PRT

<213> Homo sapiens

<400> 696

Xaa	Val	Thr	Gln	Ala	Ser	Asn	Gly	Thr	Met	Ala	Asp	Val	Val	Asn	Met
1				5					10					15	
Pro	Ser	Ser	Thr	Ile	Met	Ala	Leu	Ser	Arg	Ala	Asp	Tyr	Leu	Leu	Asp
			20					25					30		
Ile	Glu	Thr	Ser	Val	Pro	Gly	Ile	Gly	Asp	Lys	Phe	Val	Pro	Asp	Val
		35					40					45			
Trp	Gly	Lys	Leu	Lys	Leu	Gly	Lys	Asp	Asn	Glu	His	Thr	Ala	Leu	Pro
	50					55				60					
Trp	Tyr	Phe	Gly	Pro	Phe	Val	Val	Thr	Tyr	Asn	Lys	Asp	Ile	Phe	Lys
65				70				75					80		
Asp	Val	Gly	Leu	Asp	Pro	Glu	Ile	Pro	Pro	Lys	Thr	Met	Thr	Glu	Tyr
			85					90					95		
Leu	Asp	Phe	Ala	Lys	Lys	Ile	Thr	Ala	Ala	Gly	Lys	Gln	Ala	Val	Tyr
			100					105					110		
Gly	Asn	Thr	Ser	Trp	Tyr	Met	Leu	Ala	Glu	Trp	Arg	Ala	Leu	Gly	Val
		115				120						125			
Lys	Val	Met	Asn	Asp	Asp	Phe	Thr	Lys	Phe	Thr	Phe	Ala	Ser	Glu	Ser
	130					135					140				
Asn	Ala														
145															

<210> 697

<211> 368

<212> DNA

<213> Homo sapiens

<400> 697

nggcaataac gccgtcgtcg aaatccgttc ccttgatctc gaacatgccg atgaagcggc
60

tgtcggatgat ggggtcggag atgtcgccct cccacaactt gaacttgatc ggaccaaccc
 120
 tttccaccct ggagagactc gcctgccttg aaagtcttct tgcccttctt gggcaactga
 180
 tcgccctccc gaacgagata atccaagctc aagcgaccgc ccaccttgte gcgcgcctcc
 240
 acaccgacgg aatgcgatgc cgggatcgca tcgatgctag cggcgggtgcg tgcaatgaca
 300
 atcttgtctt cacgcagcga tacgggccccg ccgttggaat cgaacacaaa caccttgaag
 360
 gcgttgtn
 368

<210> 698
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 698
 Met Pro Met Lys Arg Leu Ser Val Met Gly Ser Glu Met Ser Pro Ser
 1 5 10 15
 His Asn Leu Asn Leu Ile Gly Pro Thr Leu Ser Thr Leu Glu Arg Leu
 20 25 30
 Ala Cys Leu Glu Ser Leu Leu Ala Leu Leu Gly Gln Leu Ile Ala Leu
 35 40 45
 Pro Asn Glu Ile Ile Gln Ala Gln Ala Thr Ala His Leu Val Ala Arg
 50 55 60
 Leu His Thr Asp Gly Met Arg Cys Arg Asp Arg Ile Asp Ala Ser Gly
 65 70 75 80
 Gly Ala Cys Asn Asp Asn Leu Val Phe Thr Gln Arg Tyr Gly Pro Ala
 85 90 95
 Val Gly Ile Glu His Lys His Leu Glu Gly Val Val
 100 105

<210> 699
 <211> 363
 <212> DNA
 <213> Homo sapiens

<400> 699
 nacgcgtaca caaatagtat cggaatcatt tcctatcatg ctgctatgac gagatttctc
 60
 cacacctcag attggcaact ggggatgact cggcactacc tgtcgaagcg cggcgacgac
 120
 gaccacagg cacggtttac tgccgatcga atcgagacgg tgcgcaggct gggcgacggt
 180
 gcccggaagg agggctgcga gtttgtcgtc gtcgccggag atgtcttcga aaccacaaat
 240
 gtctccactc agatcattgc ccgcgcgtgt gaggcgatag cctccattga tctccccgtg
 300
 tacctgctgc ccggaaatca cgacagctta gagccggggt gtctctggga tgggccagaa
 360
 ttc
 363

<210> 700
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 700
 Xaa Ala Tyr Thr Asn Ser Ile Gly Ile Ile Ser Tyr His Ala Ala Met
 1 5 10 15
 Thr Arg Phe Leu His Thr Ser Asp Trp Gln Leu Gly Met Thr Arg His
 20 25 30
 Tyr Leu Ser Lys Arg Gly Asp Asp Asp Pro Gln Ala Arg Phe Thr Ala
 35 40 45
 Asp Arg Ile Glu Thr Val Arg Arg Leu Gly Asp Val Ala Arg Lys Glu
 50 55 60
 Gly Cys Glu Phe Val Val Val Ala Gly Asp Val Phe Glu Thr His Asn
 65 70 75 80
 Val Ser Thr Gln Ile Ile Ala Arg Ala Cys Glu Ala Ile Ala Ser Ile
 85 90 95
 Asp Leu Pro Val Tyr Leu Leu Pro Gly Asn His Asp Ser Leu Glu Pro
 100 105 110
 Gly Cys Leu Trp Asp Gly Pro Glu Phe
 115 120

<210> 701
 <211> 585
 <212> DNA
 <213> Homo sapiens

<400> 701
 nacgcgtccg ggcacaccgt caccgaggcg acgttccacg gccacccac gctgatctat
 60
 ttcggctacg tccattgcgc ggatgtctgc ccgctgacac tgggcaacat ggtctcggcc
 120
 ctcgatcgcc tgggctcccg ggcggacggc atcgttccga tcttcattctc cgtcgatccg
 180
 gcccgcgaca caccgcgct ggtcggacag tatgtcgcgc atttctcgcc gcggatcgtc
 240
 gggctgaccg gcaccgcagc gcagctggcg ccggtactgg cggagttcca catcaccgcg
 300
 cgcgccgaac ctgcggcaca cgacatggcc gccgacatgt atgccgtcga ccacagcgcc
 360
 ctctctatc tgatggacgg caacaaccgc ctgttgcggg tgatggcggt cagcgccgac
 420
 gctgcctcgc tgacgcacca gctggcgggc ggctggccg gggcaagaat gagaccatga
 480
 aagcgatcgg accgacggac gccccgaac aggcagcgcc gggctggtcg ttcggcatca
 540
 tcctgctgct cggcatcgcc ggcattgctg atttcgtcga ccggt
 585

<210> 702
 <211> 159
 <212> PRT

<213> Homo sapiens

<400> 702

```

Xaa Ala Ser Gly His Thr Val Thr Glu Ala Thr Phe His Gly His Pro
 1           5           10           15
Thr Leu Ile Tyr Phe Gly Tyr Val His Cys Ala Asp Val Cys Pro Leu
          20           25           30
Thr Leu Gly Asn Met Val Ser Ala Leu Asp Arg Leu Gly Ser Arg Ala
          35           40           45
Asp Gly Ile Val Pro Ile Phe Ile Ser Val Asp Pro Ala Arg Asp Thr
          50           55           60
Pro Ala Leu Val Gly Gln Tyr Val Ala His Phe Ser Pro Arg Ile Val
65           70           75           80
Gly Leu Thr Gly Thr Ala Ala Gln Leu Ala Pro Val Leu Ala Glu Phe
          85           90           95
His Ile Thr Ala Arg Ala Glu Pro Ala Ala His Asp Met Ala Ala Asp
          100          105          110
Met Tyr Ala Val Asp His Ser Ala Leu Leu Tyr Leu Met Asp Gly Asn
          115          120          125
Asn Arg Leu Leu Arg Val Met Ala Val Ser Ala Asp Ala Ala Ser Leu
          130          135          140
Thr His Gln Leu Ala Ala Gly Leu Ala Gly Ala Arg Met Arg Pro
145           150           155

```

<210> 703

<211> 390

<212> DNA

<213> Homo sapiens

<400> 703

```

ttctctgctc catcacacc tcagcagaat ggcacgccc agcgcaagaa cataactctt
60
attgagatgg cccgaacgat gcttgatgag tacaagactc cgcggaagtt ctggcctgaa
120
gccattgata ctgcttgta caccatcaac cgcgtttatc ttcacaaggt tttggagaaa
180
acctcttatg agttcctaac tggtaagaaa cccaatgtaa gctatttcag agtatttggt
240
gctaggtgct ggatcaagga tcctcatcac acttcaaaat ttgcaccgaa agcacatgaa
300
ggttttatgc ttggttacgg aaaggattcg cactcctaca gagtcttcaa cctctttcac
360
tataaagtgg ttcaaactgt ggatgtgcgn
390

```

<210> 704

<211> 130

<212> PRT

<213> Homo sapiens

<400> 704

```

Phe Ser Ala Pro Tyr Thr Pro Gln Gln Asn Gly Ile Ala Glu Arg Lys
 1           5           10           15
Asn Ile Thr Leu Ile Glu Met Ala Arg Thr Met Leu Asp Glu Tyr Lys

```

```

      20      25      30
Thr Pro Arg Lys Phe Trp Pro Glu Ala Ile Asp Thr Ala Cys His Thr
      35      40      45
Ile Asn Arg Val Tyr Leu His Lys Val Leu Glu Lys Thr Ser Tyr Glu
      50      55      60
Phe Leu Thr Gly Lys Lys Pro Asn Val Ser Tyr Phe Arg Val Phe Gly
65      70      75      80
Ala Arg Cys Trp Ile Lys Asp Pro His His Thr Ser Lys Phe Ala Pro
      85      90      95
Lys Ala His Glu Gly Phe Met Leu Gly Tyr Gly Lys Asp Ser His Ser
      100      105      110
Tyr Arg Val Phe Asn Leu Phe His Tyr Lys Val Val Gln Thr Val Asp
      115      120      125
Val Arg
      130

```

<210> 705
 <211> 513
 <212> DNA
 <213> Homo sapiens

```

<400> 705
acgcgtat ttt cgtccaaatg attcaaata aaacgccgcc gttaaaaacg atgcaggcga
60
agacaatgcg aataaaaaag gtggtaaata agcatgagtt ttaaaatgac acaatctcaa
120
tacacaagtc tttatggacc aactgtagga gactccgtga gattaggaga tacgaacttg
180
tttgcacaag ttgagaaaga ctatgcaa at tatggggatg aagctacttt cggtggcgga
240
aatcaattc gtgatggat ggctcaaaat cctaattgta caagagatga taaaaatgta
300
gccgatttag ttttaactaa cgcattaatt attgattatg acaagattgt taaagcagat
360
atcgggtatta aaaatgggta tattttttaag attgggtaaag ctggaaaccc agatataatg
420
gataacgttg acatcatcat tgggtgcaaca actgatatta ttgctgctga aggtaaaatt
480
gttactgccg gcggtatcga tacacacgtg cac
513

```

<210> 706
 <211> 140
 <212> PRT
 <213> Homo sapiens

```

<400> 706
Met Ser Phe Lys Met Thr Gln Ser Gln Tyr Thr Ser Leu Tyr Gly Pro
1      5      10      15
Thr Val Gly Asp Ser Val Arg Leu Gly Asp Thr Asn Leu Phe Ala Gln
      20      25      30
Val Glu Lys Asp Tyr Ala Asn Tyr Gly Asp Glu Ala Thr Phe Gly Gly
      35      40      45
Gly Lys Ser Ile Arg Asp Gly Met Ala Gln Asn Pro Asn Val Thr Arg

```


50	55	60
Asp Asp Lys Asn Val Ala Asp Leu Val Leu Thr Asn Ala Leu Ile Ile		
65	70	75
Asp Tyr Asp Lys Ile Val Lys Ala Asp Ile Gly Ile Lys Asn Gly Tyr		80
	85	90
Ile Phe Lys Ile Gly Lys Ala Gly Asn Pro Asp Ile Met Asp Asn Val		95
	100	105
Asp Ile Ile Ile Gly Ala Thr Thr Asp Ile Ile Ala Ala Glu Gly Lys		110
	115	120
Ile Val Thr Ala Gly Gly Ile Asp Thr His Val His		125
	130	135
		140

<210> 707

<211> 409

<212> DNA

<213> Homo sapiens

<400> 707

acgcgtggca tcctcagacc accaaagaca atcctgtcct gggaggcagg gagaaagccg
60
gcacactaca cagtgcacag gtgaagccct caggggggtcc tggagcaggg ccacctccct
120
gggggatccc caggtgccat tttcatggca gtgtctatgg acggtcccc ttggcatggt
180
gctgggtggc aatcctggct gtagctgcca cccctgccc tttttgcttc cctccgaggg
240
cattgtgatc atcagtgtga gtctgttggg aaggagagcc aggtccccag gtttgggaaa
300
ggagtagggt ttcccagcct gtctggccat cccccccag ccagcccct cctgctgggt
360
gacgtgctca gttcggcccc tgctgtactg ggaggggggt aggagcata
409

<210> 708

<211> 136

<212> PRT

<213> Homo sapiens

<400> 708

Met Leu Leu Ala Pro Ser Gln Tyr Ser Arg Gly Arg Thr Glu His Val		
1	5	10
Thr Gln Gln Glu Gly Leu Gly Trp Gly Val Met Ala Arg Gln Ala Gly		15
	20	25
Lys Pro Tyr Ser Phe Pro Lys Pro Gly Asp Leu Ala Leu Leu Pro Asn		30
	35	40
Arg Leu Thr Leu Met Ile Thr Met Pro Ser Glu Gly Ser Lys Lys Gly		45
	50	55
Arg Gly Trp Gln Leu Gln Pro Gly Leu Pro Pro Ser Thr Met Pro Arg		60
65	70	75
Gly Ala Val His Arg His Cys His Glu Asn Gly Thr Trp Gly Ser Pro		80
	85	90
Arg Glu Val Ala Leu Leu Gln Asp Pro Leu Arg Ala Ser Pro Val His		95
	100	105
Cys Val Val Cys Arg Leu Ser Pro Cys Leu Pro Gly Gln Asp Cys Leu		110

115 120 125
 Trp Trp Ser Glu Asp Ala Thr Arg
 130 135

<210> 709
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 709
 acgcgtctga cggagagcct cctgagtctc cccacgcaga ggactcagaa aggggaatcgg
 60
 tgaccacacc tgggccagcg acgtgtggtg cgccagcctc cccagcggat cacctcctcc
 120
 tccccctcca ggaggagagt ttctccgaag tccccatgag tgaagcaagc tcagcgaaag
 180
 acactccact ctttaggatg gagggagagg atgcccttgt gactcagtat cagagcaaag
 240
 ccagtgacca cgaagggtta ttgtctgacc ccttgagtga ccttcagttg gtctcagatt
 300
 ttaaattctcc aatcatggcc gatctgaact taagccttcc ttccattcct gaagtcgcat
 360
 cggatgatga aagaatagat cagggtgaag atgacggaga tcagggtgaa gatgatggag
 420
 agacagcaaa gtcgtcaact ctggacatag gagctttgtc cttgggcttg gtagtcccct
 480
 gtccctgagag gggaaagggg cccagtggcg aggcagatag gttggtactg ggggagggcc
 540
 tgtgtgattt caggctgcaa gcaccccagg catctgtgac agctccttca gagcagacca
 600
 cagagttcgg aattcacaaa ccacatcttg gcaagagctc aagcttggat aaacagctgc
 660
 caggccccag tgggtggtgag gaagaaaaac cgatgggaaa tgggagtcca agcccgctc
 720
 ctggcacatc cctggacaat cctgtacca gccctcccc ttctgagatc t
 771

<210> 710
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 710
 Met Ser Glu Ala Ser Ser Ala Lys Asp Thr Pro Leu Phe Arg Met Glu
 1 5 10 15
 Gly Glu Asp Ala Leu Val Thr Gln Tyr Gln Ser Lys Ala Ser Asp His
 20 25 30
 Glu Gly Leu Leu Ser Asp Pro Leu Ser Asp Leu Gln Leu Val Ser Asp
 35 40 45
 Phe Lys Ser Pro Ile Met Ala Asp Leu Asn Leu Ser Leu Pro Ser Ile
 50 55 60
 Pro Glu Val Ala Ser Asp Asp Glu Arg Ile Asp Gln Val Glu Asp Asp
 65 70 75 80
 Gly Asp Gln Val Glu Asp Asp Gly Glu Thr Ala Lys Ser Ser Thr Leu

	85		90		95
Asp Ile Gly Ala Leu Ser Leu Gly Leu Val Val Pro Cys Pro Glu Arg					
	100		105		110
Gly Lys Gly Pro Ser Gly Glu Ala Asp Arg Leu Val Leu Gly Glu Gly					
	115		120		125
Leu Cys Asp Phe Arg Leu Gln Ala Pro Gln Ala Ser Val Thr Ala Pro					
	130		135		140
Ser Glu Gln Thr Thr Glu Phe Gly Ile His Lys Pro His Leu Gly Lys					
145		150		155	160
Ser Ser Ser Leu Asp Lys Gln Leu Pro Gly Pro Ser Gly Gly Glu Glu					
	165		170		175
Glu Lys Pro Met Gly Asn Gly Ser Pro Ser Pro Pro Pro Gly Thr Ser					
	180		185		190
Leu Asp Asn Pro Val Pro Ser Pro Ser Pro Ser Glu Ile					
	195		200		205

<210> 711
 <211> 432
 <212> DNA
 <213> Homo sapiens

<400> 711
 nnggatccga cggcgcaaag ccttaatgaa gggtaggcag ttacctcttt ttctgtagga
 60
 attctcctgt tttatatcta ctcccccta gggtcatcct actccctcat cttctgagct
 120
 aatgtgcccg ctttatttgc acttgcatgg aatatgatta tgaacacagt ttttatcatt
 180
 gatgaccacc ccgttatcag gttggcgatt cgtatgttgt tggaacacga gggttataag
 240
 gtcgttggtg aaacggacaa cggttgtgac gcgatccaaa tggttcgcga atgcctgccg
 300
 gacctgatca tcctggatat cagcatcccc aaactcgacg gcctcgaagt gctctgccga
 360
 ttcaacgcca tgaacacatc catgaaaacc ctgattctta ccgccagag tccgacgttg
 420
 ttcgccacgc gt
 432

<210> 712
 <211> 93
 <212> PRT
 <213> Homo sapiens

Met Ile Met Asn Thr Val Phe Ile Ile Asp Asp His Pro Val Ile Arg					
1	5		10		15
Leu Ala Ile Arg Met Leu Leu Glu His Glu Gly Tyr Lys Val Val Gly					
	20		25		30
Glu Thr Asp Asn Gly Cys Asp Ala Ile Gln Met Val Arg Glu Cys Leu					
	35		40		45
Pro Asp Leu Ile Ile Leu Asp Ile Ser Ile Pro Lys Leu Asp Gly Leu					
	50		55		60
Glu Val Leu Cys Arg Phe Asn Ala Met Asn Thr Ser Met Lys Thr Leu					

<400> 714																
Ile	Leu	Ile	Ala	Asn	Gly	Gly	Met	Gln	Asn	Pro	Val	Gly	Ala	Val	Phe	
1				5					10					15		
Asn	Pro	Asp	Thr	Met	Arg	Met	Glu	Met	Thr	Asp	Phe	Ala	Ala	Val	Ile	
			20					25						30		
Phe	Asn	Pro	Val	Ala	Gln	Ala	Lys	Phe	Val	His	Thr	Val	Ser	Ala	Gly	
		35					40					45				
Tyr	Val	Ala	Gly	Ala	Met	Phe	Val	Met	Ser	Ile	Ser	Ala	Trp	Tyr	Leu	
	50					55					60					
Leu	Lys	Gly	Arg	His	Thr	Asp	Leu	Ala	Lys	Arg	Ser	Met	Ala	Val	Ala	
65					70					75					80	
Ala	Ser	Phe	Gly	Leu	Ala	Ser	Ala	Leu	Ser	Val	Val	Val	Leu	Gly	Asp	
				85					90					95		
Glu	Ser	Gly	Tyr	Leu	Thr	Thr	Glu	His	Gln	Lys	Met	Lys	Ile	Ala	Ala	
			100					105					110			
Met	Glu	Ser	Met	Trp	His	Thr	Glu	Pro	Ala	Pro	Ala	Ser	Phe	Asn	Leu	
		115					120					125				
Ile	Ala	Leu	Pro	Asn	Gln	Ala	Glu	Arg	Lys	Asn	Asp	Phe	Ala	Ile	Glu	
	130					135					140					
Ile	Pro	Tyr	Val	Met	Xaa	Leu	Ile	Gly	Thr	Arg						
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<210> 715
 <211> 354
 <212> DNA
 <213> Homo sapiens

<400> 715
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 tgcaagttag taccgggggt ttccctggag ttgctcagcc aggtggacgc aggcgagctg
 180
 gactcggcga tcatcattcg cccgcccttt gatttgccca aggagttgca cgtacaggta
 240
 ctgcgcaagg agccgtttgt gttgatcgtg cccagggcgg tcgggggtga tgaccggtg
 300
 caactgctcg aagctcatcc ccacgtgcgc tacgaccgcg cttegtttgg cggg
 354

<210> 716
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 716
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 20 25 30
 Arg Gln Ala Ala Pro Thr Val Glu Cys Lys Leu Val Pro Gly Val Ser
 35 40 45
 Leu Glu Leu Leu Ser Gln Val Asp Ala Gly Glu Leu Asp Ser Ala Ile
 50 55 60
 Ile Ile Arg Pro Pro Phe Asp Leu Pro Lys Glu Leu His Val Gln Val
 65 70 75 80
 Leu Arg Lys Glu Pro Phe Val Leu Ile Val Pro Gln Ala Val Gly Gly
 85 90 95
 Asp Asp Pro Leu Gln Leu Leu Glu Ala His Pro His Val Arg Tyr Asp
 100 105 110
 Arg Ala Ser Phe Gly Gly
 115

<210> 717
 <211> 401
 <212> DNA
 <213> Homo sapiens

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 ccgttaagtc atctaaatag gccattctgt ggctctccat cagtaagaac caaatccata
 120
 ggagaagttg agcggatagt aatgcatcaa attgatgctg agaaaccgaa aaatgggaca
 180

atataatcaa gctgacaata ctgatcaaac cactcgcacg aaagctacta ccgcttgacc
 240
 accaagcaga aaaaaccaat gaaatgctta aaaataaaat cgtccaaagt aaaaagctag
 300
 accaggtggt agccagatta aaaataggcc gctctagaaa atgaaaagaa atccaatgag
 360
 attcaacggc gtagcaccag cacagcaaca tagccactag t
 401

<210> 718
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 718
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 His Phe Leu Glu Arg Pro Ile Phe Asn Leu Ala Thr Thr Trp Ser Ser
 20 25 30
 Phe Leu Leu Trp Thr Ile Leu Phe Leu Ser Ile Ser Leu Val Phe Ser
 35 40 45
 Ala Trp Trp Ser Ser Gly Ser Ser Phe His Ala Ser Gly Leu Ile Ser
 50 55 60
 Ile Val Ser Leu Ile Ile Leu Ser His Phe Ser Val Ser Gln His Gln
 65 70 75 80
 Phe Asp Ala Leu Leu Ser Ala Gln Leu Leu Leu Trp Ile Trp Phe Leu
 85 90 95
 Leu Met Glu Ser His Arg Met Ala Tyr Leu Asp Asp Leu Thr Ala Leu
 100 105 110
 Pro Gly Arg Arg Ala Leu Asn Glu Lys Leu Val Gly Leu Pro Lys Arg
 115 120 125
 Tyr Ala
 130

<210> 719
 <211> 685
 <212> DNA
 <213> Homo sapiens

<400> 719
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 ctcttgaagg cggattttca taggcgctgc gcctctcata ttcaagcatc aaggcaatcc
 120
 aatctccctg cgttggtaac tgggcaaaag aaagacctct gcagtccagc aacctcatcg
 180
 tgcaaagtcg gtggcggtgt caactctgac ggccctggaag ctgcagacct tgtcaaagga
 240
 cctcggccga aattcaccct tgatctcttt gtcttgtcca actcttgtcc ctgagaatga
 300
 aactgtcttc tgagagtcca tcaatgagac gctgactcgt gagaagtgtc gaatcacgtc
 360
 gccattttgg agacctgcca acgcagctct ggaacctgcc aggacgcctt ccacaacacc
 420

agaacgcagc gactttgcgt taaatccaag ctcaaacacc tcttgctcca caggcctgag
 480
 cataaaaagg tattctgcga cgggaaatgt aaagtctgag cttaggtgca gagtaccgcc
 540
 atcgatcagt gtctgatact gcttgctcgc gacttctttg ccgagcaatg ggtatagcgt
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 tttcaaccaa gtggaagcag tcgtttgctc accctggcga ttccggcgag ttagggacat
 660
 gaccacgtca tcgatgggat tttgc
 685

<210> 720
 <211> 161
 <212> PRT
 <213> Homo sapiens

<400> 720
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 20 25 30
 Lys Gln Tyr Gln Thr Leu Ile Asp Gly Gly Thr Leu His Leu Ser Ser
 35 40 45
 Asp Phe Thr Phe Pro Val Ala Glu Tyr Leu Phe Met Leu Arg Pro Val
 50 55 60
 Glu Gln Glu Val Phe Glu Leu Gly Phe Asn Ala Lys Ser Leu Arg Ser
 65 70 75 80
 Gly Val Val Glu Gly Val Leu Ala Gly Ser Arg Ala Ala Leu Ala Gly
 85 90 95
 Leu Gln Asn Gly Asp Val Ile Gln His Phe Ser Arg Val Ser Val Ala
 100 105 110
 Leu Met Asp Ser Gln Lys Thr Val Ser Phe Ser Gly Thr Arg Val Gly
 115 120 125
 Gln Asp Lys Glu Ile Lys Gly Glu Phe Arg Pro Arg Ser Phe Asp Lys
 130 135 140
 Val Cys Ser Phe Gln Ala Val Arg Val Asp His Ala Thr Ala Phe Ala
 145 150 155 160
 Arg

<210> 721
 <211> 579
 <212> DNA
 <213> Homo sapiens

<400> 721
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 120
 aggaacgctc tcagggtggc tgaagtctgg atggatgaat ttaaaagcca cgtctactgg
 180
 catggaacat accaggagga ctcaggaatt gacattgggg acatcactgc aaggaaggct
 240

ctcaggaaac agctgcagtg caagaccttc cgggtggtacc tggtcagcgt gtacccagag
 300
 atgaggatgt actccgacat cattgcctat ggagtgctgc agaattctct gaagactgat
 360
 ttgtgtcttg accaggggcc agatacagag aatgtcccca tcatgtacat ctgccatggg
 420
 atgacgcctc agaacgtgta ctacacgagc agtcagcaga tccatgtggg cattctgagc
 480
 cccaccgtgg atgatgatga caaccgatgc ctggtggacg tcaacagccg gccccggctc
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 atcgaatgca gctacgcca agccaagagg atgaagctt
 579

<210> 722
 <211> 193
 <212> PRT
 <213> Homo sapiens

<400> 722
 Lys Leu Gly Ile Arg Val Trp Gln Cys Gly Gly Ser Val Glu Val Leu
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 Pro Cys Ser Arg Ile Ala His Ile Glu Arg Ala His Lys Pro Tyr Thr
 20 25 30
 Glu Asp Leu Thr Ala His Val Arg Arg Asn Ala Leu Arg Val Ala Glu
 35 40 45
 Val Trp Met Asp Glu Phe Lys Ser His Val Tyr Trp His Gly Thr Tyr
 50 55 60
 Gln Glu Asp Ser Gly Ile Asp Ile Gly Asp Ile Thr Ala Arg Lys Ala
 65 70 75 80
 Leu Arg Lys Gln Leu Gln Cys Lys Thr Phe Arg Trp Tyr Leu Val Ser
 85 90 95
 Val Tyr Pro Glu Met Arg Met Tyr Ser Asp Ile Ile Ala Tyr Gly Val
 100 105 110
 Leu Gln Asn Ser Leu Lys Thr Asp Leu Cys Leu Asp Gln Gly Pro Asp
 115 120 125
 Thr Glu Asn Val Pro Ile Met Tyr Ile Cys His Gly Met Thr Pro Gln
 130 135 140
 Asn Val Tyr Tyr Thr Ser Ser Gln Gln Ile His Val Gly Ile Leu Ser
 145 150 155 160
 Pro Thr Val Asp Asp Asp Asp Asn Arg Cys Leu Val Asp Val Asn Ser
 165 170 175
 Arg Pro Arg Leu Ile Glu Cys Ser Tyr Ala Lys Ala Lys Arg Met Lys
 180 185 190
 Leu

<210> 723
 <211> 384
 <212> DNA
 <213> Homo sapiens

<400> 723
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ctcaacgaaa tgctctcgct taaaccgtgc gaaggaaccc caccgcaatg gcgcttattc
 120
 cgcgaggggg attaccaaat gcgcattgat acgcgctccg gaacgcctac gctgatgctt
 180
 accgtacaaa gtgtaaccga caaacctggt acggacgtca ctcgacaatg tcctaaatgg
 240
 gacggcaagc ccctcaccct tgacgtaacg aatacattcc cggaaggctc cgtcgtacga
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 gacttctaca gcaagcaaac cgctatgggt cagcaaggta aatcacact tcagcctgcc
 360
 gctaacagca atggcctgct gctg
 384

<210> 724
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 724
 Thr Arg Pro Leu Thr Leu Ser Phe Asp Asn Ala Cys Trp Gln Pro Thr
 1 5 10 15
 Glu Ala Val Lys Leu Asn Glu Met Leu Ser Leu Lys Pro Cys Glu Gly
 20 25 30
 Thr Pro Pro Gln Trp Arg Leu Phe Arg Glu Gly Asp Tyr Gln Met Arg
 35 40 45
 Ile Asp Thr Arg Ser Gly Thr Pro Thr Leu Met Leu Thr Val Gln Ser
 50 55 60
 Val Thr Asp Lys Pro Val Thr Asp Val Thr Arg Gln Cys Pro Lys Trp
 65 70 75 80
 Asp Gly Lys Pro Leu Thr Leu Asp Val Thr Asn Thr Phe Pro Glu Gly
 85 90 95
 Ser Val Val Arg Asp Phe Tyr Ser Lys Gln Thr Ala Met Val Gln Gln
 100 105 110
 Gly Lys Ile Thr Leu Gln Pro Ala Ala Asn Ser Asn Gly Leu Leu Leu
 115 120 125

<210> 725
 <211> 521
 <212> DNA
 <213> Homo sapiens

<400> 725
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 120
 gaaaataggt ttccttcttc cacaggcatg gagaaggaag gaaattttgc actggccttc
 180
 gggaagctga agaagagctg gggggaggct tgttctgaca aaatagtgac tctctccctg
 240
 cttgaaatgt cccacagaag gctgtttctg gttcacattt gccctctag gtccactccc
 300
 tccccttcac cctgctcact gccagagaga ctatgctggg agtggtgcat cggtggtctc
 360

caggcccttt taggctcaag gtgttcattc cctggctcct tccctgccat gtctttgttc
 420
 cttctccct ccttcccac ccagcagcca cctcctcct tccaccagac ctgggaacca
 480
 tcatcccaac cacaatcacc ccgtgggttct attacacgcg t
 521

<210> 726
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 726
 Met Glu Lys Glu Gly Asn Phe Ala Leu Ala Phe Gly Lys Leu Lys Lys
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 Ser Trp Gly Glu Ala Cys Ser Asp Lys Ile Val Thr Leu Ser Leu Leu
 20 25 30
 Glu Met Ser His Arg Arg Leu Phe Leu Val His Ile Cys Pro Ser Arg
 35 40 45
 Ser Thr Pro Ser Pro Ser Ser Cys Ser Leu Pro Glu Arg Leu Cys Trp
 50 55 60
 Glu Trp Cys Ile Gly Gly Leu Gln Ala Leu Leu Gly Ser Arg Cys Ser
 65 70 75 80
 Phe Pro Gly Ser Phe Pro Ala Met Ser Leu Phe Leu Pro Pro Ser Phe
 85 90 95
 Pro Ser Gln Gln Pro Pro Ser Ser Phe His Gln Thr Trp Glu Pro Ser
 100 105 110
 Ser Gln Pro Gln Ser Pro Arg Gly Ser Ile Thr Arg
 115 120

<210> 727
 <211> 629
 <212> DNA
 <213> Homo sapiens

<400> 727
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 tctgttgctt gacggcacgg tggctcagga ctcatctcg ggaaccttg cgactcgcg
 120
 tgccattatc gacgctggtg agttgaaggc tccgacgcac cgggcggttg cgtcaatcag
 180
 tgccgcccgc cagcaggtcc aaggagaact cgaatgaatc cgaatgacta cctggtgctc
 240
 tcggcgatct tgttcgctat cggcatcgtg ggcttcctga cgaggcgtaa tgccctggtg
 300
 gcctttatgt cgggtggagt gatgctcaac gccgcgaacc tggcgctggt gactttcgt
 360
 cacgtacacg gctctctcga cggacaggtc ggggttttct tcgtgatgat cgtggcagcc
 420
 gctgaggtgg ttgtcggttt ggcgatcatc gtcactatct tccgttcccg tcgcaccact
 480
 tcggtggacg acaccaacct gctgaagttc tgagggaggt accgtgactg tcttggaac
 540

cggtttgttc aacgtggcct ggctcatgat tgcggtgccca ctggtggttg ccgcgctgct
600
attggtgctg ggacgccgca ggcacgcgt
629

<210> 728
<211> 99
<212> PRT
<213> Homo sapiens

<400> 728
Met Asn Pro Asn Asp Tyr Leu Val Leu Ser Ala Ile Leu Phe Ala Ile
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Gly Ile Val Gly Phe Leu Thr Arg Arg Asn Ala Leu Val Ala Phe Met
20 25 30
Ser Val Glu Leu Met Leu Asn Ala Ala Asn Leu Ala Leu Val Thr Phe
35 40 45
Ala His Val His Gly Ser Leu Asp Gly Gln Val Gly Val Phe Phe Val
50 55 60
Met Ile Val Ala Ala Ala Glu Val Val Val Gly Leu Ala Ile Ile Val
65 70 75 80
Thr Ile Phe Arg Ser Arg Arg Thr Thr Ser Val Asp Asp Thr Asn Leu
85 90 95
Leu Lys Phe

<210> 729
<211> 4716
<212> DNA
<213> Homo sapiens

<400> 729
nnaggagaga agaaattgaa aagcaggcac ttgagaagtc taagagaagc tttaagacgt
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ttaaggaaat gctgcaggac agggaatccc aaaatcaaaa gtctacagtt ccgtcaagaa
120
ggagaatgta ttcttttgat gatgtgctgg aggaaggaaa gcgacccctt acaatgactg
180
tgtcagaagc aagttaccag agtgagagag tagaagagaa gggagcaact tattcttcag
240
aaattcccaa agaagattct accacttttg caaaaagaga ggaccctgtt aacaactgaa
300
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360
cgttcacgga gcacacaaat ggaatcaact cgtgtttcag cttctctccc cagaagttac
420
cggaactg atacagtcag gttaacatct gtggtcacac caagaccctt tggctctcag
480
acaaggggaa tctcatcact cccagatct tacacgatgg atgatgcttg gaagtataat
540
ggagatgttg aagacattaa gagaactcca aacaatgttg tcagcacccc tgcaccaagc
600
ccggacgcaa gccaaactggc ttcaagctta tctagccaga aagaggtagc agcaacagaa
660

gaagatgtga caaggctgcc ctctectaca tcccccttct catctctttc ccaagaccag
720
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780
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840
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1020
tcaaaagagt gggaggaagc catggctaag gctcaagaaa ctggacacct agtgatggat
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2040
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2100
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2160
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2220
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2280

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2940
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3360
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3720
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3780
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3900

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 3960
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 4080
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 4140
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 4200
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 4260
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 4320
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 4380
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 4440
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 4680
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<210> 730

<211> 797

<212> PRT

<213> Homo sapiens

<400> 730

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Thr	Asp	Thr	Val	Arg	Leu	Thr	Ser	Val	Val	Thr	Pro	Arg	Pro	Phe	Gly
			20					25					30		
Ser	Gln	Thr	Arg	Gly	Ile	Ser	Ser	Leu	Pro	Arg	Ser	Tyr	Thr	Met	Asp
		35					40					45			
Asp	Ala	Trp	Lys	Tyr	Asn	Gly	Asp	Val	Glu	Asp	Ile	Lys	Arg	Thr	Pro
	50					55					60				
Asn	Asn	Val	Val	Ser	Thr	Pro	Ala	Pro	Ser	Pro	Asp	Ala	Ser	Gln	Leu
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			85						90				95		
Val	Thr	Arg	Leu	Pro	Ser	Pro	Thr	Ser	Pro	Phe	Ser	Ser	Leu	Ser	Gln
			100						105				110		
Asp	Gln	Ala	Ala	Thr	Ser	Lys	Ala	Thr	Leu	Ser	Ser	Thr	Ser	Gly	Leu
		115					120					125			
Asp	Leu	Met	Ser	Glu	Ser	Gly	Glu	Gly	Glu	Ile	Ser	Pro	Gln	Arg	Glu
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Val	Ser	Arg	Ser	Gln	Asp	Gln	Phe	Ser	Asp	Met	Arg	Ile	Ser	Ile	Asn

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Gln Thr Pro Gly Lys Ser Leu Asp Phe Gly Phe Thr Ile Lys Trp Asp						
	165			170		175
Ile Pro Gly Ile Phe Val Ala Ser Val Glu Ala Gly Ser Pro Ala Glu						
	180			185		190
Phe Ser Gln Leu Gln Val Asp Asp Glu Ile Ile Ala Ile Asn Asn Thr						
	195			200		205
Lys Phe Ser Tyr Asn Asp Ser Lys Glu Trp Glu Glu Ala Met Ala Lys						
	210			215		220
Ala Gln Glu Thr Gly His Leu Val Met Asp Val Arg Arg Tyr Gly Lys						
	225			230		235
Ala Gly Ser Pro Glu Thr Lys Trp Ile Asp Ala Thr Ser Gly Ile Tyr						
	245			250		255
Asn Ser Glu Lys Ser Ser Asn Leu Ser Val Thr Thr Asp Phe Ser Glu						
	260			265		270
Ser Leu Gln Ser Ser Asn Ile Glu Ser Lys Glu Ile Asn Gly Ile His						
	275			280		285
Asp Glu Ser Asn Ala Phe Glu Ser Lys Ala Ser Glu Ser Ile Ser Leu						
	290			295		300
Lys Asn Leu Lys Arg Arg Ser Gln Phe Phe Glu Gln Gly Ser Ser Asp						
	305			310		315
Ser Val Val Pro Asp Leu Pro Val Pro Thr Ile Ser Ala Pro Ser Arg						
	325			330		335
Trp Val Trp Asp Gln Glu Glu Glu Arg Lys Arg Gln Glu Arg Trp Gln						
	340			345		350
Lys Glu Gln Asp Arg Leu Leu Gln Glu Lys Tyr Gln Arg Glu Gln Glu						
	355			360		365
Lys Leu Arg Glu Glu Trp Gln Arg Ala Lys Gln Glu Ala Glu Arg Glu						
	370			375		380
Asn Ser Lys Tyr Leu Asp Glu Glu Leu Met Val Leu Ser Ser Asn Ser						
	385			390		395
Met Ser Leu Thr Thr Arg Glu Pro Ser Leu Ala Thr Trp Glu Ala Thr						
	405			410		415
Trp Ser Glu Gly Ser Lys Ser Ser Asp Arg Glu Gly Thr Arg Ala Gly						
	420			425		430
Glu Glu Glu Arg Arg Gln Pro Gln Glu Glu Val Val His Glu Asp Gln						
	435			440		445
Gly Lys Lys Pro Gln Asp Gln Leu Val Ile Glu Arg Glu Arg Lys Trp						
	450			455		460
Glu Gln Gln Leu Gln Glu Glu Gln Glu Gln Lys Arg Leu Gln Ala Glu						
	465			470		475
Ala Glu Glu Gln Lys Arg Pro Ala Glu Glu Gln Lys Arg Gln Ala Glu						
	485			490		495
Ile Glu Arg Glu Thr Ser Val Arg Ile Tyr Gln Tyr Arg Arg Pro Val						
	500			505		510
Asp Ser Tyr Asp Ile Pro Lys Thr Glu Glu Ala Ser Ser Gly Phe Leu						
	515			520		525
Pro Gly Asp Arg Asn Lys Ser Arg Ser Thr Thr Glu Leu Asp Asp Tyr						
	530			535		540
Ser Thr Asn Lys Asn Gly Asn Asn Lys Tyr Leu Asp Gln Ile Gly Asn						
	545			550		555
Thr Thr Ser Ser Gln Arg Arg Ser Lys Lys Glu Gln Val Pro Ser Gly						
	565			570		575
Ala Glu Leu Glu Arg Gln Gln Ile Leu Gln Glu Met Arg Lys Arg Thr						

			580					585					590						
Pro	Leu	His	Asn	Asp	Asn	Ser	Trp	Ile	Arg	Gln	Arg	Ser	Ala	Ser	Val				
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Leu	Asp	Asn	Leu	Asp	Ser	Pro	Arg	Ser	Asn	Ser	Trp	Arg	Gln	Pro	Pro				
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Phe	Ser	Arg	Pro	Pro	Pro	Gln	Leu	Val	Ser	Thr	Ser	Asn	Arg	Ala	Tyr				
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Lys	Thr	Ser	Thr	Thr	Gly	Val	Ala	Thr	Thr	Gln	Ser	Pro	Thr	Pro	Arg				
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Ser	His	Ser	Pro	Ser	Ala	Ser	Gln	Ser	Gly	Ser	Gln	Leu	Arg	Asn	Arg				
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Ser	Val	Ser	Gly	Lys	Arg	Ile	Cys	Ser	Tyr	Cys	Asn	Asn	Ile	Leu	Gly				
			725				730						735						
Lys	Gly	Ala	Ala	Met	Ile	Ile	Glu	Ser	Leu	Gly	Leu	Cys	Tyr	His	Leu				
		740				745						750							
His	Cys	Phe	Lys	Cys	Val	Ala	Cys	Glu	Cys	Asp	Leu	Gly	Gly	Ser	Ser				
	755					760					765								
Ser	Gly	Ala	Glu	Val	Arg	Ile	Arg	Asn	His	Gln	Leu	Tyr	Cys	Asn	Asp				
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<210> 731

<211> 513

<212> DNA

<213> Homo sapiens

<400> 731

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513

<210> 732

<211> 113
 <212> PRT
 <213> Homo sapiens

<400> 732
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 35 40 45
 Leu Ile Leu Pro Pro Pro Leu His Thr Tyr Leu Glu Leu Lys Glu Gln
 50 55 60
 His Met Cys Thr Cys Ser Ser Arg Lys His Phe Pro Leu Ser Phe Leu
 65 70 75 80
 Trp Pro Asp Lys Val Leu Thr Pro Ser Arg Gln Pro Glu Ser Val Phe
 85 90 95
 Pro Thr Ile Cys Phe Pro Ser Gln Ser Phe Glu Glu Ser Arg Glu Ala
 100 105 110
 Glu

<210> 733
 <211> 4366
 <212> DNA
 <213> Homo sapiens

<400> 733
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<210> 734

<211> 364

<212> PRT

<213> Homo sapiens

<400> 734

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			20					25					30		
Ala	His	Ile	Arg	Ala	Ser	Phe	Arg	Asp	Gly	Asp	Pro	Val	His	Arg	His
		35					40					45			
Arg	Gln	Leu	Ala	Lys	Leu	Leu	Tyr	Val	His	Met	Leu	Gly	Tyr	Pro	Ala
	50				55						60				
His	Phe	Gly	Gln	Met	Glu	Cys	Leu	Lys	Leu	Ile	Ala	Ser	Ser	Arg	Phe
65				70					75					80	
Thr	Asp	Lys	Arg	Val	Gly	Tyr	Leu	Gly	Ala	Met	Leu	Leu	Leu	Asp	Glu
			85					90						95	
Arg	His	Asp	Ala	His	Leu	Leu	Ile	Thr	Asn	Ser	Ile	Lys	Asn	Asp	Leu
			100					105					110		
Ser	Gln	Gly	Ile	Gln	Pro	Val	Gln	Gly	Leu	Ala	Leu	Cys	Thr	Leu	Ser
		115					120					125			
Thr	Met	Gly	Ser	Ala	Glu	Met	Cys	Arg	Asp	Leu	Ala	Pro	Glu	Val	Glu
	130					135					140				
Lys	Leu	Leu	Leu	Gln	Pro	Ser	Pro	Tyr	Val	Arg	Lys	Lys	Ala	Ile	Leu
145				150						155				160	
Thr	Ala	Val	His	Met	Ile	Arg	Lys	Val	Pro	Glu	Leu	Ser	Ser	Val	Phe
			165					170						175	
Leu	Pro	Pro	Cys	Ala	Gln	Leu	Leu	His	Glu	Arg	His	His	Gly	Ile	Leu
		180						185					190		
Leu	Gly	Thr	Ile	Thr	Leu	Ile	Thr	Glu	Leu	Cys	Glu	Arg	Ser	Pro	Ala
	195						200					205			
Ala	Leu	Arg	His	Phe	Arg	Lys	Val	Val	Pro	Gln	Leu	Val	His	Ile	Leu
	210					215					220				
Arg	Thr	Leu	Val	Thr	Met	Gly	Tyr	Ser	Thr	Glu	His	Ser	Ile	Ser	Gly
225				230						235				240	
Val	Ser	Asp	Pro	Phe	Leu	Gln	Val	Gln	Ile	Leu	Arg	Leu	Leu	Arg	Ile
			245					250						255	
Leu	Gly	Arg	Asn	His	Glu	Glu	Ser	Ser	Glu	Thr	Met	Asn	Asp	Leu	Leu
		260						265					270		
Ala	Gln	Val	Ala	Thr	Asn	Thr	Asp	Thr	Ser	Arg	Asn	Ala	Gly	Asn	Ala

275	280	285
Val Leu Phe Glu Thr	Val Leu Thr Ile Met Asp	Ile Arg Ser Ala Ala
290	295	300
Gly Leu Arg Val Leu Ala	Val Asn Ile Leu Gly Arg	Phe Leu Leu Asn
305	310	315
Ser Asp Arg Asn Ile Arg Tyr Val	Ala Leu Thr Ser Leu Leu Arg	Leu
325	330	335
Val Gln Ser Asp His Ser Ala	Val Gln Arg His Arg Pro Thr	Val Val
340	345	350
Glu Cys Leu Arg Glu Thr Asp	Ala Ser Leu Ser Arg	
355	360	

<210> 735

<211> 597

<212> DNA

<213> Homo sapiens

<400> 735

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<210> 736

<211> 175

<212> PRT

<213> Homo sapiens

<400> 736

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Thr Gln Asp Ile Leu Ser Ala Ile His Asp Val Ala Ala Pro Leu Ala
35 40 45
Leu Pro Ile Phe Val Val Gly Ala Thr Ala Arg Asp Ile Leu Leu Thr
50 55 60
His Val Phe Gly Ile Glu Thr Gly Arg Ala Thr Leu Asp Val Asp Phe

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65              70              75              80
Ala Val Ala Val Glu His Trp Pro Gln Phe Glu Asn Ile Lys Gln His
              85              90              95
Leu Leu Ala Asn Asp His Phe Asp Ser Ala Ala Ser Ile Thr His Arg
              100             105             110
Leu Leu Tyr Arg Thr Ser Asp Asn Thr Ile Ala Arg Pro Ile Asp Leu
              115             120             125
Ile Pro Phe Gly Gly Ile Glu Gln Pro Pro Ala Thr Ile Lys Trp Pro
              130             135             140
Pro Asp Met Ala Val Met Met Asn Val Ala Gly Tyr Ala Asp Ala Trp
145              150              155              160
Arg Ala Ala Val Glu Val Glu Phe Val Pro Gly Arg Ser Ile Arg
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<210> 737
 <211> 497
 <212> DNA
 <213> Homo sapiens

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<400> 737
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360
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497

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<210> 738
 <211> 165
 <212> PRT
 <213> Homo sapiens

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<400> 738
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Pro His Ala Asp Arg Ala Asp Leu His Pro Ala Leu Ser Trp Ile Ser
              35              40              45
His Val Thr Phe Val Lys Thr Val Ser Val Gly Asp Thr Ile Gly Tyr
              50              55              60
Gly Arg Thr Trp Thr Ala Ser Glu Thr Thr Lys Ile Ala Thr Val Pro

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65		70		75		80									
Val	Gly	Tyr	Ala	Asp	Gly	Leu	Ser	Arg	Gly	Leu	Ser	Asn	Lys	Gly	His
			85						90					95	
Val	Leu	Ile	Arg	Gly	Ser	Val	His	Pro	Ile	Val	Gly	Arg	Ile	Cys	Met
			100					105					110		
Asp	Gln	Phe	Met	Val	Asp	Leu	Gly	Pro	Asp	Ser	Asn	Val	Thr	Val	Gly
		115					120					125			
Asp	Glu	Val	Val	Leu	Ile	Gly	Thr	Gln	Glu	Asp	Glu	Thr	Leu	Thr	Ala
	130					135					140				
Asp	Asp	Met	Ala	Glu	Leu	Leu	Gly	Thr	Ile	Ser	Tyr	Glu	Ile	Thr	Cys
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Ala	Ile	Ser	Lys	Arg											
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<210> 739

<211> 438

<212> DNA

<213> Homo sapiens

<400> 739

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 gccgaccagc ccccgctctg cgccccgag gacgacgcc agctccagct ggcccttagt
 240
 ttgagccgag aagagcatga taaggaggag cggatccgtc gcggggatga cctgcggctg
 300
 cagatggcaa tcgaggagag caagagggag actgggggca aggaggagtc gtcctcatg
 360
 gaccttgctg acgtcttcac gccccagct cctgccccga ccacagaccc ctggggggggc
 420
 ccagcaccca tggctgct
 438

<210> 740

<211> 146

<212> PRT

<213> Homo sapiens

<400> 740

Arg	Leu	Arg	Glu	Glu	Arg	Ala	His	Ala	Leu	Lys	Thr	Lys	Glu	Lys	Leu
1				5					10					15	
Ala	Gln	Thr	Ala	Thr	Ala	Ser	Ser	Ala	Ala	Val	Gly	Ser	Gly	Pro	Pro
			20					25					30		
Pro	Glu	Ala	Glu	Gln	Ala	Trp	Pro	Gln	Ser	Ser	Gly	Glu	Glu	Glu	Leu
		35				40					45				
Gln	Leu	Gln	Leu	Ala	Leu	Ala	Met	Ser	Lys	Glu	Glu	Ala	Asp	Gln	Pro
	50					55				60					
Pro	Ser	Cys	Gly	Pro	Glu	Asp	Asp	Ala	Gln	Leu	Gln	Leu	Ala	Leu	Ser
65					70				75					80	
Leu	Ser	Arg	Glu	Glu	His	Asp	Lys	Glu	Glu	Arg	Ile	Arg	Arg	Gly	Asp

	85		90		95										
Asp	Leu	Arg	Leu	Gln	Met	Ala	Ile	Glu	Glu	Ser	Lys	Arg	Glu	Thr	Gly
			100					105					110		
Gly	Lys	Glu	Glu	Ser	Ser	Leu	Met	Asp	Leu	Ala	Asp	Val	Phe	Thr	Pro
		115				120					125				
Pro	Ala	Pro	Ala	Pro	Thr	Thr	Asp	Pro	Trp	Gly	Gly	Pro	Ala	Pro	Met
	130				135						140				
Ala	Ala														
145															

<210> 741
 <211> 726
 <212> DNA
 <213> Homo sapiens

<400> 741
 gcctctctcc gaccgcgttg ttgtaaggat gtcgcgacgg tgcgcaaaaa tgaatatgtg
 60
 aatttgccgg tcattctgct cgtcggggccc actgctagcg gaaaatcagg gctagcgggtg
 120
 cgagtgtgcc gccgcttgta tgcgatgag caccgcccg aaattattaa tactgactcg
 180
 atggtggtgt atcgcgggat ggacattggc actgccaccc ctacactgcg cgagcagcgc
 240
 acggtagtgc atcacctggt gtcgattctt gatgtgactg tgccctcctc gctagtactg
 300
 atgcagacgc tggcccgtga tgccgtcgag gattgtctgt cgcggtggtgt catccctgtc
 360
 ttggtgggag ggtctgcgct gtacaccaag gccatcattg acgaaatgtc catcccgcca
 420
 actgatccgg aagtgagggc tcggtggcag gagaagctag atgccgaggg gccgcgagtt
 480
 ctgcatgacg agcttgcccc tcgcatccc aaggcggctg agtcaatctt gcccggaac
 540
 ggcaggcgaa tcgtttcgtg ccctcgaagt ttattgaccc tgacagggtc ctttactgcc
 600
 accgatcccc gacgggaccc tccactggcc aagacggtgc aaatgggctt agaactgtcg
 660
 cgcaaagaca tagaccagcg tattgccgat cgggttgacc agatgtgggc atacggtttc
 720
 gtcgac
 726

<210> 742
 <211> 242
 <212> PRT
 <213> Homo sapiens

<400> 742															
Ala	Ser	Leu	Arg	Pro	Arg	Cys	Cys	Lys	Asp	Val	Ala	Thr	Val	Arg	Lys
1				5				10						15	
Asn	Glu	Tyr	Val	Asn	Leu	Pro	Val	Ile	Cys	Leu	Val	Gly	Pro	Thr	Ala
			20					25				30			
Ser	Gly	Lys	Ser	Gly	Leu	Ala	Val	Arg	Val	Cys	Arg	Arg	Leu	Tyr	Val


```

      35      40      45
Asp Glu His Pro Ala Glu Ile Ile Asn Thr Asp Ser Met Val Val Tyr
  50      55      60
Arg Gly Met Asp Ile Gly Thr Ala Thr Pro Thr Leu Arg Glu Gln Arg
  65      70      75      80
Thr Val Val His His Leu Val Ser Ile Leu Asp Val Thr Val Pro Ser
      85      90      95
Ser Leu Val Leu Met Gln Thr Leu Ala Arg Asp Ala Val Glu Asp Cys
      100      105      110
Leu Ser Arg Gly Val Ile Pro Val Leu Val Gly Gly Ser Ala Leu Tyr
      115      120      125
Thr Lys Ala Ile Ile Asp Glu Met Ser Ile Pro Pro Thr Asp Pro Glu
      130      135      140
Val Arg Ala Arg Trp Gln Glu Lys Leu Asp Ala Glu Gly Pro Arg Val
      145      150      155      160
Leu His Asp Glu Leu Ala Arg Arg Asp Pro Lys Ala Ala Glu Ser Ile
      165      170      175
Leu Pro Gly Asn Gly Arg Arg Ile Val Ser Cys Pro Arg Ser Leu Leu
      180      185      190
Thr Leu Thr Gly Ser Phe Thr Ala Thr Asp Pro Arg Arg Asp Pro Pro
      195      200      205
Leu Ala Lys Thr Val Gln Met Gly Leu Glu Leu Ser Arg Lys Asp Ile
      210      215      220
Asp Gln Arg Ile Ala Asp Arg Val Asp Gln Met Trp Ala Tyr Gly Phe
      225      230      235      240
Val Asp

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<210> 743
 <211> 430
 <212> DNA
 <213> Homo sapiens

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<400> 743
naaaaaagtg atggtttcgg atctgtggcc agtcgtcttg caagaaatca ttatgacgtg
60
gatgagggca acagcancat tcatgttaat caagacattg cgcgcagaac agggacggga
120
aagctattgg tacgagtgtg cccggcgcac gtgtactcag aggagcccga tggcactatt
180
tccgtggagt acgcagcgtg tctggagtgt ggcacttgtc tggcggttgc tgcgccaggg
240
tcgcttgaat ggcactatcc cgcaggtgca atgggtatatt cgttcagaga aggatgaagt
300
ccttgtgggc gactgtaaag cgacatggcc gtcgctcggg aggaggaatt gtggtgtccg
360
caccaaatag tgctcaggat gaagttcgtc atggaaatcc ggctccaacc gtttcgggag
420
ctgggtcgga
430

```

<210> 744
 <211> 98
 <212> PRT

<213> Homo sapiens

<400> 744

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Xaa Lys Ser Asp Gly Phe Gly Ser Val Ala Ser Arg Leu Ala Arg Asn
 1           5           10           15
His Tyr Asp Val Asp Glu Gly Asn Ser Xaa Ile His Val Asn Gln Asp
          20           25           30
Ile Ala Arg Arg Thr Gly Thr Gly Lys Leu Leu Val Arg Val Cys Pro
          35           40           45
Ala His Val Tyr Ser Glu Glu Pro Asp Gly Thr Ile Ser Val Glu Tyr
          50           55           60
Ala Ala Cys Leu Glu Cys Gly Thr Cys Leu Ala Val Ala Ala Pro Gly
65           70           75           80
Ser Leu Glu Trp His Tyr Pro Ala Gly Ala Met Gly Ile Ser Phe Arg
          85           90           95
Glu Gly

```

<210> 745

<211> 362

<212> DNA

<213> Homo sapiens

<400> 745

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cggccgattg aagcgtcgct gcggtttgag tcggtgatgg atgcggtgga cggtgcttcg
60
gcgtcgtggt ggcgcatggc gcggtatttc atcgccgagc ttgaacgcag cagcgagttg
120
tatgagcagg cggcgtttac ccgcgatctg gaaagctcgc tgatcaaggg cctgacctc
180
gccagccga acaactactc cgaagaactg cgcgacgtac tcggcgtgaa gctgccgcat
240
tacttgattc gcgcgcggca gtacatccac gacaacgccc gcgaagccgt gcatctggaa
300
gacctggaaa ccgctgccgg ggtatcgcgg ttcaagttgt tcgatgcggt tcgcaaatac
360
tt
362

```

<210> 746

<211> 108

<212> PRT

<213> Homo sapiens

<400> 746

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Met Asp Ala Val Asp Gly Ala Ser Ala Ser Trp Trp Arg Met Ala Arg
 1           5           10           15
Tyr Phe Ile Ala Glu Leu Glu Arg Ser Ser Glu Leu Tyr Glu Gln Ala
          20           25           30
Ala Phe Thr Arg Asp Leu Glu Ser Ser Leu Ile Lys Gly Leu Ile Leu
          35           40           45
Ala Gln Pro Asn Asn Tyr Ser Glu Glu Leu Arg Asp Val Leu Gly Val
          50           55           60
Lys Leu Pro His Tyr Leu Ile Arg Ala Arg Gln Tyr Ile His Asp Asn

```

65		70		75		80									
Ala	Arg	Glu	Ala	Val	His	Leu	Glu	Asp	Leu	Glu	Thr	Ala	Ala	Gly	Val
			85					90						95	
Ser	Arg	Phe	Lys	Leu	Phe	Asp	Ala	Phe	Arg	Lys	Tyr				
			100					105							

<210> 747
 <211> 416
 <212> DNA
 <213> Homo sapiens

<400> 747
 nacgcgttga tcgccgccga ccgtttcatc ccgcaatcac ccgacatggc ggcctatttt
 60
 ctgaatgccg atggcacgcc taaagccacc ggcacgctgc tcaagaaccc agcgctggcc
 120
 gccgtgttca aacgtatcgc caaggaagga ccggacgcgc tgtaccacgg gccgattgcc
 180
 gacgagatcg cgcgcaaggt tcagggcaac cgcaatgcgg gcagcctgtc gcaagcggac
 240
 ctcaaggctt acaccgcaa ggaacgcacg ccgctgtgca ccgactacaa gcaatatcag
 300
 gtgtgcggca tgccaccgcc gtcgtcaggc gggattgcgg tggcgcagat cctcggcacg
 360
 ctgcaggccg tggaagcccg cgacccacgc ctggccatcg ccccatgaa accggt
 416

<210> 748
 <211> 138
 <212> PRT
 <213> Homo sapiens

<400> 748
 Xaa Ala Leu Ile Ala Ala Asp Arg Phe Ile Pro Gln Ser Pro Asp Met
 1 5 10 15
 Ala Ala Tyr Phe Leu Asn Ala Asp Gly Thr Pro Lys Ala Thr Gly Thr
 20 25 30
 Leu Leu Lys Asn Pro Ala Leu Ala Ala Val Phe Lys Arg Ile Ala Lys
 35 40 45
 Glu Gly Pro Asp Ala Leu Tyr His Gly Pro Ile Ala Asp Glu Ile Ala
 50 55 60
 Arg Lys Val Gln Gly Asn Arg Asn Ala Gly Ser Leu Ser Gln Ala Asp
 65 70 75 80
 Leu Lys Ala Tyr Thr Ala Lys Glu Arg Thr Pro Leu Cys Thr Asp Tyr
 85 90 95
 Lys Gln Tyr Gln Val Cys Gly Met Pro Pro Pro Ser Ser Gly Gly Ile
 100 105 110
 Ala Val Ala Gln Ile Leu Gly Thr Leu Gln Ala Val Glu Ala Arg Asp
 115 120 125
 Pro Arg Leu Ala Ile Ala Pro Met Lys Pro
 130 135

<210> 749
 <211> 1211

<212> DNA

<213> Homo sapiens

<400> 749

nagtcctaga cgccagaccc gctcagaccc tcctgccagg tgacagccgc caagatgggg
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tcttgggccc tgctgtggcc tcccctgctg ttcaccgggc tgctcgtccg acccccgggg
120
accatggccc aggcccagta ctgctctgtg aacaaggaca tctttgaagt agaggagAAC
180
acaaatgtca ccgagccgct ggtggacatc cacgtcccgg agggccagga ggtgaccctc
240
ggagccttgt ccaccccctt tgcatttcgg atccaggga accagctgtt tctcaacgtg
300
actcctgatt acgaggagaa gtcactgctt gaggctcagc tgctgtgtca gagcggaggc
360
acattggtga cccagctaag ggtgttcgtg tcagtgtctg acgtcaatga caatgcccc
420
gaattcccct ttaagaccaa ggagataagg gtggaggagg acacgaaagt gaactccacc
480
gtcatccccg agacgcaact gcaggctgag gaccgcgaca aggacgacat tctgttctac
540
accctccagg aaatgacagc aggtgccagt gactacttct ccctgggtgag tgtaaaccgt
600
cccgccctga ggctggaccg gcccctggac ttctacgagc ggccgaacat gaccttctgg
660
ctgctggtgc gggacactcc gggggagaat gtggaaccca gccacactgc caccgccaca
720
ctagtgtga acgtggtgcc cggcgacctg cggccccctg ggttcctgcc ctgcaccttc
780
tcagatggct acgtctgcat tcaagctcag taccacgggg ctgtccccac ggggcacata
840
ctgccatctc ccctcgtcct gcgtcccga cccatctacg ctgaggacgg agaccgcggc
900
atcaaccagc ccatcatcta cagcatcttt aggggaaacg tgaatggtac attcatcatc
960
caccagact cgggcaacct caccgtggcc aggagtgtcc ccagcccat gaccttcctt
1020
ctgctggtga agggccaaca ggccgacctt gccgctact cagtgacca ggtcaccgtg
1080
gagggtgtg gctgcggccg ggagcccgcc ccgcttcccc cagagcctgt atcgtggcac
1140
cgtggcgctg ggcgctggag cgggcgttgt ggtcaaggat gcagctgccc cttttcagcc
1200
tctgaggatc c
1211

<210> 750

<211> 385

<212> PRT

<213> Homo sapiens

<400> 750

Met Gly Ser Trp Ala Leu Leu Trp Pro Pro Leu Leu Phe Thr Gly Leu

1	5	10	15
Leu Val Arg Pro Pro Gly Thr Met Ala Gln Ala Gln Tyr Cys Ser Val			
20	25	30	
Asn Lys Asp Ile Phe Glu Val Glu Glu Asn Thr Asn Val Thr Glu Pro			
35	40	45	
Leu Val Asp Ile His Val Pro Glu Gly Gln Glu Val Thr Leu Gly Ala			
50	55	60	
Leu Ser Thr Pro Phe Ala Phe Arg Ile Gln Gly Asn Gln Leu Phe Leu			
65	70	75	80
Asn Val Thr Pro Asp Tyr Glu Glu Lys Ser Leu Leu Glu Ala Gln Leu			
85	90	95	
Leu Cys Gln Ser Gly Gly Thr Leu Val Thr Gln Leu Arg Val Phe Val			
100	105	110	
Ser Val Leu Asp Val Asn Asp Asn Ala Pro Glu Phe Pro Phe Lys Thr			
115	120	125	
Lys Glu Ile Arg Val Glu Glu Asp Thr Lys Val Asn Ser Thr Val Ile			
130	135	140	
Pro Glu Thr Gln Leu Gln Ala Glu Asp Arg Asp Lys Asp Asp Ile Leu			
145	150	155	160
Phe Tyr Thr Leu Gln Glu Met Thr Ala Gly Ala Ser Asp Tyr Phe Ser			
165	170	175	
Leu Val Ser Val Asn Arg Pro Ala Leu Arg Leu Asp Arg Pro Leu Asp			
180	185	190	
Phe Tyr Glu Arg Pro Asn Met Thr Phe Trp Leu Leu Val Arg Asp Thr			
195	200	205	
Pro Gly Glu Asn Val Glu Pro Ser His Thr Ala Thr Ala Thr Leu Val			
210	215	220	
Leu Asn Val Val Pro Ala Asp Leu Arg Pro Pro Trp Phe Leu Pro Cys			
225	230	235	240
Thr Phe Ser Asp Gly Tyr Val Cys Ile Gln Ala Gln Tyr His Gly Ala			
245	250	255	
Val Pro Thr Gly His Ile Leu Pro Ser Pro Leu Val Leu Arg Pro Gly			
260	265	270	
Pro Ile Tyr Ala Glu Asp Gly Asp Arg Gly Ile Asn Gln Pro Ile Ile			
275	280	285	
Tyr Ser Ile Phe Arg Gly Asn Val Asn Gly Thr Phe Ile Ile His Pro			
290	295	300	
Asp Ser Gly Asn Leu Thr Val Ala Arg Ser Val Pro Ser Pro Met Thr			
305	310	315	320
Phe Leu Leu Leu Val Lys Gly Gln Gln Ala Asp Leu Ala Arg Tyr Ser			
325	330	335	
Val Thr Gln Val Thr Val Glu Gly Cys Gly Cys Gly Arg Glu Pro Ala			
340	345	350	
Pro Leu Pro Pro Glu Pro Val Ser Trp His Arg Gly Ala Trp Arg Trp			
355	360	365	
Ser Gly Arg Cys Gly Gln Gly Cys Ser Cys Pro Phe Ser Ala Ser Glu			
370	375	380	
Asp			
385			

<210> 751

<211> 345

<212> DNA

<213> Homo sapiens

<400> 751

cgcgctcgcg tcacgtcaa cgacatgagc gaggtcaaca tcgacgcggc gctggtggcg
60
gcaggcgcg ggctgtcgcg caccgaggag aagctcgctg agatgtcgaa cggctgcac
120
tgctgcacgc tgcgcgacga cctgatgcag gaagtggcga gactggcggg cgaaggccgc
180
ttcgatgcgc tggatcatga gagcaccggc gtgtccgagc cgatgccggc cgccgccacg
240
ttcgatttcc gtgaccagga cggcgtctcg ctcgccgacg tcgcgcggct ggataccatg
300
gtcaccgtcg tcgacgcgcg gtccttcctg cgcgactacg gctcg
345

<210> 752

<211> 115

<212> PRT

<213> Homo sapiens

<400> 752

Arg	Val	Ala	Val	Ile	Val	Asn	Asp	Met	Ser	Glu	Val	Asn	Ile	Asp	Ala
1				5				10						15	
Ala	Leu	Val	Ala	Ala	Gly	Gly	Gly	Leu	Ser	Arg	Thr	Glu	Glu	Lys	Leu
			20					25						30	
Val	Glu	Met	Ser	Asn	Gly	Cys	Ile	Cys	Cys	Thr	Leu	Arg	Asp	Asp	Leu
		35					40						45		
Met	Gln	Glu	Val	Ala	Arg	Leu	Ala	Gly	Glu	Gly	Arg	Phe	Asp	Ala	Leu
	50					55					60				
Val	Ile	Glu	Ser	Thr	Gly	Val	Ser	Glu	Pro	Met	Pro	Val	Ala	Ala	Thr
65					70					75				80	
Phe	Asp	Phe	Arg	Asp	Gln	Asp	Gly	Val	Ser	Leu	Ala	Asp	Val	Ala	Arg
			85						90					95	
Leu	Asp	Thr	Met	Val	Thr	Val	Val	Asp	Ala	Ala	Ser	Phe	Leu	Arg	Asp
			100					105						110	
Tyr	Gly	Ser													
			115												

<210> 753

<211> 352

<212> DNA

<213> Homo sapiens

<400> 753

gcgcgccagt acgccaagac cgtccgcaag gaccgcaagg gcgaacggcg gcgtcggggc
60
gcgtcggact agtccacgat gcatccgaac cgcgccttcc gctttgccga tgatgtctcg
120
atgctcgatt tcgcggccaa gcgagccttt gcgcacatct tcgtgagcac gcccgagggg
180
cctatggtag cgcattgccc gggtacgccc ttcgacggag ccttcgctt ccatgtcgcg
240
cgcggaatc ggatcgcgcg gcacctggat ggcgcgacgc tgctgctcag catcagcgcg
300

accgacggct atatcagccc gagctggtac gccgaccgc agggaccaca gt
352

<210> 754

<211> 91

<212> PRT

<213> Homo sapiens

<400> 754

Met	His	Pro	Asn	Arg	Ala	Phe	Arg	Phe	Ala	Asp	Asp	Val	Ser	Met	Leu
1			5					10					15		
Asp	Phe	Ala	Ala	Lys	Arg	Ala	Phe	Ala	His	Ile	Phe	Val	Ser	Thr	Pro
		20					25				30				
Glu	Gly	Pro	Met	Val	Ala	His	Ala	Pro	Val	Thr	Pro	Phe	Asp	Gly	Ala
		35				40					45				
Phe	Arg	Phe	His	Val	Ala	Arg	Gly	Asn	Arg	Ile	Ala	Arg	His	Leu	Asp
	50				55				60						
Gly	Ala	Thr	Leu	Leu	Leu	Ser	Ile	Ser	Ala	Thr	Asp	Gly	Tyr	Ile	Ser
65				70				75						80	
Pro	Ser	Trp	Tyr	Ala	Asp	Pro	Gln	Gly	Pro	Gln					
				85				90							

<210> 755

<211> 301

<212> DNA

<213> Homo sapiens

<400> 755

tgggatgcag ggtctttctt ctccaaggat ttcattcctg gagggagaaa agggccccag
60
ctgtctgcca tcaaaccggg ttgccgggct ggagctcctc ccaggcccgt gtgaggaaga
120
gcaaaggccg gcaggggctc gatgggacca gtcgctcgct caggcccagg aaaaccacac
180
agctgggggc tgtcaggatt ggaccagggt caggccggcc aggcgatggc gggaaaagca
240
ggcccactct gcagacctca atgtctcagg tgcactgcag ggcaaccccc cctacccccg
300
g
301

<210> 756

<211> 99

<212> PRT

<213> Homo sapiens

<400> 756

Met	Gln	Gly	Leu	Ser	Ser	Pro	Arg	Ile	Ser	Phe	Leu	Glu	Gly	Glu	Lys
1			5					10					15		
Gly	Pro	Ser	Cys	Leu	Pro	Ser	Asn	Arg	Val	Ala	Gly	Leu	Glu	Leu	Leu
		20					25				30				
Pro	Gly	Pro	Cys	Glu	Glu	Glu	Gln	Arg	Pro	Ala	Gly	Ala	Arg	Trp	Asp
	35					40				45					
Gln	Ser	Leu	Ala	Gln	Ala	Gln	Glu	Asn	His	Thr	Ala	Gly	Gly	Cys	Gln

50 55 60
 Asp Trp Thr Arg Val Arg Pro Ala Arg Arg Trp Arg Glu Lys Gln Ala
 65 70 75 80
 His Ser Ala Asp Leu Asn Val Ser Gly Ala Leu Gln Gly Asn Pro Ala
 85 90 95
 Tyr Pro Gly

<210> 757
 <211> 311
 <212> DNA
 <213> Homo sapiens

<400> 757
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 60
 gtctccgatg ttctctacgt catcgaggcc aaccccaggg catcgcgcac agtcccccttc
 120
 gtctcaaagg catccggcgt gcagctcgcc aaagcggcgg ccctcatcat gacaggggag
 180
 acgatcgctt cgctcaggcg ctccggccac ctgcccaggg ccgacgccgc cgtcaccgat
 240
 cccgatgacc cgatcgccgt caaggaggcg gtctaccct tcaaacgatt ccgcaccacc
 300
 gagggacgcg t
 311

<210> 758
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 758
 Thr Glu Ala Ile Ala Arg Gly Val Gly Val Arg Gly Leu Leu Asn Ile
 1 5 10 15
 Gln Phe Ala Leu Val Ser Asp Val Leu Tyr Val Ile Glu Ala Asn Pro
 20 25 30
 Arg Ala Ser Arg Thr Val Pro Phe Val Ser Lys Ala Ser Gly Val Gln
 35 40 45
 Leu Ala Lys Ala Ala Ala Leu Ile Met Thr Gly Glu Thr Ile Ala Ser
 50 55 60
 Leu Arg Arg Ser Gly His Leu Pro Glu Ala Asp Ala Ala Val Thr Asp
 65 70 75 80
 Pro Asp Asp Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Lys Arg
 85 90 95
 Phe Arg Thr Thr Glu Gly Arg
 100

<210> 759
 <211> 391
 <212> DNA
 <213> Homo sapiens

<400> 759

gtgcacaccg gcaagctggt gtggaactgg gacagcggca acccggacga cactacgccg
60
attgccgagg gcaagaccta cacccgcaac tcgccgaaca tgtgggtccat gttcgccgtc
120
gacgaaaaac tcggcatgct ctacctgccg atgggcaacc agaccccgga ccagttcggg
180
ggctaccgca cgcctgcgtc ggaactgcac gctgccggcc tgacagcgct ggatatcgac
240
actggtaaag tgcgctggca ctaccagttc acccaccatg acctgtggga catggacgtg
300
ggcggccagc cgagcctgat cgacatcaag accgccgccg gcgtgaaaca agccgtgatg
360
gcctcgacca agcaaggcag catctacgcy t
391

<210> 760
<211> 130
<212> PRT
<213> Homo sapiens

<400> 760
Val His Thr Gly Lys Leu Val Trp Asn Trp Asp Ser Gly Asn Pro Asp
1 5 10 15
Asp Thr Thr Pro Ile Ala Glu Gly Lys Thr Tyr Thr Arg Asn Ser Pro
20 25 30
Asn Met Trp Ser Met Phe Ala Val Asp Glu Lys Leu Gly Met Leu Tyr
35 40 45
Leu Pro Met Gly Asn Gln Thr Pro Asp Gln Phe Gly Gly Tyr Arg Thr
50 55 60
Pro Ala Ser Glu Leu His Ala Ala Gly Leu Thr Ala Leu Asp Ile Asp
65 70 75 80
Thr Gly Lys Val Arg Trp His Tyr Gln Phe Thr His His Asp Leu Trp
85 90 95
Asp Met Asp Val Gly Gly Gln Pro Ser Leu Ile Asp Ile Lys Thr Ala
100 105 110
Ala Gly Val Lys Gln Ala Val Met Ala Ser Thr Lys Gln Gly Ser Ile
115 120 125
Tyr Ala
130

<210> 761
<211> 324
<212> DNA
<213> Homo sapiens

<400> 761
cctaggtagg cccaaagggg cctaactttc ttgctgcctt ggtggagcaa gaaatatctt
60
ctaggagagg ccaatccttc cctgccccac agctccttct ctgcaaagct cagggggcaa
120
tcaggtacct cctgcccgaag aggcccccat ggttcctcgc ctaaggaagg cagggcgggg
180
cattgggagc cgttgacagc tgggctcagc tggggggagg ggtcagtttg ggagcaggtg
240

cagatttcag ggaggggggg gcctaaaggg aagtagggat cttggtaggc tgcaaaattt
 300
 tcctcccat ccccatcca caga
 324

<210> 762
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 762
 Met Gly Asp Gly Glu Glu Asn Phe Ala Ala Tyr Gln Asp Pro Tyr Phe
 1 5 10 15
 Pro Leu Gly Pro Pro Leu Pro Glu Ile Cys Thr Cys Ser Gln Thr Asp
 20 25 30
 Pro Ser Pro Gln Leu Ser Pro Ala Val Asn Gly Ser Gln Cys Pro Ala
 35 40 45
 Leu Pro Ser Leu Gly Glu Glu Pro Trp Gly Pro Leu Gly Gln Glu Val
 50 55 60
 Pro Asp Cys Pro Leu Ser Phe Ala Glu Lys Glu Leu Trp Gly Arg Glu
 65 70 75 80
 Gly Leu Ala Ser Pro Arg Arg Tyr Phe Leu Leu His Gln Gly Ser Lys
 85 90 95
 Lys Val Arg Pro Leu Trp Ala Tyr Leu
 100 105

<210> 763
 <211> 301
 <212> DNA
 <213> Homo sapiens

<400> 763
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 120
 ccgcggtggc cgccaccggc tttaccgagg ccaccggcgg cctcggctgc ttctgctgg
 180
 gcgctgcctt gggcaccatt gccggcctgg ccatgagcaa cattggcgcg gacacagggc
 240
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 300
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 301

<210> 764
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 764
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20 25 30
 Pro Ala Met Val Pro Lys Ala Ala Pro Ser Arg Lys Gln Pro Arg Pro
 35 40 45
 Pro Val Ala Ser Val Lys Pro Val Ala Ala Thr Ala Ala Ala Val Ala
 50 55 60
 Pro Ala Val Ile Ala Ile Leu Ala Ala Thr Ser Ser Thr Pro Pro Arg
 65 70 75 80
 Met Ser Ala Ile Ile Glu Val Trp Asp Ser Ala Ser Pro Ile Arg Ala
 85 90 95
 Ala His Asn Ala
 100

<210> 765
 <211> 831
 <212> DNA
 <213> Homo sapiens

<400> 765
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 120
 agcctccaga atcacaatca ccagctgaaa ggggaggtcc tgagatataa gcggaaattg
 180
 agagaagccc agtctgacct gaacaagaca cgcctgcgta gtggtagtgc cctcctgcag
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 360
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 420
 agagaacggg agaaggagaa ggagagagaa cgagagaagc agaagctaaa agagtcagaa
 480
 aaagagagag attctgctaa ggataaagag aaaggcaaac atgatgatgg acggaaaaag
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 gaagcagaaa ttatcaaaca attgaagatt gaactcaaga aggcacagga gagccaaaag
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 660
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 720
 aaggatctgg aagataaaga gaagaaagag aacaagaaaa tggctgatga ggatgccttg
 780
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 831

<210> 766
 <211> 243
 <212> PRT
 <213> Homo sapiens

<400> 766
 Met Arg His Leu Ile Ser Ser Leu Gln Asn His Asn His Gln Leu Lys

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20	25	30	
Leu Asn Lys Thr Arg	Leu Arg Ser Gly Ser Ala	Leu Leu Gln Ser	Gln
35	40	45	
Ser Ser Thr Glu Asp Pro	Lys Asp Glu Pro Ala	Glu Leu Lys Pro	Asp
50	55	60	
Ser Gly Asp Leu Ser Ser	Gln Ser Ser Ala Ser	Lys Ala Ser Gln	Glu
65	70	75	80
Asp Ala Asn Glu Ile Lys	Ser Lys Arg Asp Glu	Glu Glu Arg Glu	Arg
85	90	95	
Glu Arg Arg Glu Lys Glu	Arg Glu Arg Glu Arg	Glu Arg Glu Lys	Glu
100	105	110	
Lys Glu Arg Glu Arg Glu	Lys Gln Lys Leu Lys	Glu Ser Glu Lys	Glu
115	120	125	
Arg Asp Ser Ala Lys Asp	Lys Glu Lys Gly Lys	His Asp Asp Gly	Arg
130	135	140	
Lys Lys Glu Ala Glu Ile	Ile Lys Gln Leu Lys	Ile Glu Leu Lys	Lys
145	150	155	160
Ala Gln Glu Ser Gln Lys	Glu Met Lys Leu Leu	Leu Asp Met Tyr	Arg
165	170	175	
Ser Ala Pro Lys Glu Gln	Arg Asp Lys Val Gln	Leu Met Ala Ala	Glu
180	185	190	
Lys Lys Ser Lys Ala Glu	Leu Glu Asp Leu Arg	Gln Arg Leu Lys	Asp
195	200	205	
Leu Glu Asp Lys Glu Lys	Lys Glu Asn Lys Lys	Met Ala Asp Glu	Asp
210	215	220	
Ala Leu Arg Lys Ile Arg	Ala Val Glu Glu Gln	Ile Glu Tyr Leu	Gln
225	230	235	240
Lys Lys Leu			

<210> 767

<211> 431

<212> DNA

<213> Homo sapiens

<400> 767

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120
gaggccggca gctggcgctg gggatccctg ctcttcgctc tcttctggc tgcgtcccta
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240
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431

<210> 768
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 768
 Met Gly Val Pro Thr Ala Pro Glu Ala Gly Ser Trp Arg Trp Gly Ser
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 20 25 30
 Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro Glu Gly Gln
 35 40 45
 Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val Asp Lys Gly His
 50 55 60
 Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser Ser Arg Gly Glu Val
 65 70 75 80
 Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg Asn Leu Thr Phe Gln Asp
 85 90 95
 Leu His Leu His His Gly Gly His Gln Ala Ala Asn Thr Ser
 100 105 110

<210> 769
 <211> 422
 <212> DNA
 <213> Homo sapiens

<400> 769
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 120
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 180
 aaaaatcccg ggtcggccca caaataaatc aattgcgccc ctcctccgag ttcttccatg
 240
 tcaacgatct cccctggctg ctcaagccaa ggccctcgcg gccgtgggac tccaagggttg
 300
 acgttgaccc gactgatttc ggaccagttg gcgtcggtat tgggggcagg gtagttaccg
 360
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 422

<210> 770
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 770
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 1 5 10 15
 Thr Ser Lys Lys Ser Arg Val Gly Pro Gln Ile Asn Gln Leu Arg Arg

			20					25				30							
Ser	Ser	Glu	Phe	Phe	His	Val	Asn	Asp	Leu	Pro	Trp	Leu	Leu	Lys	Pro				
		35					40					45							
Arg	Pro	Ser	Arg	Pro	Trp	Asp	Ser	Lys	Val	Asp	Val	Asp	Pro	Thr	Asp				
	50					55				60									
Phe	Gly	Pro	Val	Gly	Val	Gly	Ile	Gly	Gly	Arg	Val	Val	Thr	Ala	His				
65					70					75					80				
Val	Asp	Asp	Leu	His	Arg	His	Arg	Gln	Arg	Val	Phe	Val	Val	Val	Met				
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<210> 771

<211> 369

<212> DNA

<213> Homo sapiens

<400> 771

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360

ttgattaat

369

<210> 772

<211> 123

<212> PRT

<213> Homo sapiens

<400> 772

Ala Tyr Ala Gln Phe Leu Ala Gly Met Ala Phe Asn Asn Ala Ser Leu
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20 25 30Pro His Gly Val Cys Asn Ala Ile Leu Leu Pro His Val Gln Thr Phe
35 40 45Asn Cys Lys Val Ala Ala Ser Arg Leu Arg Asp Cys Ala Gln Ala Met
50 55 60Gly Val Asp Val Ser Gln Met Thr Ala Glu Gln Gly Ala Gln Ala Cys
65 70 75 80Ile Ala Glu Ile Arg Ser Leu Ala Arg Gln Val Asn Ile Pro Val Gly
85 90 95Leu Arg Asp Leu Asn Val Lys Glu Ala Asp Phe Pro Ile Leu Ala Thr
100 105 110

Asn Ala Leu Lys Asp Pro Val Gly Leu Ile Asn

115

120

<210> 773
 <211> 309
 <212> DNA
 <213> Homo sapiens

<400> 773
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 180
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 309

<210> 774
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 774
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 Ala Ala Asp Ile Gly Tyr Leu Ile Arg Val Glu Pro Gly Val Gln Thr
 20 25 30
 Pro Glu Phe Thr Leu Glu Asn Ala Ser Gly Ser Cys Arg Asp Ser Ala
 35 40 45
 Trp Leu Leu Val Gln Leu Leu Arg Asn Leu Gly Leu Ala Ala Arg Phe
 50 55 60
 Val Ser Gly Tyr Leu Ile Gln Leu Thr Ala Asp Val Lys Ala Leu Asp
 65 70 75 80
 Gly Pro Ser Gly Thr Glu Val Asp Phe Thr Asp Leu His Ala Trp Cys
 85 90 95
 Glu Val Tyr Leu Pro Gly Ala
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<210> 775
 <211> 4125
 <212> DNA
 <213> Homo sapiens

<400> 775
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 120
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 180

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240
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300
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<210> 776

<211> 483

<212> PRT

<213> Homo sapiens

<400> 776

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			20					25					30		
Ser	Glu	Asp	Ser	Asp	Leu	Ser	Met	Arg	Thr	Leu	Ser	Thr	Pro	Ser	Pro
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Ala	Leu	Ile	Cys	Pro	Pro	Asn	Leu	Pro	Gly	Phe	Gln	Asn	Gly	Arg	Gly
	50					55					60				
Ser	Ser	Thr	Ser	Ser	Ser	Ser	Ile	Thr	Gly	Glu	Thr	Val	Ala	Met	Val
65					70				75					80	
His	Ser	Pro	Pro	Pro	Thr	Arg	Leu	Thr	His	Pro	Leu	Ile	Arg	Leu	Ala
				85					90					95	
Ser	Arg	Pro	Gln	Lys	Asp	Gln	Ala	Ser	Ile	Asp	Arg	Leu	Pro	Asp	His
		100						105					110		
Ser	Met	Val	Gln	Ile	Phe	Ser	Phe	Leu	Pro	Thr	Asn	Gln	Leu	Cys	Arg
	115						120				125				
Cys	Ala	Arg	Val	Cys	Arg	Arg	Trp	Tyr	Asn	Leu	Ala	Trp	Asp	Pro	Arg
	130					135					140				
Leu	Trp	Arg	Thr	Ile	Arg	Leu	Thr	Gly	Glu	Thr	Ile	Asn	Val	Asp	Arg
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Ala	Leu	Lys	Val	Leu	Thr	Arg	Arg	Leu	Cys	Gln	Asp	Thr	Pro	Asn	Val
			165					170					175		
Cys	Leu	Met	Leu	Glu	Thr	Val	Thr	Val	Ser	Gly	Cys	Arg	Arg	Leu	Thr

			180					185					190				
Asp	Arg	Gly	Leu	Tyr	Thr	Ile	Ala	Gln	Cys	Cys	Pro	Glu	Leu	Arg	Arg		
		195					200					205					
Leu	Glu	Val	Ser	Gly	Cys	Tyr	Asn	Ile	Ser	Asn	Glu	Ala	Val	Phe	Asp		
	210					215					220						
Val	Val	Ser	Leu	Cys	Pro	Asn	Leu	Glu	His	Leu	Asp	Val	Ser	Gly	Cys		
225					230					235				240			
Ser	Lys	Val	Thr	Cys	Ile	Ser	Leu	Thr	Arg	Glu	Ala	Ser	Ile	Lys	Leu		
			245						250					255			
Ser	Pro	Leu	His	Gly	Lys	Gln	Ile	Ser	Ile	Arg	Tyr	Leu	Asp	Met	Thr		
		260					265					270					
Asp	Cys	Phe	Val	Leu	Glu	Asp	Glu	Gly	Leu	His	Thr	Ile	Ala	Ala	His		
	275						280					285					
Cys	Thr	Gln	Leu	Thr	His	Leu	Tyr	Leu	Arg	Arg	Cys	Val	Arg	Leu	Thr		
	290					295					300						
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Leu	Ser	Val	Ser	Asp	Cys	Arg	Phe	Val	Ser	Asp	Phe	Gly	Leu	Arg	Glu		
			325						330					335			
Ile	Ala	Lys	Leu	Glu	Ser	Arg	Leu	Arg	Tyr	Leu	Ser	Ile	Ala	His	Cys		
		340						345					350				
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	355						360					365					
Lys	Leu	Arg	Tyr	Leu	Asn	Ala	Arg	Gly	Cys	Glu	Gly	Ile	Thr	Asp	His		
	370				375					380							
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385					390					395				400			
Ile	Gly	Lys	Cys	Pro	Leu	Val	Ser	Asp	Thr	Gly	Leu	Glu	Cys	Leu	Ala		
			405					410						415			
Leu	Asn	Cys	Phe	Asn	Leu	Lys	Arg	Leu	Ser	Leu	Lys	Ser	Cys	Glu	Ser		
		420						425					430				
Ile	Thr	Gly	Gln	Gly	Leu	Gln	Ile	Val	Ala	Ala	Asn	Cys	Phe	Asp	Leu		
	435						440						445				
Gln	Thr	Leu	Asn	Val	Gln	Asp	Cys	Glu	Val	Ser	Val	Glu	Ala	Leu	Arg		
	450					455					460						
Phe	Val	Lys	Arg	His	Cys	Lys	Arg	Cys	Val	Ile	Glu	His	Thr	Asn	Pro		
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Ala	Phe	Phe															

<210> 777

<211> 705

<212> DNA

<213> Homo sapiens

<400> 777

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 240

actcagcaaa aggagagctc tgaaggtccc tgaggcggca cgggccagca ttattaggtc
 300
 acatggtatg acctgaaaca aatacgttct tcccaaagt ggcaggaccg ggagagcttc
 360
 tcaccaggag ggaaccgccg caatgaccgc cggacgtcca gcaacacttg ttggtagtcc
 420
 ttgctcatct gccgtaggtt cttccctgat ataggaggtg ggtcattggc attgacattg
 480
 aggagcttgg gccacacttt tcgtctgac tcatcagtea ggagccctcc ttcactgata
 540
 gccatgcgtc taagggcagc cacatcagtg ggatcactgt tcagagcctg gtgtatctct
 600
 aacactttct ttttcctttt ggcgttaaag tctgccttct ccgcgccgcc gtcccagtgg
 660
 ccggaggtgg gccgtccct gcgcactccg gaggccatcc ccggg
 705

<210> 778
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 778
 Met Ala Ser Gly Val Arg Arg Gly Arg Pro Thr Ser Gly His Trp Asp
 1 5 10 15
 Gly Gly Ala Glu Lys Ala Asp Phe Asn Ala Lys Arg Lys Lys Lys Val
 20 25 30
 Leu Glu Ile His Gln Ala Leu Asn Ser Asp Pro Thr Asp Val Ala Ala
 35 40 45
 Leu Arg Arg Met Ala Ile Ser Glu Gly Gly Leu Leu Thr Asp Glu Ile
 50 55 60
 Arg Arg Lys Val Trp Pro Lys Leu Leu Asn Val Asn Ala Asn Asp Pro
 65 70 75 80
 Pro Pro Ile Ser Gly Lys Asn Leu Arg Gln Met Ser Lys Asp Tyr Gln
 85 90 95
 Gln Val Leu Leu Asp Val Arg Arg Ser Leu Arg Arg Phe Pro Pro Gly
 100 105 110
 Glu Lys Leu Ser Arg Ser Cys His Ile Trp Glu Glu Arg Ile Cys Phe
 115 120 125
 Arg Ser Tyr His Val Thr
 130

<210> 779
 <211> 322
 <212> DNA
 <213> Homo sapiens

<400> 779
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 gactgtgagt gattctgagg ataccgttgc gccgtcccag ctggttcgat cccctcgtaa
 120
 cgccttgctt ttgaaggaac ccagtgggaa ggctagacca agtaaatatg aatcaccaaa
 180

cgccagcaac ttcatcgtca ggcattgtggc aactggcaaa gagggcactg atgatgagta
 240
 tgctaactca aactactact actcgatgtc tgccaatcga ctaggagacg aggaaacgga
 300
 ggaaatgata ggtttggcta cc
 322

<210> 780
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 780
 Met Cys Lys Gln Phe Asn Asp Val Val Arg Arg His Gly Val His His
 1 5 10 15
 Ser Val Thr Val Ser Asp Ser Glu Asp Thr Val Ala Pro Ser Gln Leu
 20 25 30
 Val Arg Ser Pro Arg Asn Ala Leu Pro Leu Lys Glu Pro Ser Gly Lys
 35 40 45
 Ala Arg Pro Ser Lys Tyr Glu Ser Pro Asn Ala Ser Asn Phe Ile Val
 50 55 60
 Arg His Val Ala Thr Gly Lys Glu Gly Thr Asp Asp Glu Tyr Ala Asn
 65 70 75 80
 Ser Asn Tyr Tyr Tyr Ser Met Ser Ala Asn Arg Leu Gly Asp Glu Glu
 85 90 95
 Thr Glu Glu Met Ile Gly Leu Ala Thr
 100 105

<210> 781
 <211> 297
 <212> DNA
 <213> Homo sapiens

<400> 781
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 gtgtgtatgn gaatatgtgt gtgtatgnga atgtgtgtgt gtgtttggaa tgtgtgtatg
 120
 gaatgtgtgt ctgtgtatgg aatatgtgtg agtatngaa tgtgtgtgtg tgtttggaat
 180
 gtatcgaatg tgtgtctgtg tgtaaggaat gtgtgtgtat ggaatgtgtt tacgtgcatg
 240
 tgtctggaat gtgtgtgtat ggaatgtgtg tgtatgtgta tgngaattgt tgtgtgt
 297

<210> 782
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 782
 Xaa Arg Val Pro Gly Met Cys Val Cys Val Cys Val Cys Met Tyr Val
 1 5 10 15
 Cys Met Glu Cys Val Cys Met Xaa Ile Cys Val Cys Met Xaa Met Cys

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<400> 784
Met Ser Ile Cys Val Pro Gly Thr Gly Ser Ser Glu Leu Pro Ser Ser
 1             5             10             15
Lys Pro Thr Thr Ser Val Thr Arg Pro Ile Thr Leu Leu Ser Thr Ser
      20             25             30
Met Thr Gly Asn Phe Lys Glu Ile Gln Val Arg Thr Cys Ala Val Arg
      35             40             45
Thr Lys Ile Gly Trp Val Ser Ile Asn Cys Gly Leu Pro Ile Ala Glu

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      50      55      60
Phe Ala Arg Phe Asp Asp Thr Cys Leu His Arg Asp Ile Gln Gln Pro
65      70      75      80
Gln Tyr Val His Arg Gln Leu Asp Gly His Arg Ala Gly Phe Val Gly
      85      90      95
Gln Leu His Lys Ala Leu Asn Gln Val Glu Gln Leu Gln Val Asp Val
      100      105      110
Gln Gly Ala Leu Val Arg Ala Val Leu Tyr Ile Asp Gln Val Ala Gln
      115      120      125
Val Gln Asp Leu Arg Ala Trp Gly Asn Gln Leu Asp Cys Phe Glu Val
      130      135      140
Ile Asp His His Leu Asp Arg Ile Thr Ala Gln Leu Glu His Ile Asp
145      150      155      160
Gly Gly Leu Asp Gln Leu Ala Asp Gly Arg Val Gly Leu Glu Gln Leu
      165      170      175
Val Val Val Ala Gly Ala Asp Val Glu Ala Asp Gly Arg Arg
      180      185      190

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<210> 785
 <211> 408
 <212> DNA
 <213> Homo sapiens

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<400> 785
accttggact acttcactat cgaccctcgg ctaggcgacg acgatgactt cgatcacctg
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cttcaggccg cccacgctcg tggctctgtca gtactgctcg acgggggtggt caaccacgtc
120
tcgcgtcgca accgcatcgt gcaggatgcg cagagtgcgt ggccagattc agacgccggc
180
cgtatggttc gctgggtgtga ggggcgcctc gacgttttcg agggtcatag tgacctggtc
240
gcactcaacc acgacaaccc cgcagtgcgg gaacatgtca cccggatcat gaactattgg
300
tgcggtcgcg gtggttgacgg ctggcggctg gacgccgcta ttccgtcaat cctgagttct
360
gggctgcggt gctgcctccg gtgcgagaga agcgccctga cgtgagga
408

```

<210> 786
 <211> 134
 <212> PRT
 <213> Homo sapiens

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<400> 786
Thr Leu Asp Tyr Phe Thr Ile Asp Pro Arg Leu Gly Asp Asp Asp Asp
1      5      10      15
Phe Asp His Leu Leu Gln Ala Ala His Ala Arg Gly Leu Ser Val Leu
20      25      30
Leu Asp Gly Val Val Asn His Val Ser Arg Arg Asn Arg Ile Val Gln
35      40      45
Asp Ala Gln Ser Ala Gly Pro Asp Ser Asp Ala Gly Arg Met Val Arg
50      55      60
Trp Cys Glu Gly Arg Leu Asp Val Phe Glu Gly His Ser Asp Leu Val

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65		70		75		80									
Ala	Leu	Asn	His	Asp	Asn	Pro	Ala	Val	Arg	Glu	His	Val	Thr	Arg	Ile
				85					90					95	
Met	Asn	Tyr	Trp	Cys	Gly	Arg	Gly	Val	Asp	Gly	Trp	Arg	Leu	Asp	Ala
			100					105					110		
Ala	Ile	Pro	Ser	Ile	Leu	Ser	Ser	Gly	Leu	Arg	Cys	Cys	Leu	Arg	Cys
		115					120					125			
Glu	Arg	Ser	Ala	Leu	Thr										
		130													

<210> 787
 <211> 310
 <212> DNA
 <213> Homo sapiens

<400> 787
 acgcgtgaag ggggaatgaaa gggtttttcc tggatcaaaa tgatgcttgt ggcagacaca
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 gttggaacca cagacgatgc cacgcttggtg tcagcagtgc gacactggcc cacgtggcgt
 120
 ccttggtctc tcttcattgc tgccgtcact gtgtgctggg catgccctgc agttacccca
 180
 aagctttatg tcacaacatt gaggctggcg gagaaagacc ggccccttca ccccacctta
 240
 gacttcctgg aagggccgcc cgggtccaca acctggcccc ttaactccct gggcagctgc
 300
 tgggggagaa
 310

<210> 788
 <211> 90
 <212> PRT
 <213> Homo sapiens

<400> 788
Met Met Leu Val Ala Asp Thr Val Gly Thr Thr Asp Asp Ala Thr Leu
1 5 10 15
Val Ser Ala Val Arg His Trp Pro Thr Trp Arg Pro Trp Ser Leu Leu
20 25 30
Ile Ala Ala Val Thr Val Cys Trp Ala Cys Pro Ala Val Thr Pro Lys
35 40 45
Leu Tyr Val Thr Thr Leu Arg Leu Ala Glu Lys Asp Arg Pro Leu His
50 55 60
Pro Thr Leu Asp Phe Leu Glu Gly Pro Pro Gly Ser Thr Thr Trp Pro
65 70 75 80
Val Asn Ser Leu Gly Ser Cys Trp Gly Arg
85 90

<210> 789
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 789

acgcgtgaag ttgcagcagc aagcaatctg cctcgcttct ggtgccacc gaaaccaagg
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tctgccagac agcagcgctg ggacctctcc cctccccagc aggatgggccc ggctctggaa
120
gcacgaggtg ttccaaagtg caaacaagct gctgttaaata aattattccc aaacgccaaa
180
gcccttgctg gtttgcttgc ttgctttttt ctttttttgc ctcgcacaga tatcgctagg
240
gcagagtatt gacatttcgt tttctttttg ttatgggtga taaagcacgg tgtttcttgt
300
gagtgtatgc ctgtatttcc ctgcagagct gattgccagt ccattttctt ctatcccatc
360
cccattttc
369

<210> 790

<211> 114

<212> PRT

<213> Homo sapiens

<400> 790

Met	Asp	Trp	Gln	Ser	Ala	Leu	Gln	Gly	Asn	Thr	Gly	Ile	His	Ser	Gln
1				5				10						15	
Glu	Thr	Pro	Cys	Phe	Ile	Thr	His	Asn	Lys	Lys	Lys	Thr	Lys	Cys	Gln
			20					25					30		
Tyr	Ser	Ala	Leu	Ala	Ile	Ser	Val	Arg	Gly	Lys	Lys	Arg	Lys	Lys	Gln
		35					40					45			
Ala	Ser	Lys	Pro	Ala	Arg	Ala	Leu	Ala	Phe	Gly	Asn	Asn	Tyr	Leu	Thr
	50					55				60					
Ala	Ala	Cys	Leu	His	Phe	Gly	Thr	Pro	Arg	Ala	Ser	Arg	Ala	Gly	Pro
65				70					75					80	
Ser	Cys	Trp	Gly	Gly	Glu	Arg	Ser	Gln	Arg	Cys	Cys	Leu	Ala	Asp	Leu
			85					90						95	
Gly	Phe	Gly	Gly	His	Gln	Lys	Arg	Gly	Arg	Leu	Leu	Ala	Ala	Ala	Thr
			100					105					110		
Ser	Arg														

<210> 791

<211> 420

<212> DNA

<213> Homo sapiens

<400> 791

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120
agaatcaaaa tggaaagagt gggtaatgtg tgttcactgg aaattttctaa cattcaaaaa
180
ggagaagggg gagagtacat gtgtcatgct gtaaacaatca taggggaagc aaagagcttt
240
gcaaatgtag acataatgcc ccaggaagaa agagtgggtgg cactaccacc tccagtaaca
300

catcagcatg tcatggagtt tgatttggaa cacaccacat catcaagaac accttctcct
360

caagaaattg tcctggaagt tgaattaagt gaaaaagacg ttaaagaatt tgagaagcag
420

<210> 792

<211> 138

<212> PRT

<213> Homo sapiens

<400> 792

Thr	Lys	Arg	Lys	Val	Tyr	Glu	Asn	Thr	Thr	Leu	Gly	Phe	Ile	Val	Glu
1				5					10					15	
Val	Glu	Gly	Leu	Pro	Val	Pro	Gly	Val	Lys	Trp	Tyr	Arg	Asn	Lys	Ser
			20					25					30		
Leu	Leu	Glu	Pro	Asp	Glu	Arg	Ile	Lys	Met	Glu	Arg	Val	Gly	Asn	Val
		35					40					45			
Cys	Ser	Leu	Glu	Ile	Ser	Asn	Ile	Gln	Lys	Gly	Glu	Gly	Gly	Glu	Tyr
	50					55					60				
Met	Cys	His	Ala	Val	Asn	Ile	Ile	Gly	Glu	Ala	Lys	Ser	Phe	Ala	Asn
65					70					75				80	
Val	Asp	Ile	Met	Pro	Gln	Glu	Glu	Arg	Val	Val	Ala	Leu	Pro	Pro	Pro
				85					90					95	
Val	Thr	His	Gln	His	Val	Met	Glu	Phe	Asp	Leu	Glu	His	Thr	Thr	Ser
			100					105					110		
Ser	Arg	Thr	Pro	Ser	Pro	Gln	Glu	Ile	Val	Leu	Glu	Val	Glu	Leu	Ser
		115					120						125		
Glu	Lys	Asp	Val	Lys	Glu	Phe	Glu	Lys	Gln						
		130					135								

<210> 793

<211> 479

<212> DNA

<213> Homo sapiens

<400> 793

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ccgcgaacag tactgcgagg acccaaacga tcatttttaa cccagacgt ccctgaacca
120
aagccaaagt ctacaggtca ctggggcaga ggccgcccga aaccagcttc ccctcccggc
180
ctaggcgcg caggtccccg cccagccggg gcgatccttt ggtcggacag tgagggtggg
240
agcccaccgc acccaagtcc gccgcatcca cccggcgag gcgacccccg acgggcagcc
300
gctcaccttc tcctggcccc ggcttcagga aaactgcctg gaggtggccg gggttccta
360
gcggaggctg ggcgggcgggc ttcgcgcctg cctcagtctc cccatccgtg gcccggggga
420
tgagagccgc tgcgcgcaga ggctgcggca ggtcccagcc aggtgccttg gaacgtgga
479

<210> 794

<211> 159
 <212> PRT
 <213> Homo sapiens

<400> 794
 Xaa Ala Cys Arg Phe Ser Glu Ile His Tyr Gly Asn Val Arg Val Val
 1 5 10 15
 Glu Met Leu Arg Pro Arg Thr Val Leu Arg Glu Pro Lys Arg Ser Phe
 20 25 30
 Leu Thr Pro Asp Val Pro Glu Pro Lys Pro Lys Ser Thr Gly His Trp
 35 40 45
 Gly Arg Gly Arg Pro Lys Pro Ala Ser Pro Pro Gly Leu Gly Ala Pro
 50 55 60
 Gly Pro Arg Pro Ala Gly Ala Ile Leu Trp Ser Asp Ser Glu Val Gly
 65 70 75 80
 Ser Pro Pro His Pro Ser Pro Pro His Pro Pro Gly Ala Gly Asp Pro
 85 90 95
 Arg Arg Ala Ala Ala His Leu Leu Leu Ala Pro Ala Ser Gly Lys Leu
 100 105 110
 Pro Gly Gly Gly Arg Gly Ser Leu Ala Glu Ala Gly Arg Arg Ala Ser
 115 120 125
 Arg Leu Pro Gln Ser Pro His Pro Trp Pro Gly Gly Trp Ser Pro Leu
 130 135 140
 Arg Ala Glu Ala Ala Ala Gly Pro Ser Gln Val Pro Trp Asn Val
 145 150 155

<210> 795
 <211> 1418
 <212> DNA
 <213> Homo sapiens

<400> 795
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 ccggactacg aggcgctgcc ggctggagcc actgtcacca cgcacatggt ggcaggcgcc
 120
 gtggcagggg tccctggagca ctgcgtgatg taccceatcg actgcgtcaa gacccggatg
 180
 cagagtctac agcctgaccc agctgcccgc tatcgcaatg tggttgaggc cctctggagg
 240
 attataagaa cggagggcct atggaggccc atgagggggc tgaacgtcac agcaacaggc
 300
 gcagggcctg cccacgccct ttattttgcc tgctacgaaa agttaaaaaa gacattgagt
 360
 gatgtaatcc accctggggg caatagccat attgccaatg gtgcggccgg gtgtgtggca
 420
 acattacttc atgatgcagc catgaaccct gcggaaggct gatctgctga cttggggctc
 480
 tgaatctgga tactctccat caccgggttg ctgctgtcac catttccttc ctcgttgatg
 540
 gcactactag tgggtcaagca gaggatgcag atgtacaact caccatacca ccgggtgaca
 600
 gactgtgtac gggcagtgtg gcaaaatgaa ggggccgggg ccttttaccg cagctacacc
 660

acccagctga ccatgaacgt tcctttccaa gccattcact tcatgaccta tgaattcctg
 720
 caggagcact ttaacccccca gagacggtac aacccaagct cccacgtcct ctctggagct
 780
 tgcgcaggag ctgtagctgc cgcagccaca accccactgg acgtttgcaa aacactgctc
 840
 aacacccagg agtccttggc tttgaactca cacattacag gacatatcac aggcattggct
 900
 agtgccttca ggacggtata tcaagtaggt ggggtgaccg cctatttccg aggggtgcag
 960
 gccagagtaa tttaccagat cccctccaca gccatcgcat ggtctgtgta tgagttcttc
 1020
 aaatacctaa tcactaaaag gcaagaagag tggagggctg gcaagtgaag tagcactgaa
 1080
 cgaagccagg ggttcagatg aactgctgc atcctggta cattctctgt ctctgggaat
 1140
 gctccacact caagtggagt tagaaggaag gtagaggggc tctccccag gattttggtg
 1200
 ttttgactaa caccagttcc tgccaacctc tgttgccacc acctttcctt ccaggcccta
 1260
 agcacgtgca gcaaagcaca ccacagcacc tttgataacc tctctccatc ctgggcctga
 1320
 tgacctgctc tagactgtta tagagggata agcagctcat tcccctgggt cctaataaaa
 1380
 agcctttaaa ttaaaaaaaaa aaaaaaaaaa aaaaaaaaa
 1418

<210> 796

<211> 176

<212> PRT

<213> Homo sapiens

<400> 796

Met	Ala	Leu	Leu	Val	Val	Lys	Gln	Arg	Met	Gln	Met	Tyr	Asn	Ser	Pro
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Tyr	His	Arg	Val	Thr	Asp	Cys	Val	Arg	Ala	Val	Trp	Gln	Asn	Glu	Gly
			20					25					30		
Ala	Gly	Ala	Phe	Tyr	Arg	Ser	Tyr	Thr	Thr	Gln	Leu	Thr	Met	Asn	Val
		35					40					45			
Pro	Phe	Gln	Ala	Ile	His	Phe	Met	Thr	Tyr	Glu	Phe	Leu	Gln	Glu	His
	50					55				60					
Phe	Asn	Pro	Gln	Arg	Arg	Tyr	Asn	Pro	Ser	Ser	His	Val	Leu	Ser	Gly
65				70					75					80	
Ala	Cys	Ala	Gly	Ala	Val	Ala	Ala	Ala	Ala	Thr	Thr	Pro	Leu	Asp	Val
			85					90					95		
Cys	Lys	Thr	Leu	Leu	Asn	Thr	Gln	Glu	Ser	Leu	Ala	Leu	Asn	Ser	His
			100					105					110		
Ile	Thr	Gly	His	Ile	Thr	Gly	Met	Ala	Ser	Ala	Phe	Arg	Thr	Val	Tyr
		115				120						125			
Gln	Val	Gly	Gly	Val	Thr	Ala	Tyr	Phe	Arg	Gly	Val	Gln	Ala	Arg	Val
		130				135					140				
Ile	Tyr	Gln	Ile	Pro	Ser	Thr	Ala	Ile	Ala	Trp	Ser	Val	Tyr	Glu	Phe
145				150				155						160	
Phe	Lys	Tyr	Leu	Ile	Thr	Lys	Arg	Gln	Glu	Glu	Trp	Arg	Ala	Gly	Lys

165

170

175

<210> 797

<211> 585

<212> DNA

<213> Homo sapiens

<400> 797

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 120
 gagatgctgc cggaagttaa gtcgtcttca gaaatctacg gccgcaccaa aagcggatc
 180
 gctatcggcg gcatcgcggg cgaccaacag gctgctctgt tcggccagat gtgcgtggaa
 240
 gccgggcagg ccaagaacac ttatggcacc ggctgcttcc tgctgatgaa caccggcgac
 300
 aaagccgtca aatccaaaca cggcattgctc accaccatcg cctgcgggtcc acgcggcgaa
 360
 gtggcttatg cgctggaagg cgcggtgttc aacggtggtt ccccgtgca gtggctgcgt
 420
 gatgagctga agatcatcgc ggacgccacc gacaccgaat acttcgccgg caaggtcaag
 480
 gacagcaacg gcgtctacct ggtgccggcc ttaccggcc tgggcgctcc gtactgggac
 540
 ccgtatgccc gtggcgcttt gtttggcctg actcgtggcg tacgc
 585

<210> 798

<211> 195

<212> PRT

<213> Homo sapiens

<400> 798

Lys	Phe	Thr	Gly	Gly	Lys	Thr	His	Val	Thr	Asp	Tyr	Thr	Asn	Ala	Ser
1				5					10					15	
Arg	Thr	Met	Leu	Phe	Asn	Ile	His	Thr	Leu	Glu	Trp	Asp	Ala	Lys	Met
			20					25					30		
Leu	Glu	Ile	Leu	Asp	Val	Pro	Arg	Glu	Met	Leu	Pro	Glu	Val	Lys	Ser
		35					40				45				
Ser	Ser	Glu	Ile	Tyr	Gly	Arg	Thr	Lys	Ser	Gly	Ile	Ala	Ile	Gly	Gly
	50					55				60					
Ile	Ala	Gly	Asp	Gln	Gln	Ala	Ala	Leu	Phe	Gly	Gln	Met	Cys	Val	Glu
65				70					75					80	
Ala	Gly	Gln	Ala	Lys	Asn	Thr	Tyr	Gly	Thr	Gly	Cys	Phe	Leu	Leu	Met
			85					90					95		
Asn	Thr	Gly	Asp	Lys	Ala	Val	Lys	Ser	Lys	His	Gly	Met	Leu	Thr	Thr
		100					105					110			
Ile	Ala	Cys	Gly	Pro	Arg	Gly	Glu	Val	Ala	Tyr	Ala	Leu	Glu	Gly	Ala
		115				120					125				
Val	Phe	Asn	Gly	Gly	Ser	Pro	Val	Gln	Trp	Leu	Arg	Asp	Glu	Leu	Lys
	130					135					140				
Ile	Ile	Ala	Asp	Ala	Thr	Asp	Thr	Glu	Tyr	Phe	Ala	Gly	Lys	Val	Lys

145		150		155		160									
Asp	Ser	Asn	Gly	Val	Tyr	Leu	Val	Pro	Ala	Phe	Thr	Gly	Leu	Gly	Ala
			165						170					175	
Pro	Tyr	Trp	Asp	Pro	Tyr	Ala	Arg	Gly	Ala	Leu	Phe	Gly	Leu	Thr	Arg
			180					185					190		
Gly	Val	Arg													
		195													

<210> 799
 <211> 2152
 <212> DNA
 <213> Homo sapiens

<400> 799
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 120
 acgccgagag cccagaccag gattccaaac acactgcacg agaatattgt ggatccgctg
 180
 tcaggtaagt gtccgtcact gacccagacg ctgttacgtg gcacatgact gtacagtgcc
 240
 acgtaacagc actgtacttt tctcccataa acagttacct gccatgtatc tacatgattc
 300
 agaacatttt gaacagttaa ttctgacact tgaataatcc catcaaaaac cgtaaaatca
 360
 ctttgatggt gtaacgacaa catagcatca ctttacgaca gaatcatctg gaaaaacaga
 420
 acaacgaata catacatctt aaaaaatgct ggggtgggcc aggcacagct cagcctgta
 480
 atcccagcac tttgggaggc tgaggcgggt ggatcacgta atcccagcac tttgaggggc
 540
 agaggtggac agatcatgag gtcaagagat caagaccatc ctggtcaaaa tggtgaaacc
 600
 ccgtctctac taaaaataca aaaattagct gagcttagtg gcacacacct gtagtcccag
 660
 ctacttggga ggctgaggca ggagaatcgc ttgaaccag gagacacagg ctgcagtgac
 720
 tcgagatcac gccactgcac tccagcctgg cgacagagcg agactccatc tcaaaaaaaaa
 780
 aaaccaacaa aaaaactggg gtgaaaatct aacggataat tcagcattgc cgcataaaaa
 840
 cctccgcaaa accggccaaa caaacgcgga caggcggccc tggcgtcagc gcacgacagt
 900
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<212> PRT

<213> Homo sapiens

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Pro	Leu	Pro	Gly	His	Leu	Ala	Ser	Ala	Gly	Pro	Leu	Ala	Ser	Ala	Glu				
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Ser	Leu	Glu	Pro	Val	Ser	Trp	Arg	Glu	Gly	Pro	Ser	Gly	His	Ser	Thr				
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Leu	Pro	Arg	Ser	Pro	Arg	Asp	Ala	Pro	Cys	Ser	Ala	Ser	Ser	Glu	Leu				
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Ser	Gly	Pro	Ser	Thr	Pro	Leu	His	Thr	Ser	Ser	Pro	Val	Gln	Gly	Lys				
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Glu	Ser	Thr	Arg	Arg	Gln	Asp	Thr	Arg	Ser	Pro	Thr	Ser	Ala	Pro	Thr				
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Gln	Arg	Leu	Ser	Pro	Gly	Glu	Ala	Leu	Pro	Pro	Val	Ser	Gln	Ala	Gly				
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Thr	Gly	Lys	Ala	Pro	Glu	Leu	Pro	Ser	Gly	Ser	Gly	Pro	Glu	Pro	Leu				
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Ala	Pro	Ser	Pro	Val	Ser	Pro	Thr	Phe	Pro	Pro	Ser	Ser	Pro	Ser	Asp				
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Trp	Pro	Gln	Glu	Arg	Ser	Pro	Gly	Gly	His	Ser	Asp	Gly	Ala	Ser	Pro				
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Gln	Gly	Pro	Arg	Gly	Pro	Pro	Asp	Ser	Pro	Asp	Gly	Ser	Pro	Leu	Thr				
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Ser	Arg	Asp	Gln	Ala	Ile	Ala	Leu	Leu	Lys	Asp	Lys	Asp	Pro	Gly	Ala				
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Phe	Leu	Ile	Arg	Asp	Ser	His	Ser	Phe	Gln	Gly	Ala	Tyr	Gly	Leu	Ala				

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 Cys Leu Arg Ile Pro Ser Lys Asp Pro Leu Glu Glu Thr Pro Glu Ala
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 Pro Val Pro Thr Asn Met Ser Thr Ala Ala Asp Leu Leu Arg Gln Gly
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 Thr Gly Pro Gln Ala Val Ala Arg Ala Ser Ser Ala Ala Leu Ser Cys
 1285 1290 1295
 Ser Pro Arg Pro Thr Pro Ala Val Val His Phe Lys Val Ser Ala Gln
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 Gly Ile Thr Leu Thr Asp Asn Gln Arg Lys Leu Phe Phe Arg Arg His
 1315 1320 1325
 Tyr Pro Val Asn Ser Ile Thr Phe Ser Ser Thr Asp Pro Gln Asp Arg
 1330 1335 1340
 Arg Trp Thr Asn Pro Asp Gly Thr Thr Ser Lys Ile Phe Gly Phe Val
 1345 1350 1355 1360
 Ala Lys Lys Pro Gly Ser Pro Trp Glu Asn Val Cys His Leu Phe Ala
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 Glu Leu Asp Pro Asp Gln Pro Ala Gly Ala Ile Val Thr Phe Ile Thr
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 Lys Val Leu Leu Gly Gln Arg Lys
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<210> 805
 <211> 550
 <212> DNA
 <213> Homo sapiens

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 aatggacctt gccaggacac tcagtcacag gtttcacacc caaagagaag acagcccaac
 420
 ccagaccctc aaaagagagc acctggggga agggagcgtg gaaaccagga ctcagaaaga
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cacaagagaa aaagaagctg tacactgggg aggcttccgg ggtacctgtg cctgccatgt
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<210> 806
 <211> 118
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Met Leu Gly Arg Ala Thr Pro Met Asp Leu Ala Arg Thr Leu Ser His
 50 55 60
 Arg Phe His Thr Gln Arg Glu Asp Ser Pro Thr Gln Thr Leu Lys Arg
 65 70 75 80
 Glu His Leu Gly Glu Gly Ser Val Glu Thr Arg Thr Gln Lys Asp Thr
 85 90 95
 Arg Glu Lys Glu Ala Val His Trp Gly Gly Phe Arg Gly Thr Cys Ala
 100 105 110
 Cys His Val Ser Glu Gly
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<210> 807
 <211> 287
 <212> DNA
 <213> Homo sapiens

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<210> 808
 <211> 93
 <212> PRT
 <213> Homo sapiens

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Leu	Ser	Asp	Ala	Met	Thr	Glu	Trp	Val	Glu	Ala	Gln	Thr	Gly	Thr	Gly	
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Arg	Tyr	Thr	Ser	Ala	Ser	Asp	Tyr	Ile	Cys	Ala	Leu	Ile	Arg	Gln	Asp	
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Gln	Glu	Arg	Ser	Asp	Gly	Leu	Arg	Gln	Leu	Gln	Thr	Leu	Ile	Thr	Glu	
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Gly	Phe	Asp	Ser	Gly	Ile	Ser	Ala	Ser	Ser	Leu	Asp	Asp				
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<210> 809

<211> 405

<212> DNA

<213> Homo sapiens

<400> 809

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gacgcgtggt cgcgtaaagt ggagagacga tcggtgccgc ccttgcccca cgatcctgat
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240
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300
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405

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<210> 810

<211> 135

<212> PRT

<213> Homo sapiens

<400> 810

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			20				25				30					
Gly	Val	Tyr	Ser	Gln	Gly	Gln	Gln	Asp	Ala	Trp	Ser	Arg	Gln	Met	Glu	
	35					40					45					
Arg	Arg	Ser	Val	Pro	Pro	Leu	Pro	His	Asp	Pro	Asp	Gly	Pro	Glu	Ile	
	50				55					60						
Pro	Asp	Asp	Val	Thr	Thr	Leu	Ala	Gln	Gln	Val	Met	Gly	Leu	Pro	Arg	
65				70					75					80		
His	Leu	Gly	Ile	His	Ser	Ala	Gly	Met	Val	Leu	Thr	Arg	Glu	Pro	Val	
			85				90					95				
Gly	Arg	Ile	Cys	Pro	Ile	Glu	Pro	Ala	Arg	Met	Phe	Gly	Arg	Thr	Gly	
		100					105					110				
Leu	Gln	Trp	Asp	Lys	Xaa	Asn	Cys	Ala	Trp	Met	Gly	Leu	Gly	Lys	Phe	
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130

135

<210> 811
 <211> 642
 <212> DNA
 <213> Homo sapiens

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 420
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<210> 812
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 812
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 20 25 30
 Ala His Pro Glu Val Leu Glu Ser Phe Leu Gln Glu Leu Arg Pro Lys
 35 40 45
 Ala Ser Arg Lys Glu Arg Xaa Thr Thr Asn Leu Ile Phe Thr Pro Phe
 50 55 60
 Pro Cys His Leu Val Phe Pro Val Ile Phe Asn Pro Ile Leu Cys Ala
 65 70 75 80
 Ala Gly Ala Ala Ala Leu Trp Ala Thr Pro Leu Val Ala Gly Val Glu
 85 90 95
 Val Thr Gly Ser Ser Ala Leu Tyr His Ser
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<210> 813
 <211> 558

<212> DNA

<213> Homo sapiens

<400> 813

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<210> 814

<211> 151

<212> PRT

<213> Homo sapiens

<400> 814

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20      25      30
Ala Phe Gly Pro Leu Ala Phe Gly Gln Arg Ala Ala Gln Phe Gly Val
35      40      45
Glu Asp Asp Pro Arg Pro Phe Asp Leu Asp His Asp Leu Gln Leu Pro
50      55      60
Ala Ile Val Phe Ala Ala Asp Ile Gln Arg Ala Ala Ala His Gln Arg
65      70      75      80
Leu Ala Gly Asp Gln Gly Glu Val Gln His His Leu Gln Arg Gly Leu
85      90      95
Gly Gln Arg Leu Arg Phe His Pro Pro Val Glu Leu Arg Ala Leu Ile
100     105     110
Val Gly Asn Gln Pro Leu Val Arg Gly Phe Arg Phe Ala Arg Val Asp
115     120     125
Leu Phe Ala Glu Pro Ala Gly Gly Ala Glu Gly Glu Ala Glu Glu Phe
130     135     140
Glu Leu Val Gly Gly Tyr Ala
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<210> 815

<211> 315

<212> DNA

<213> Homo sapiens

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<210> 816

<211> 90

<212> PRT

<213> Homo sapiens

<400> 816

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Pro	His	Thr	Asp	Gly	Ser	Glu	Pro	Gly	Gln	Ala	Ser	Ala	Gly	Glu	Ser
			20					25					30		
Arg	Asp	Leu	Thr	Ser	Glu	Ala	Asp	Ser	Ala	Ser	Ala	Gln	Pro	Ser	Thr
		35					40					45			
His	Ala	Glu	Val	Ser	Ser	Glu	Val	Thr	Ala	Thr	Ser	Ser	Ile	Asp	Glu
	50					55				60					
Gln	Val	Asp	Leu	Ile	Ala	Ala	Pro	Leu	Ser	Glu	Glu	Ser	Asn	Val	Ser
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Lys	Leu	Gly	Pro	Ser	Pro	Glu	Ala	Asp	Thr						
				85				90							

<210> 817

<211> 321

<212> DNA

<213> Homo sapiens

<400> 817

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180
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300
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321

<210> 818
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 818
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 35 40 45
 Ile Asn Gln Ser Ile Ile Phe Cys Asn Ser Val Asn Ser Val Glu Leu
 50 55 60
 Leu Ala Lys Lys Ile Thr Glu Leu Gly Tyr Ser Cys Phe Tyr Ile His
 65 70 75 80
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 85 90 95
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<210> 819
 <211> 3422
 <212> DNA
 <213> Homo sapiens

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 420
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<210> 820

<211> 494

<212> PRT

<213> Homo sapiens

<400> 820

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Phe	Thr	Ser	Pro	Glu	Ala	Leu	Gln	Pro	Gly	Gly	Thr	Ala	Leu	Ala	Pro
			20					25					30		
Lys	Lys	Arg	Ser	Arg	Lys	Gly	Arg	Ala	Gly	Ala	His	Gly	Leu	Ser	Lys
		35				40					45				
Gly	Pro	Leu	Glu	Lys	Arg	Pro	Tyr	Leu	Gly	Pro	Ala	Leu	Pro	Leu	Thr
	50				55					60					
Pro	Arg	Asp	Arg	Ala	Ser	Gly	Thr	Gln	Gly	Ala	Ser	Glu	Asp	Asn	Ser
65				70					75					80	
Gly	Gly	Gly	Gly	Lys	Lys	Pro	Lys	Met	Glu	Glu	Leu	Gly	Leu	Ala	Ser

$\langle 210 \rangle$ 821
 $\langle 211 \rangle$ 420

<213> Homo sapiens

acgcgtcccg tcacctgcgg tatggaccaa gtgagttgtg tgctcgacaa tggggttcgcc
60
gccatcatgg atgtgccggg tttcaactat cgcgcccatc gttacaccga agcctatcgg
120
cgtttgccgc aaaatgtggg gctaggttcg gaaacgacct cgacggtgag cagccgtggg
180
gtctacaagt ttctgtttgt gctgaagtcc gatgccatct atcccgacca tcagtcgtca
240
ggctacgaca cagagtattg ttcgtgggtcg aacacccccg atgtcgattt cgccttcgcc
300
gaagactatc cctggacgat ggggcagttt gtctggacgg gcttcgacta cctcggtgaa
360
ccttcgcctt acgacaccga tgccctggccc tctcacgcct ccctcttcgg cattgtcgac
420

<213> Homo sapiens

[illegible]

<213> Homo sapiens

tctagattct tgggcagccg agccccctctt gaattcctca gcctaccatc atgatcaaca
60
cctcccatgt tccgtccatg aatgaccgca ctgacagcac tggagagatt taatgggtca
120

ccaattgagg cagtgaaggc actcatggca ctcagagctg gaatggggct gatctgagtt
 180
 gtactgttga ctgcagtggg gatgacaacc tgcattcctt tgctggctgc atcgacaact
 240
 gctttgtaaa tggcatctac ggaagcatca cctggggccac ccacaacgag gccatccttc
 300
 acctgttgac caagagatgg gtcaatcctc ggttgcaact cacaaggtgt atcttgaaaa
 360
 ggtggaagtg tagtgtttgg attctcagga agtgctgtga gcccaggctg agtgcttatt
 420
 cttttgttta ggagagctgc atcttcctgc attctcacct gaaagttctg aaacagacaa
 480
 gccatggggg tattgttagc tgggcaagga attgtggact gtccttgga cgcctggaga
 540
 ttctggtacc
 550

<210> 824
 <211> 161
 <212> PRT
 <213> Homo sapiens

<400> 824
 Met Ala Cys Leu Phe Gln Asn Phe Gln Val Arg Met Gln Glu Asp Ala
 1 5 10 15
 Ala Leu Leu Asn Lys Arg Ile Ser Thr Gln Pro Gly Leu Thr Ala Leu
 20 25 30
 Pro Glu Asn Pro Asn Thr Thr Leu Pro Pro Phe Gln Asp Thr Pro Cys
 35 40 45
 Glu Leu Gln Pro Arg Ile Asp Pro Ser Leu Gly Gln Gln Val Lys Asp
 50 55 60
 Gly Leu Val Val Gly Gly Pro Gly Asp Ala Ser Val Asp Ala Ile Tyr
 65 70 75 80
 Lys Ala Val Val Asp Ala Ala Ser Lys Gly Met Gln Val Val Ile Thr
 85 90 95
 Thr Ala Val Asn Ser Thr Thr Gln Ile Ser Pro Ile Pro Ala Leu Ser
 100 105 110
 Ala Met Ser Ala Phe Thr Ala Ser Ile Gly Asp Pro Leu Asn Leu Ser
 115 120 125
 Ser Ala Val Ser Ala Val Ile His Gly Arg Asn Met Gly Gly Val Asp
 130 135 140
 His Asp Gly Arg Leu Arg Asn Ser Arg Gly Ala Arg Leu Pro Lys Asn
 145 150 155 160
 Leu

<210> 825
 <211> 327
 <212> DNA
 <213> Homo sapiens

<400> 825
 gcgtttgcga ccggccgtaa cccgcagaat gcggcggtgt gttgcactga gggatattttg
 60

cagttgctgg atgagcgcgga gatgcgcggc gtgctcggcc acgagctgat gcacgtgtac
 120
 aaccgcgata tcctcacctc ttcggtggcg gcgggtatcg cctccatcat cggtacgatt
 180
 gcgcagattc tttcgtttgg cgcgatgttc ggtggatcca accgcgatgg tgaacgttcc
 240
 aacccccctcg ccatgttcgt ggttgctatg ctggctccca ttgctactca ggtcatccag
 300
 atggctatta gccgcacccg tgaattc
 327

<210> 826
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 826
 Ala Phe Ala Thr Gly Arg Asn Pro Gln Asn Ala Ala Val Cys Cys Thr
 1 5 10 15
 Glu Gly Ile Leu Gln Leu Leu Asp Glu Arg Glu Met Arg Gly Val Leu
 20 25 30
 Gly His Glu Leu Met His Val Tyr Asn Arg Asp Ile Leu Thr Ser Ser
 35 40 45
 Val Ala Ala Gly Ile Ala Ser Ile Ile Gly Thr Ile Ala Gln Ile Leu
 50 55 60
 Ser Phe Gly Ala Met Phe Gly Gly Ser Asn Arg Asp Gly Glu Arg Ser
 65 70 75 80
 Asn Pro Leu Ala Met Phe Val Val Ala Met Leu Ala Pro Ile Ala Thr
 85 90 95
 Gln Val Ile Gln Met Ala Ile Ser Arg Thr Arg Glu Phe
 100 105

<210> 827
 <211> 534
 <212> DNA
 <213> Homo sapiens

<400> 827
 nacgcgtacg tcaatatgca tcgtccagtc gttatcgcaa cgccgaaatc gatgctgcgc
 60
 aacaagatgg cgacctcgga tcccgaagag ttcaccaccg gtaggtggcg tcctgttcta
 120
 cccgacccat cgatcaccca cccgacggcc gttacgagga ttatcttggt ctctggcaag
 180
 gcgcggtggg agctggtcaa gcaacgtaag gccgccagtc ttgacggaca gctcgccatc
 240
 atcccgatgg agcgtctcta cccgctacca gtcgacgagt tggctgaggt ttttgcgcct
 300
 tacaccaacg tcacggatgt ccgctgggtc caagaagagc cagagaacca gggcgccctgg
 360
 tactacatgc tgaccacact gccccaggcc atgtcggaga agctgccagg attctttgat
 420
 gggttagtcg gcatcaccgg cccaccgtcc tcagctccgt cggtgggaca gcacagcgtc
 480

cacatccgtg aagagcagga gttactcgag aaggctatag cctgagcgac ctga
534

<210> 828
<211> 174
<212> PRT
<213> Homo sapiens

<400> 828
Xaa Ala Tyr Val Asn Met His Arg Pro Val Val Ile Ala Thr Pro Lys
1 5 10 15
Ser Met Leu Arg Asn Lys Met Ala Thr Ser Asp Pro Glu Glu Phe Thr
20 25 30
Thr Gly Arg Trp Arg Pro Val Leu Pro Asp Pro Ser Ile Thr Asp Pro
35 40 45
Thr Ala Val Thr Arg Ile Ile Leu Cys Ser Gly Lys Ala Arg Trp Glu
50 55 60
Leu Val Lys Gln Arg Lys Ala Ala Ser Leu Asp Gly Gln Leu Ala Ile
65 70 75 80
Ile Pro Met Glu Arg Leu Tyr Pro Leu Pro Val Asp Glu Leu Ala Glu
85 90 95
Val Phe Ala Pro Tyr Thr Asn Val Thr Asp Val Arg Trp Val Gln Glu
100 105 110
Glu Pro Glu Asn Gln Gly Ala Trp Tyr Tyr Met Leu Thr His Leu Pro
115 120 125
Gln Ala Met Ser Glu Lys Leu Pro Gly Phe Phe Asp Gly Leu Val Gly
130 135 140
Ile Thr Arg Pro Pro Ser Ser Ala Pro Ser Val Gly Gln His Ser Val
145 150 155 160
His Ile Arg Glu Glu Gln Glu Leu Leu Glu Lys Ala Ile Ala
165 170

<210> 829
<211> 492
<212> DNA
<213> Homo sapiens

<400> 829
nagtggccgg gtggccggcg ggtgccagcc gccatggagg ccgtgccccg catgccccatg
60
atctggctgg acctgaagga ggccggtgac ttctacttcc agccagctgt gaagaagttt
120
gtcctgaaga attatggaga gaaccagaa gcctacaatg aagaactgaa gaagctggag
180
ttgctcagac agaatgctgt ccgtgtccca cgagactttg agggctgtag tgcctccgc
240
aagtacctcg gccagcttca ttacctgcag agtcgggtcc ccatgggctc gggccaggag
300
gccgctgtcc ctgtcacatg gacagagatc ttctcaggca agtctgtggc ccatgaggac
360
atcaagtacg agcaggcctg tattttctcc aacnttgag cgctgcactc catgctgggg
420
gccatggaca agcgggtgtc tgaggagggc atgaaggtct cctgtacca tttccagtgc
480

gcagccggcg cc
492

<210> 830
<211> 164
<212> PRT
<213> Homo sapiens

<400> 830
Xaa Trp Pro Gly Gly Arg Arg Val Pro Ala Ala Met Glu Ala Val Pro
1 5 10 15
Arg Met Pro Met Ile Trp Leu Asp Leu Lys Glu Ala Gly Asp Phe His
20 25 30
Phe Gln Pro Ala Val Lys Lys Phe Val Leu Lys Asn Tyr Gly Glu Asn
35 40 45
Pro Glu Ala Tyr Asn Glu Glu Leu Lys Lys Leu Glu Leu Leu Arg Gln
50 55 60
Asn Ala Val Arg Val Pro Arg Asp Phe Glu Gly Cys Ser Val Leu Arg
65 70 75 80
Lys Tyr Leu Gly Gln Leu His Tyr Leu Gln Ser Arg Val Pro Met Gly
85 90 95
Ser Gly Gln Glu Ala Ala Val Pro Val Thr Trp Thr Glu Ile Phe Ser
100 105 110
Gly Lys Ser Val Ala His Glu Asp Ile Lys Tyr Glu Gln Ala Cys Ile
115 120 125
Phe Ser Asn Xaa Gly Ala Leu His Ser Met Leu Gly Ala Met Asp Lys
130 135 140
Arg Val Ser Glu Glu Gly Met Lys Val Ser Cys Thr His Phe Gln Cys
145 150 155 160
Ala Ala Gly Ala

<210> 831
<211> 303
<212> DNA
<213> Homo sapiens

<400> 831
gcgttgctgc ggcgtggcga gaccatgacg gcggagaatc agcgtgccaa tgtgcgcac
60
gccgcaaacc acatcaagga ggttgccggtc gatcaccgagg tcgttgtagc ccatggta
120
ggcccccagg taggtctggt ggctctgcaa tcgacagcct acgaggaagt cggtatctat
180
ccgctggatg tcctgggcgc agagtcacag gccatgatcg gctacatgat cgagcaggaa
240
ctcggcaatg tgatgcctca ggatcagcag atcgtcacca tgatcacgat gacagtcgtc
300
gac
303

<210> 832
<211> 101
<212> PRT

<213> Homo sapiens

<400> 832

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Ala Leu Leu Arg Arg Gly Glu Thr Met Thr Ala Glu Asn Gln Arg Ala
 1           5           10           15
Asn Val Arg Ile Ala Ala Asn His Ile Lys Glu Val Ala Val Asp His
          20           25           30
Glu Val Val Val Ala His Gly Asn Gly Pro Gln Val Gly Leu Leu Ala
          35           40           45
Leu Gln Ser Thr Ala Tyr Glu Glu Val Gly Ile Tyr Pro Leu Asp Val
          50           55           60
Leu Gly Ala Glu Ser Gln Ala Met Ile Gly Tyr Met Ile Glu Gln Glu
65           70           75           80
Leu Gly Asn Val Met Pro Gln Asp Gln Gln Ile Val Thr Met Ile Thr
          85           90           95
Met Thr Val Val Asp
          100

```

<210> 833

<211> 466

<212> DNA

<213> Homo sapiens

<400> 833

```

nngatccgcg cgatcgacga ggcgggtgcg tgatgttgac agcgaaaatg cgcagccggc
60
catttgacga gggctgaaaa cgtcttctac cggctctgctg tgccgcctgg tgtcagcaaa
120
cgacgccatg atcgtccagt gggatatgat ttgttctgcg gcgctggggg attcagttgc
180
ggattccacc aggccgggtg gcatgttgcg gcggcggttg agcacgacgt gtcggcgtct
240
ctgacctatg tcatgaatct cgctcggccc ggcgtcaaga ttcacatcga ccccgagcac
300
ccggagctgg gcccaagacc accgcgaacc aagaagaaga gcggcggcgc agtgccgttc
360
gatgcgcatg tcggaactgg gtggatcgcc agcgagcccg ccgacgatcc cggctgcgaa
420
cacttctacg tgtacgacgt caagaacctc agcggcgagc ggatcc
466

```

<210> 834

<211> 142

<212> PRT

<213> Homo sapiens

<400> 834

```

Gln Arg Lys Cys Ala Ala Gly His Leu Thr Arg Ala Glu Asn Val Phe
 1           5           10           15
Tyr Arg Ser Ala Val Pro Pro Gly Val Ser Lys Arg Arg His Asp Arg
          20           25           30
Pro Val Gly Ile Asp Leu Phe Cys Gly Ala Gly Gly Phe Ser Cys Gly
          35           40           45
Phe His Gln Ala Gly Trp His Val Ala Ala Ala Val Glu His Asp Val

```

50		55		60											
Ser	Ala	Ser	Leu	Thr	Tyr	Val	Met	Asn	Leu	Ala	Arg	Pro	Gly	Val	Lys
65					70				75						80
Ile	His	Ile	Asp	Pro	Glu	His	Pro	Glu	Leu	Gly	Pro	Arg	Pro	Pro	Arg
			85						90					95	
Thr	Lys	Lys	Lys	Ser	Gly	Gly	Ala	Val	Pro	Phe	Asp	Ala	His	Val	Gly
			100					105					110		
Thr	Gly	Trp	Ile	Ala	Ser	Glu	Pro	Ala	Asp	Asp	Pro	Gly	Cys	Glu	His
		115					120					125			
Phe	Tyr	Val	Tyr	Asp	Val	Lys	Asn	Leu	Ser	Gly	Glu	Arg	Ile		
	130					135					140				

<210> 835
 <211> 482
 <212> DNA
 <213> Homo sapiens

<400> 835
 acgcgtgaag ggattttgat caccagaac aaccacctgt ctttttagat caagaagcag
 60
 aagctcagag caaagaacat cacaccacgt ccctcagtga ttgaagcagt gattgagtca
 120
 cagaataaat ctggaactca ggtcttctga tctttgctcc agatgtaga gacaaaacta
 180
 aaagtaaaat accaagtga atcaaagcat cacgattgag ccagaacat gaaaaagaac
 240
 ttcttgccc acttgagaaa ctgttaaacc ggacatacct ttggggactt cttcccttct
 300
 ctggaataag attgatgttt ccatgctgtg aaagacgatg atgttccttc tcccagattc
 360
 ctgctgtctt caaaaggcct agcaaaaacc actgctgctg ggtgcagttg agaaagggaa
 420
 tgaagaacaa tcccatggcc atgcaggcac tcctcccctc cacctctctg cccttcacgc
 480
 gt
 482

<210> 836
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 836
 Met Ala Met Gly Leu Phe Phe Ile Pro Phe Leu Asn Cys Thr Gln Gln
 1 5 10 15
 Gln Trp Phe Leu Leu Gly Leu Leu Lys Thr Ala Gly Ile Trp Glu Lys
 20 25 30
 Glu His His Arg Leu Ser Gln His Gly Asn Ile Asn Leu Ile Pro Glu
 35 40 45
 Lys Gly Arg Ser Pro Gln Arg Tyr Val Arg Phe Asn Ser Phe Ser Ser
 50 55 60
 Gly Pro Gly Ser Ser Phe Ser Cys Ser Gly Leu Asn Arg Asp Ala Leu
 65 70 75 80
 Ile Ser Leu Gly Ile Leu Leu Leu Val Leu Ser Leu Thr Ser Gly Ala

				85						90					95				
Lys	Ile	Arg	Arg	Pro	Glu	Phe	Gln	Ile	Tyr	Ser	Val	Thr	Gln	Ser	Leu				
				100				105							110				
Leu	Gln	Ser	Leu	Arg	Asp	Val	Val												
				115				120											

<210> 837
 <211> 509
 <212> DNA
 <213> Homo sapiens

<400> 837
 acgcgtggac ccccgttctg cccgcctttg cagtcacgc cctccctgaa gtcaccgctg
 60
 cagaaatacg caggcactga cctgggggta cagccaggca agggagagac gaggggctca
 120
 ctctgcacca gccaaaggcct gtgtcctggc atggctcccc caggaagcga ggatggcggt
 180
 gcctggcggt cgagcccctc ttatcctggg gaatgctggg gggcgcttct gagcagacct
 240
 gcctgctgcc cctgctggct ggcactgcc ctccccggg gaaagggttg gtggtcccc
 300
 caggggaact caaagcaggg gagcccctgg agggcccaag tccctggaat atcttggcgc
 360
 tcagatggcc cccctcgaac accctcacac gggggggccg cgcggtggga ggtgaccag
 420
 cagccactct tacttggcga agacttttct cccaatgcga gcgcgggttg tatcagcctg
 480
 agccttcagg ttggtgaggc tgggggtacc
 509

<210> 838
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 838
 Met Ala Pro Pro Gly Ser Glu Asp Gly Gly Ala Trp Arg Ser Ser Pro
 1 5 10 15
 Ser Tyr Pro Gly Glu Cys Trp Gly Ala Phe Leu Ser Arg Pro Ala Cys
 20 25 30
 Cys Pro Cys Trp Leu Ala Leu Pro Leu Pro Arg Gly Lys Val Gly Trp
 35 40 45
 Ser Pro Gln Gly Asn Ser Lys Gln Gly Ser Pro Trp Arg Pro Gln Val
 50 55 60
 Pro Gly Ile Ser Trp Arg Ser Asp Gly Pro Pro Arg Thr Pro Ser His
 65 70 75 80
 Gly Gly Ala Ala Arg Trp Glu Val Thr Gln Gln Pro Leu Leu Leu Gly
 85 90 95
 Glu Asp Phe Ser Pro Asn Ala Ser Ala Gly Gly Ile Ser Leu Ser Leu
 100 105 110
 Gln Val Gly Glu Ala Gly Val
 115

<210> 839
 <211> 347
 <212> DNA
 <213> Homo sapiens

<400> 839
 acgcgtctcg tgttcgtgcg gcacggcagg acggcggttca atgtggaggg tcggctccag
 60
 ggccgtctcg acatgccggtt ggatgaggtg gggcgccgtc aggcactcac agtggctcaa
 120
 gtcacgccc agatggaacc tgacgcgatc atggcctctc cgctacaacg tgcgcgcgac
 180
 acagctcagg caatcggtgc ttgtgctgga ttgggcgtac agctggatga tcgactcatc
 240
 gagatcgatg tcggacgttg gtcgggacaa cgggctgcgg acctgcgtcg caacgatcct
 300
 gagtacgcag caagtgtggt cagccctatc gattaccggg tcggagn
 347

<210> 840
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 840
 Thr Arg Leu Val Phe Val Arg His Gly Arg Thr Ala Phe Asn Val Glu
 1 5 10 15
 Gly Arg Leu Gln Gly Arg Leu Asp Met Pro Leu Asp Glu Val Gly Arg
 20 25 30
 Arg Gln Ala Leu Thr Val Ala Gln Val Ile Ala Glu Met Glu Pro Asp
 35 40 45
 Ala Ile Met Ala Ser Pro Leu Gln Arg Ala Arg Asp Thr Ala Gln Ala
 50 55 60
 Ile Gly Ala Cys Ala Gly Leu Gly Val Gln Leu Asp Asp Arg Leu Ile
 65 70 75 80
 Glu Ile Asp Val Gly Arg Trp Ser Gly Gln Arg Ala Ala Asp Leu Arg
 85 90 95
 Arg Asn Asp Pro Glu Tyr Ala Ala Ser Val Val Ser Pro Ile Asp Tyr
 100 105 110
 Arg Val Gly
 115

<210> 841
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 841
 tccggaactc accccgacgc cgtcattatg gacgtcatga tgccgcgtct agatggcttg
 60
 gaagccaccc ggatgctgcg cagcaatggc aacgacgtcc cgatcctcgt cctcaccgcc
 120
 cgcgatgctg tcgacgatcg cgttgacggc ctcgacgctg gcgccgatga ctacatggtc
 180

aagcccttcg ccctcgacga actcctcgct cgcctacgcy ccctcactcg tcgttcccgt
 240
 cccgagccag agcaaaacga ggcccctgaa caactctcct tcgctgacct cacccttgat
 300
 ccaggcaccc gcgagatcac ccgcgggaac cgtcgcatca gtttgacgcy t
 351

<210> 842
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 842
 Ser Gly Thr His Pro Asp Ala Val Ile Met Asp Val Met Met Pro Arg
 1 5 10 15
 Leu Asp Gly Leu Glu Ala Thr Arg Met Leu Arg Ser Asn Gly Asn Asp
 20 25 30
 Val Pro Ile Leu Val Leu Thr Ala Arg Asp Ala Val Asp Asp Arg Val
 35 40 45
 Asp Gly Leu Asp Ala Gly Ala Asp Asp Tyr Met Val Lys Pro Phe Ala
 50 55 60
 Leu Asp Glu Leu Leu Ala Arg Leu Arg Ala Leu Thr Arg Arg Ser Arg
 65 70 75 80
 Pro Glu Pro Glu Gln Asn Glu Ala Pro Glu Gln Leu Ser Phe Ala Asp
 85 90 95
 Leu Thr Leu Asp Pro Gly Thr Arg Glu Ile Thr Arg Gly Asn Arg Arg
 100 105 110
 Ile Ser Leu Thr Arg
 115

<210> 843
 <211> 393
 <212> DNA
 <213> Homo sapiens

<400> 843
 ctagcccagg ctctcgcca cgaggggctg cgcgctgtgg cctctggggc aaaccgggtc
 60
 ggcccaagc gcggtatcga gaaggctgtc gacgccgttg tggaggagct ccgctctatc
 120
 tcgcgcgcca tcgacaccac ctcggacatg gccagcggtg ccaccatctc cagccgtgac
 180
 gagaccatcg gcgccctcat cgctgaggcc ttcgacaagg ttggttaagga cgggggttatc
 240
 accgtcgacg agtcgcagac cttcggcact gagcttgact tcaccgaggg catgcagttc
 300
 gacaagggtt acctgtcgcc ctacatggtc accgaccagg ttcgcatgga ggctgtgatc
 360
 gaggatcctt acatcctcat tcaactcccgc aag
 393

<210> 844
 <211> 131
 <212> PRT

<213> Homo sapiens

<400> 844

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Leu Ala Gln Ala Leu Val His Glu Gly Leu Arg Ala Val Ala Ser Gly
 1           5           10           15
Ala Asn Pro Val Gly Leu Lys Arg Gly Ile Glu Lys Ala Val Asp Ala
 20           25           30
Val Val Glu Glu Leu Arg Ser Ile Ser Arg Ala Ile Asp Thr Thr Ser
 35           40           45
Asp Met Ala Ser Val Ala Thr Ile Ser Ser Arg Asp Glu Thr Ile Gly
 50           55           60
Ala Leu Ile Ala Glu Ala Phe Asp Lys Val Gly Lys Asp Gly Val Ile
 65           70           75           80
Thr Val Asp Glu Ser Gln Thr Phe Gly Thr Glu Leu Asp Phe Thr Glu
 85           90           95
Gly Met Gln Phe Asp Lys Gly Tyr Leu Ser Pro Tyr Met Val Thr Asp
 100          105          110
Gln Val Arg Met Glu Ala Val Ile Glu Asp Pro Tyr Ile Leu Ile His
 115          120          125
Ser Arg Lys
 130

```

<210> 845

<211> 505

<212> DNA

<213> Homo sapiens

<400> 845

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gccacctgcc caaggctgga tgacgggcct agggcacatc taaggaacaa ggacaggaca
60
gaagcaaagc cacagctgct ggggcagggt gggggccggt atgtctggcc agcagcatca
120
cccctgcccc cggcggggct ccaggaccgg gagactcatc agccggaagc tcttgaggga
180
ggcggctgcc gtgaagacag gcacccttgc tcctgagagg ggcacccaga gaaccaagac
240
tcagcagagg gaacacaggg ctacgcccag gcccaggcc tgatatccag agtctaaatc
300
ccacctcagc ccagggggga gccttgagag gagctatgtc cctcatggac ccagtttcc
360
tctgcatacg ggctccgagc cctgcactgc ctccagggta gttcccaagg tcttttccca
420
ttacctccta cgtgagcact cagtaaacca atacacatac acaagggtga cattaattcc
480
agccacagaa tcccaggcca cgcgt
505

```

<210> 846

<211> 130

<212> PRT

<213> Homo sapiens

<400> 846

```

Met Gly Lys Asp Leu Gly Asn Tyr Pro Gly Gly Ser Ala Gly Leu Gly

```


1	5	10	15
Ala Arg Met Gln Arg Lys Leu Gly Ser Met Arg Asp Ile Ala Pro Leu			
	20	25	30
Lys Ala Pro Pro Trp Ala Glu Val Gly Phe Arg Leu Trp Ile Ser Gly			
	35	40	45
Leu Gly Pro Gly Arg Ser Pro Val Phe Pro Leu Leu Ser Leu Gly Ser			
	50	55	60
Leu Gly Ala Pro Leu Arg Ser Lys Gly Ala Cys Leu His Gly Ser Arg			
65	70	75	80
Leu Leu Gln Glu Leu Pro Ala Asp Glu Ser Pro Gly Pro Gly Ala Pro			
	85	90	95
Pro Gly Ala Gly Val Met Leu Leu Ala Arg His Thr Gly Pro His Pro			
	100	105	110
Ala Pro Ala Ala Val Ala Leu Leu Leu Ser Cys Pro Cys Ser Leu Asp			
	115	120	125
Val Pro			
130			

<210> 847

<211> 448

<212> DNA

<213> Homo sapiens

<400> 847

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aagcttttaa aggagcaaga aaacatgaaa gagctagtag tcaaccttct ccgcatgact
60
caaatcaaaa ttgatgaaaa ggaacaaaag tccaaggatt tcctgaaagc tcagcaaaaa
120
tacaccaaca ttgttaaaga aatgaaagca aaggatcttg aaatcaggat acacaagaag
180
aaaaaatgtg aaatttatcg gagactgaga gagcttgcta aactgtatga caccattcga
240
aatgaaagaa acaaatttgt taacttactc cacaaagctc atcagaaagt aaatgaaata
300
aaagaaaggc ataaaatgtc attaaatgaa cttgaaattc tgagaaatag tgccgtagt
360
caagaaagaa agctacaaaa ttccatgctg aaacacgcc acaatgttac catcagagag
420
agcatgcaaa acgatgtgcg caaaattt
448

```

<210> 848

<211> 149

<212> PRT

<213> Homo sapiens

<400> 848

Lys Leu Leu Lys Glu Gln Glu Asn Met Lys Glu Leu Val Val Asn Leu			
1	5	10	15
Leu Arg Met Thr Gln Ile Lys Ile Asp Glu Lys Glu Gln Lys Ser Lys			
	20	25	30
Asp Phe Leu Lys Ala Gln Gln Lys Tyr Thr Asn Ile Val Lys Glu Met			
	35	40	45
Lys Ala Lys Asp Leu Glu Ile Arg Ile His Lys Lys Lys Lys Cys Glu			

```

      50              55              60
Ile Tyr Arg Arg Leu Arg Glu Leu Ala Lys Leu Tyr Asp Thr Ile Arg
65              70              75              80
Asn Glu Arg Asn Lys Phe Val Asn Leu Leu His Lys Ala His Gln Lys
      85              90              95
Val Asn Glu Ile Lys Glu Arg His Lys Met Ser Leu Asn Glu Leu Glu
      100             105             110
Ile Leu Arg Asn Ser Ala Val Ser Gln Glu Arg Lys Leu Gln Asn Ser
      115             120             125
Met Leu Lys His Ala Asn Asn Val Thr Ile Arg Glu Ser Met Gln Asn
      130             135             140
Asp Val Arg Lys Ile
145

```

<210> 849
 <211> 463
 <212> DNA
 <213> Homo sapiens

```

<400> 849
nnacgcgtga ttgttggggc caaggaatgc catgtggaga gtgcaggtga agtgataagt
60
cttttggaga tggggaatgc agccagacat acaggtacca ctcaaataaa tgagcactcc
120
agcagatcac atgcaatttt tacaatcagc atttgtcaag ttcataaaaa tatggaggca
180
gctgaagatg gatcatggta ttcccctcgg catattgtct caaagttcca ctttgtggat
240
ttggcaggat cagaaagagt aaccaaaccg gggaatactg gtgaacggtt caaagaatcc
300
attcaaataca atagtggatt gctggcttta ggaaatgtaa taagcgctct tggggacca
360
cgcaggaaga gttcacatat tccatatagg gatgctaaaa ttaccggct tctgaaagat
420
tctctgggag gcagtgtctaa gactgtcatg atcacatgtg tca
463

```

<210> 850
 <211> 154
 <212> PRT
 <213> Homo sapiens

```

<400> 850
Xaa Arg Val Ile Val Gly Ala Lys Glu Cys His Val Glu Ser Ala Gly
1      5      10      15
Glu Val Ile Ser Leu Leu Glu Met Gly Asn Ala Ala Arg His Thr Gly
      20      25      30
Thr Thr Gln Met Asn Glu His Ser Ser Arg Ser His Ala Ile Phe Thr
      35      40      45
Ile Ser Ile Cys Gln Val His Lys Asn Met Glu Ala Ala Glu Asp Gly
      50      55      60
Ser Trp Tyr Ser Pro Arg His Ile Val Ser Lys Phe His Phe Val Asp
65      70      75      80
Leu Ala Gly Ser Glu Arg Val Thr Lys Thr Gly Asn Thr Gly Glu Arg

```

				85					90					95					
Phe	Lys	Glu	Ser	Ile	Gln	Ile	Asn	Ser	Gly	Leu	Leu	Ala	Leu	Gly	Asn				
				100				105						110					
Val	Ile	Ser	Ala	Leu	Gly	Asp	Pro	Arg	Arg	Lys	Ser	Ser	His	Ile	Pro				
			115				120						125						
Tyr	Arg	Asp	Ala	Lys	Ile	Thr	Arg	Leu	Leu	Lys	Asp	Ser	Leu	Gly	Gly				
	130					135					140								
Ser	Ala	Lys	Thr	Val	Met	Ile	Thr	Cys	Val										
145					150														

<210> 851
 <211> 372
 <212> DNA
 <213> Homo sapiens

<400> 851
 aaatttcctg tttctgatcg acgaaataaa gtttagcgtg atgagtgagc tgcttatgca
 60
 gttcctccat tcgcttataa acagttttat ttctcatttc gaaaactctc gatgcagaat
 120
 aaaggctaga gtctggggac caagtcccca gctccgttta cgcgacttcc ttgaccttgt
 180
 ttgttatgct gataaggta ttcagcttga cgatttggtc gtggtctttc aaccgttttg
 240
 cagctggtcg acgatattcc tggtaggaac tacgatagaa gaccagcatc ggaagaactt
 300
 tgtagatgct gaacaaacac ccaccgatca cttcagcctc gaagtaaggg ttatactgtc
 360
 taaccacgc gt
 372

<210> 852
 <211> 110
 <212> PRT
 <213> Homo sapiens

Met	Ser	Glu	Leu	Leu	Met	Gln	Phe	Leu	His	Ser	Leu	Ile	Asn	Ser	Phe				
1				5				10					15						
Ile	Ser	His	Phe	Glu	Asn	Ser	Arg	Cys	Arg	Ile	Lys	Ala	Arg	Val	Trp				
			20					25					30						
Gly	Pro	Ser	Pro	Gln	Leu	Arg	Leu	Arg	Asp	Phe	Leu	Asp	Leu	Val	Cys				
		35				40					45								
Tyr	Ala	Asp	Lys	Val	Ile	Gln	Leu	Asp	Asp	Leu	Phe	Val	Val	Phe	Gln				
	50					55				60									
Pro	Phe	Cys	Ser	Trp	Ser	Thr	Ile	Phe	Leu	Val	Gly	Thr	Thr	Ile	Glu				
65					70				75					80					
Asp	Gln	His	Arg	Lys	Asn	Phe	Val	Asp	Ala	Glu	Gln	Thr	Pro	Thr	Asp				
			85			90							95						
His	Phe	Ser	Leu	Glu	Val	Arg	Val	Ile	Leu	Ser	Asn	Pro	Arg						
			100				105						110						

<210> 853
 <211> 423

<212> DNA

<213> Homo sapiens

<400> 853

acgcgttcag aaacttatgg tgaaatggcc gaactagaaa acctagtcga cgaatattac
 60
 caagctatgg gcatggatgt gcgtcgagaa acctggctgc gcgagcagat actcaagaaa
 120
 gtccaagaaa cgcatttggt agaagagctt gcaggcatag aatcagggtga tgatggcgca
 180
 gtggtggaag agagcgtatt agaaggcctc gatacctatt tatgtgagat aaaagaagca
 240
 cagattcgtc atggattgca tcgtcttgga gaattaccag aagacgataa attggccgat
 300
 accttggtcg ccttattgcy tttaccccggt ggcagtgaca ttaccagcaa gggaattttg
 360
 catgccttaa tggcagattt agagttagaa caagacgatt ttgacccaat gcaaagcacg
 420
 cgt
 423

<210> 854

<211> 141

<212> PRT

<213> Homo sapiens

<400> 854

Thr	Arg	Ser	Glu	Thr	Tyr	Gly	Glu	Met	Ala	Glu	Leu	Glu	Asn	Leu	Val
1				5					10					15	
Asp	Glu	Tyr	Tyr	Gln	Ala	Met	Gly	Met	Asp	Val	Arg	Arg	Glu	Thr	Trp
			20					25					30		
Leu	Arg	Glu	Gln	Ile	Leu	Lys	Lys	Val	Gln	Glu	Thr	His	Leu	Leu	Glu
		35					40					45			
Glu	Leu	Ala	Gly	Ile	Glu	Ser	Gly	Asp	Asp	Gly	Ala	Val	Val	Glu	Glu
	50					55					60				
Ser	Val	Leu	Glu	Gly	Leu	Asp	Thr	Tyr	Leu	Cys	Glu	Ile	Lys	Glu	Ala
65					70					75				80	
Gln	Ile	Arg	His	Gly	Leu	His	Arg	Leu	Gly	Glu	Leu	Pro	Glu	Asp	Asp
			85					90					95		
Lys	Leu	Ala	Asp	Thr	Leu	Val	Ala	Leu	Leu	Arg	Leu	Pro	Arg	Gly	Ser
		100						105					110		
Asp	Ile	Thr	Ser	Lys	Gly	Ile	Leu	His	Ala	Leu	Met	Ala	Asp	Leu	Glu
	115					120					125				
Leu	Glu	Gln	Asp	Asp	Phe	Asp	Pro	Met	Gln	Ser	Thr	Arg			
	130					135					140				

<210> 855

<211> 338

<212> DNA

<213> Homo sapiens

<400> 855

acgcgtgaag ggggagctca aagtagatgg acctctgact agatggagct ctgagtaaga
 60

tgaatgtctg tgcggatgtt gctcacagca agatagtgtt tggagcgatt ggcacttcga
 120
 acaagatgga gcatggagca gatggagctc tgagcaagat ggagcgtgga gtagatagag
 180
 cttggagcaa gaaggagctc caagcaagat ggagcttgca gcaggtgctt ctcagtgtaa
 240
 gatggagctc agagaagatg atgctcagag taagattgag ctcggtgatt ggcactccaa
 300
 acattgctct gagcccattg gagnctctga gcagaaag
 338

<210> 856

<211> 93

<212> PRT

<213> Homo sapiens

<400> 856

Met	Asn	Val	Cys	Ala	Asp	Val	Ala	His	Ser	Lys	Ile	Val	Leu	Gly	Ala
1				5					10					15	
Ile	Gly	Thr	Ser	Asn	Lys	Met	Glu	His	Gly	Ala	Asp	Gly	Ala	Leu	Ser
			20					25					30		
Lys	Met	Glu	Arg	Gly	Val	Asp	Arg	Ala	Trp	Ser	Lys	Lys	Glu	Leu	Gln
		35					40					45			
Ala	Arg	Trp	Ser	Leu	Gln	Gln	Val	Leu	Leu	Ser	Val	Arg	Trp	Ser	Ser
	50					55				60					
Glu	Lys	Met	Met	Leu	Arg	Val	Arg	Leu	Ser	Ser	Val	Ile	Gly	Thr	Pro
65					70				75					80	
Asn	Ile	Ala	Leu	Ser	Pro	Leu	Glu	Xaa	Leu	Ser	Arg	Lys			
				85					90						

<210> 857

<211> 435

<212> DNA

<213> Homo sapiens

<400> 857

ccggacagtg ggccaccagt gtttgccccc agcaatcatg tcagtgaagc ccaacctcgg
 60
 gagacacccc ggccctcat gcctcctacc aagcctttcc tagcacctga gaccaccagc
 120
 cctggtgaca ggggtggagac ccctgtgggg gagagagccc caaccctgt ctcagcaagc
 180
 tctgaggtct cccctgagag ccaagaggac tcagagaccc cagcagagga ggacagtggc
 240
 tctgagcagc ctccaacag cgtcctgcct gacaaactga aggtgagctg ggagaacccc
 300
 agccccagc aggcccctgc tgcagagagt gcagaaccgt cccaggcacc ctgttctgag
 360
 acttctgagg ctgccccag ggaggggtggg aagcccccta caccaccacc caagatctta
 420
 tcagagaaac tgaaa
 435

<210> 858

<211> 145

<212> PRT

<213> Homo sapiens

<400> 858

```

Pro Asp Ser Gly Pro Pro Val Phe Ala Pro Ser Asn His Val Ser Glu
 1           5           10           15
Ala Gln Pro Arg Glu Thr Pro Arg Pro Leu Met Pro Pro Thr Lys Pro
          20           25           30
Phe Leu Ala Pro Glu Thr Thr Ser Pro Gly Asp Arg Val Glu Thr Pro
          35           40           45
Val Gly Glu Arg Ala Pro Thr Pro Val Ser Ala Ser Ser Glu Val Ser
          50           55           60
Pro Glu Ser Gln Glu Asp Ser Glu Thr Pro Ala Glu Glu Asp Ser Gly
65           70           75           80
Ser Glu Gln Pro Pro Asn Ser Val Leu Pro Asp Lys Leu Lys Val Ser
          85           90           95
Trp Glu Asn Pro Ser Pro Gln Glu Ala Pro Ala Ala Glu Ser Ala Glu
          100          105          110
Pro Ser Gln Ala Pro Cys Ser Glu Thr Ser Glu Ala Ala Pro Arg Glu
          115          120          125
Gly Gly Lys Pro Pro Thr Pro Pro Pro Lys Ile Leu Ser Glu Lys Leu
          130          135          140
Lys
145

```

<210> 859

<211> 561

<212> DNA

<213> Homo sapiens

<400> 859

```

nacgcgtggt gtggtaatcc gggtttctggt ggcgacggct gccacccctc gtggcaagac
60
atgccgttgc gtgccgatat gccatacgaa gcttggccta gtgcgaaaag ctcgctggaa
120
ccctcgaaga ggcagggctcg gcagggtacc gtggtcggtg tacgcacgtt ttcgacgatg
180
aaccaccattc tgggagcaga tatgacgacg taccagtacc tcattgtcgg tggcgggatg
240
gccgctgatt ctgccgcccg cggatatccgc gacatcgaca agaaagggtc gatcgccatc
300
ctcagcgctg acgtcgacgc cccgtatcct cggccagcgc tgagcaagaa gctgtggact
360
gaccctgagt tcacctggga ccaggtegac cttgctactg tcgctgacac cggcgcgga
420
ttgcggctcg gcactgaggt gctcagcatt gaccgtgacg gcaagaccgt cctgaccgct
480
tccggccagg tattcggcta ccagaagttg ctgctcgta cggccttac cccgtcgcgc
540
attgacgacg acggcgatgc c
561

```

<210> 860

<211> 187

<212> PRT

<213> Homo sapiens

<400> 860

```

Xaa Ala Trp Cys Gly Asn Pro Val Ser Gly Gly Asp Gly Cys His Pro
 1           5           10           15
Ser Trp Gln Asp Met Pro Leu Arg Ala Asp Met Pro Tyr Glu Ala Trp
          20           25           30
Pro Ser Ala Lys Ser Ser Leu Glu Pro Ser Lys Arg Gln Gly Arg Gln
          35           40           45
Val Thr Val Val Gly Val Arg Ile Val Ser Thr Met Asn Pro Ile Leu
          50           55           60
Gly Ala Asp Met Thr Thr Tyr Gln Tyr Leu Ile Val Gly Gly Gly Met
65           70           75           80
Ala Ala Asp Ser Ala Ala Arg Gly Ile Arg Asp Ile Asp Lys Lys Gly
          85           90           95
Ser Ile Ala Ile Leu Ser Ala Asp Val Asp Ala Pro Tyr Pro Arg Pro
          100          105          110
Ala Leu Ser Lys Lys Leu Trp Thr Asp Pro Glu Phe Thr Trp Asp Gln
          115          120          125
Val Asp Leu Ala Thr Val Ala Asp Thr Gly Ala Glu Leu Arg Leu Gly
          130          135          140
Thr Glu Val Leu Ser Ile Asp Arg Asp Gly Lys Thr Val Leu Thr Ala
145          150          155          160
Ser Gly Gln Val Phe Gly Tyr Gln Lys Leu Leu Leu Val Thr Gly Leu
          165          170          175
Thr Pro Ser Arg Ile Asp Asp Asp Gly Asp Ala
          180          185

```

<210> 861

<211> 352

<212> DNA

<213> Homo sapiens

<400> 861

```

ccatggggttt ctatgctctg aggtttcatc tgtggggaac agtattgact tacttacaaa
60
gagataatgg tcatacccta tggtcactca ccatagtctg gcggtacatg gacttctcag
120
ccccagtaag atctgtatcc acaggacact taaagtcacc ttacagaggg ctatcccagt
180
gcctgaggcc tattagaggc gtctcttttc agccatcagt gttagaggcc atctgcatgg
240
gatcccagag cctgcctcgg gaatggcaga agctggctgg tgcttggcgt gggctttgcc
300
tgtttcactg ctttcaggga ggcctgccac aggggagaaa ctgggggggg ga
352

```

<210> 862

<211> 116

<212> PRT

<213> Homo sapiens

<400> 862

```

Met Gly Phe Tyr Ala Leu Arg Phe His Leu Trp Gly Thr Val Leu Thr
 1           5           10           15
Tyr Leu Gln Arg Asp Asn Gly His Thr Leu Trp Ser Leu Thr Ile Val
          20           25           30
Trp Arg Tyr Met Asp Phe Ser Ala Pro Val Arg Ser Val Ser Thr Gly
          35           40           45
His Leu Lys Ser Pro Tyr Arg Gly Leu Ser Gln Cys Leu Arg Pro Ile
          50           55           60
Arg Gly Val Ser Phe Gln Pro Ser Val Leu Glu Ala Ile Cys Met Gly
65           70           75           80
Ser Gln Ser Leu Pro Arg Glu Trp Gln Lys Leu Ala Gly Ala Trp Arg
          85           90           95
Gly Leu Cys Leu Phe His Cys Phe Gln Gly Gly Leu Pro Gln Gly Arg
          100          105          110
Asn Trp Gly Gly
          115

```

<210> 863

<211> 327

<212> DNA

<213> Homo sapiens

<400> 863

```

tccggatcga cccggacgaa ttccacggtc cagccattga cttccaaatg ctctttgaca
60
tacgccgtga catgttcaat gtccaactta cgcattgtcca cccgctcacc ggtctcattg
120
agtttgagct gcgagtagac gttgcggttag ttctcgttga ccgactgctc atacgagatg
180
tgcagaagca tcggtttgcg gccatcctcg gacggcattg gcttggttgta catggccgct
240
tggcggaaca tggttcagggt aaagcccgac ttgaagttgt gcgacagggc agaaacacac
300
agcatttctg accggcgatg acccatn
327

```

<210> 864

<211> 108

<212> PRT

<213> Homo sapiens

<400> 864

```

Met Gly His Arg Arg Ser Glu Met Leu Cys Val Ser Ala Leu Ser His
 1           5           10           15
Asn Phe Lys Ser Gly Phe Thr Leu Asn Met Phe Arg Gln Ala Ala Met
          20           25           30
Tyr Asn Lys Pro Met Pro Ser Glu Asp Gly Arg Lys Pro Met Leu Leu
          35           40           45
His Ile Ser Tyr Glu Gln Ser Val Asn Glu Asn Tyr Arg Asn Val Tyr
          50           55           60
Ser Gln Leu Lys Leu Asn Glu Thr Gly Glu Arg Val Asp Met Arg Lys
65           70           75           80
Leu Asp Ile Glu His Val Thr Ala Tyr Val Lys Glu His Leu Glu Val

```

	85	90	95
Asn Gly Trp Thr Val Glu Phe Val Arg Val Asp Pro			
	100	105	

<210> 865
 <211> 729
 <212> DNA
 <213> Homo sapiens

<400> 865
 acgcgtcatc ctcattcaag aggccagga ggagcaccac cctccgcata ttgcgcgtgc
 60
 agctctcgtt ctggtctctg agcatgccca cggegtctg cacacagctt ctcagcagcc
 120
 tggtggtgtc caggatcgac acatcactgc ctccgagttc agaggtttcc tttcccacct
 180
 tctcagaact ttctgtttcc atggcctcct ctgccacctc tgcacacctc cctgatgtgc
 240
 tggcctccgt ctccatcgcc tctcatggc cgtcttccgc ccggtgttcc aagcccagct
 300
 caggcaagtc tccgggcgcg aacagctggc tgatggtgac atgctgcagc ctggtcacat
 360
 cagaaaccat gaggggtggat ctccggaggt catcgatgtg gacagactgc cacagccctc
 420
 cgtggaagcc cacataggct gttcctcttc ccacccggga cagttttgtg atgaaataga
 480
 cgaagatacg gtcctcattt tctcgtattt tgttgatttc atttataaca gaatacttag
 540
 ctgaggcaat gagctgggcg ctacggattc catcttcaaa atctgtctga aaaatgagga
 600
 ttttacattt ggctgtattc gttaaacagt ttcggacttc tttgaggaat gagtactcgg
 660
 tgtcaaactg ctgcagccac aggagtgtgg gtttcggagc cctgcctgtg acctctgatt
 720
 ctaaaattt
 729

<210> 866
 <211> 83
 <212> PRT
 <213> Homo sapiens

<400> 866
 Ala Cys Pro Arg Arg Ser Ala His Ser Phe Ser Ala Ala Trp Trp Cys
 1 5 10 15
 Pro Gly Ser Thr His His Cys Leu Arg Val Gln Arg Phe Pro Phe Pro
 20 25 30
 Pro Ser Gln Asn Phe Leu Phe Pro Trp Pro Pro Leu Pro Pro Leu Pro
 35 40 45
 Pro Pro Leu Met Cys Trp Pro Pro Ser Pro Ser Pro Pro His Gly Arg
 50 55 60
 Leu Pro Pro Gly Val Pro Ser Pro Ala Gln Ala Ser Leu Arg Ala Arg
 65 70 75 80
 Thr Ala Gly

<210> 867
 <211> 640
 <212> DNA
 <213> Homo sapiens

<400> 867
 nntccggaac atcaagatcc aggcgcagaa gaccgtcaga agctgcactg gccacctcct
 60
 tcaggtggac tctcggttggg ggccggcgctc gctggccccc tcgcacccgg tcccgtgtca
 120
 catgctccag ggcgcagctc ttgtccacct ttacctcatc gaaagccttg tttttgcctc
 180
 ggttaatccc ttcatagagg gctttgatcc aggattcctt ctctctcccc gtgggtgcct
 240
 ggaatttgat gtcgctgacc ttgttccctg gggatcgag caggataaag cgggtgtttc
 300
 gcttgaggag ggcacgaagg tcctggcact tctcatagct gccagctcc acagtctcca
 360
 cacacttctg atcatcctca ttctcataga ccagcagctg ggcctggcag aggagcagat
 420
 atcgggtcttt ccagaaaccc aggaggcccc cactgctctt cttgatccag ccagccttgt
 480
 ccaccatctg tgctccccga ggcttctcac cggttctctt cacaccctcc tcctccatgg
 540
 cgagtcgcgc gaggtccgcg cgtccgcga ctcgcttcca gcgccgcgcg ggctctgcca
 600
 ccgcgtctac gcccgccag gcggcgactc tccgcgttct
 640

<210> 868
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 868
 Gly Gly His Glu Gly Pro Gly Thr Ser His Ser Cys Pro Ala Pro Gln
 1 5 10 15
 Ser Pro His Thr Ser Asp His Pro His Ser His Arg Pro Ala Ala Gly
 20 25 30
 Pro Gly Arg Gly Ala Asp Ile Gly Leu Ser Arg Asn Pro Gly Gly Pro
 35 40 45
 His Cys Ser Ser
 50

<210> 869
 <211> 321
 <212> DNA
 <213> Homo sapiens

<400> 869
 ngggtgatgc tgctcgcggc attgagcatc tttgtgctca gcgcgctgtt tatcgacaac
 60

ttcctgtcgc cgctgaatat gcgcgggctg ggcctggcga tttcgacggt gggcatcgct
 120
 gcgtgcacca tgctgttctg cctggcgctg gggcatttcg acttgtcggg gggctcgggtg
 180
 atcgccctgtg ccggtgtggg cgcggggatt gtgattcgtg acaccgatag cgtggcactc
 240
 ggcgtgtccg ctgcgttggc catgggcctg gtagtggggc tgatcaacgg catcgtgatc
 300
 gccaaagctgc gcatcaacgc g
 321

<210> 870
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 870
 Xaa Val Met Leu Leu Ala Ala Leu Ser Ile Phe Val Leu Ser Ala Leu
 1 5 10 15
 Phe Ile Asp Asn Phe Leu Ser Pro Leu Asn Met Arg Gly Leu Gly Leu
 20 25 30
 Ala Ile Ser Thr Val Gly Ile Ala Ala Cys Thr Met Leu Phe Cys Leu
 35 40 45
 Ala Ser Gly His Phe Asp Leu Ser Val Gly Ser Val Ile Ala Cys Ala
 50 55 60
 Gly Val Val Ala Gly Ile Val Ile Arg Asp Thr Asp Ser Val Ala Leu
 65 70 75 80
 Gly Val Ser Ala Ala Leu Ala Met Gly Leu Val Val Gly Leu Ile Asn
 85 90 95
 Gly Ile Val Ile Ala Lys Leu Arg Ile Asn Ala
 100 105

<210> 871
 <211> 320
 <212> DNA
 <213> Homo sapiens

<400> 871
 agatcttcag agtcctcgtc ttttaaattgg gggtaacagc agcaagtcct cagaggtgtc
 60
 ctgagcctca aaacacatcc tggtttgtaa cgtccgcagc ctcagcaggg gctaggcaca
 120
 gaacaagcat tcaggacctg gaaggtagca gcgacacctg gtcctccctt cccaggcaca
 180
 aggagcccc tctccattca agctctgccc cagcccagca aagagagggg tcttcagcca
 240
 ctgccccac cactaccaca atcatactca cctctcctgg tccatacgtg acaaaggacc
 300
 tgccacggcc agggagacaa
 320

<210> 872
 <211> 98
 <212> PRT

<213> Homo sapiens

<400> 872

```

Met Gly Val Thr Ala Ala Ser Pro Gln Arg Cys Pro Glu Pro Gln Asn
 1           5           10           15
Thr Ser Trp Phe Val Thr Ser Ala Ala Ser Ala Gly Ala Arg His Arg
 20           25           30
Thr Ser Ile Gln Asp Leu Glu Gly Thr Ser Asp Thr Trp Ser Ser Leu
 35           40           45
Pro Arg His Lys Ala Ala Pro Leu His Ser Ser Ser Ala Pro Ala Gln
 50           55           60
Gln Arg Glu Gly Ser Ser Ala Thr Ala Pro Thr Thr Thr Thr Ile Ile
 65           70           75           80
Leu Thr Ser Pro Gly Pro Tyr Val Thr Lys Asp Leu Pro Arg Pro Gly
 85           90           95
Arg Gln

```

<210> 873

<211> 363

<212> DNA

<213> Homo sapiens

<400> 873

```

nttgtttagc atcgtttttt acgggtgtat cagcgcgttt agcagcgttt ttagcggatg
60
catcagcatg ttttgcgtca cgtttttacaa ctgtgctacc gtgttttagca tcatttttga
120
cggaggtatc aatacgttta gcatcgtttt taacagatgt atcaacacgg ggttcatccg
180
cttttagcaga atccccagct ctagtagcca ctttagatac ttcagatttt atatgagtcg
240
cagttgtttc agcgtgagcc atgctgaatg tagaaccaag ggccaatgta attgctaaag
300
acaaagataa tttatttagt ttcatgttcg gagagaagtg tgccaattcg gcgatacagt
360
cag
363

```

<210> 874

<211> 108

<212> PRT

<213> Homo sapiens

<400> 874

```

Met Lys Leu Asn Lys Leu Ser Leu Ser Leu Ala Ile Thr Leu Ala Leu
 1           5           10           15
Gly Ser Thr Phe Ser Met Ala His Ala Glu Thr Thr Ala Thr His Ile
 20           25           30
Lys Ser Glu Val Ser Lys Val Ala Thr Arg Ala Gly Asp Ser Ala Lys
 35           40           45
Ala Asp Glu Pro Arg Val Asp Thr Ser Val Lys Asn Asp Ala Lys Arg
 50           55           60
Ile Asp Thr Ser Val Lys Asn Asp Ala Lys His Gly Ser Thr Val Val

```


65 70 75 80
 Lys Arg Asp Ala Lys His Ala Asp Ala Ser Ala Lys Asn Ala Ala Lys
 85 90 95
 Arg Ala Asp Thr Pro Val Lys Asn Asp Ala Lys Gln
 100 105

<210> 875
 <211> 355
 <212> DNA
 <213> Homo sapiens

<400> 875
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 120
 cccgccaagc accagctcaa gcgcaggtcc ccgggaaaaa gcgcgggctt ctctctccca
 180
 gcgctcagaa tccctgagcc ggaggccccg cgggattcag accgccagat ccccaggag
 240
 tgacaaatcg ccgcagaaac ttgggggaca actcggccct ggcaccgcgc ggcttcagg
 300
 cgcgggcagg cgcgcgccaa ctttccccgc gtgccacccc gcggctcccc cggen
 355

<210> 876
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 876
 Met Arg Ala Arg Leu Pro Gln Thr His Cys Leu Gly Glu Lys Lys Ser
 1 5 10 15
 Arg Lys Gln Leu Glu Ser Leu Pro Phe Arg Thr Asn Pro Pro Ser Thr
 20 25 30
 Ser Ser Ser Ala Gly Pro Arg Glu Lys Ala Arg Ala Ser Leu Ser Gln
 35 40 45
 Arg Ser Glu Ser Leu Ser Arg Arg Pro Arg Gly Ile Gln Thr Ala Arg
 50 55 60
 Ser Pro Gly Ser Asp Lys Ser Pro Gln Lys Leu Gly Gly Gln Leu Gly
 65 70 75 80
 Pro Gly Thr Ala Arg Leu Pro Gly Ala Gly Arg Arg Ala Pro Thr Phe
 85 90 95
 Pro Ala Cys His Pro Ala Ala Pro Pro Ala
 100 105

<210> 877
 <211> 487
 <212> DNA
 <213> Homo sapiens

<400> 877
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caatccacct atgctaaacg tggtcagcaa gggtatctca cacgagaatt ctttggtttg
 120
 ttggccaata ccatgggaga tcaaatacctt ttagtacagg cgtacagaga aggcgaagcg
 180
 atcgccgcgt cgtggtgttt ctttgatgat cattcactat atgggcgtta ttggggctgt
 240
 atggaagaag tggattgcct gcattttgaa gcttggttatt accaaggaat cgagttttgt
 300
 ctcgaaaaag ggttacagca tttcgatccg ggtacacaag gggaacacaa gattgcgcgc
 360
 ggctttgaac ctgttttttag ccacagcgtg cattacattg ctcataagg ttttcgtgaa
 420
 gcgattggga atttctgtga ggaagaagcg caagctgtgc gcgagtatca tcaagatacc
 480
 cacgcgt
 487

<210> 878
 <211> 162
 <212> PRT
 <213> Homo sapiens

<400> 878
 Thr Arg Thr Leu Gly Asn Glu Leu Thr Thr Ala Glu Ile Asp Cys Leu
 1 5 10 15
 Tyr Leu Cys Tyr Gln Ser Thr Tyr Ala Lys Arg Gly Gln Gln Gly Tyr
 20 25 30
 Leu Thr Arg Glu Phe Phe Gly Leu Leu Ala Asn Thr Met Gly Asp Gln
 35 40 45
 Ile Leu Leu Val Gln Ala Tyr Arg Glu Gly Glu Ala Ile Ala Ala Ser
 50 55 60
 Trp Cys Phe Phe Asp Asp His Ser Leu Tyr Gly Arg Tyr Trp Gly Cys
 65 70 75 80
 Met Glu Glu Val Asp Cys Leu His Phe Glu Ala Cys Tyr Tyr Gln Gly
 85 90 95
 Ile Glu Phe Cys Leu Glu Lys Gly Leu Gln His Phe Asp Pro Gly Thr
 100 105 110
 Gln Gly Glu His Lys Ile Ala Arg Gly Phe Glu Pro Val Phe Ser His
 115 120 125
 Ser Val His Tyr Ile Ala His Gln Gly Phe Arg Glu Ala Ile Gly Asn
 130 135 140
 Phe Cys Glu Glu Glu Ala Gln Ala Val Arg Glu Tyr His Gln Asp Thr
 145 150 155 160
 His Ala

<210> 879
 <211> 993
 <212> DNA
 <213> Homo sapiens

<400> 879
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agccagtcca gtagggctct gacccctcct tcctacagta ctgctaaaaa ttcattggga
 120
 tcaagatcca gtgaatcctt tgggaagtac acatcgccag taatgagtga gcatggggac
 180
 gagcacaggc agctcctctc tcaccaatg caaggccctg gactccgtgc agctacctca
 240
 tccaaccact ctgtggacga gcaactgaag aatactgaca cgcacctcat cgacctggta
 300
 accaatgaga ttatcaccca aggacctcca gtggactgga atgacattgc tgggtctcgac
 360
 ctggtgaagg ctgtcattaa agaggaggtt ttatggccag tgttgaggtc agacgcgttc
 420
 agtggactga cggccttacc tcggagcatc cttttatttg gacctcgggg gacaggcaaa
 480
 acattattgg gcagatgcat cgctagtcag ctggggggcca catttttcaa aattgccggt
 540
 tctggactag tcgccaaggg gttaggagaa gcagagaaaa ttatccatgc ctcttttctt
 600
 gtggccaggt gtcgccagcc ctcggtgatt tttgttagtg acattgacat gcttctctcc
 660
 tctcaagtga atgaggaaca tagtccagtc agtcggatga gaaccgaatt tctgatgcaa
 720
 ctggacactg tactaacttc ggctgaggac caaatcgtag taatttgtgc caccagtaaa
 780
 ccagaagaaa tagatgaatc ccttcggagg tacttcatga aacgactttt aatcccactt
 840
 cctgacagca cagcgaggca ccagataata gtacaactgc tctcacagca caattactgt
 900
 ctcaatgaca aggagtttgc actgctcgtc cagcgcacag aaggcttttc tggactagat
 960
 gtgggtcatt tgtgtcagga agcagtgggtg ggc
 993

<210> 880

<211> 331

<212> PRT

<213> Homo sapiens

<400> 880

Xaa	Leu	Ala	Phe	Lys	Pro	Thr	Arg	Gln	Leu	Met	Ser	Ser	Glu	Gln	Gln
1				5					10					15	
Arg	Lys	Phe	Ser	Ser	Gln	Ser	Ser	Arg	Ala	Leu	Thr	Pro	Pro	Ser	Tyr
			20					25					30		
Ser	Thr	Ala	Lys	Asn	Ser	Leu	Gly	Ser	Arg	Ser	Ser	Glu	Ser	Phe	Gly
		35					40					45			
Lys	Tyr	Thr	Ser	Pro	Val	Met	Ser	Glu	His	Gly	Asp	Glu	His	Arg	Gln
	50					55				60					
Leu	Leu	Ser	His	Pro	Met	Gln	Gly	Pro	Gly	Leu	Arg	Ala	Ala	Thr	Ser
65					70					75					80
Ser	Asn	His	Ser	Val	Asp	Glu	Gln	Leu	Lys	Asn	Thr	Asp	Thr	His	Leu
			85						90					95	
Ile	Asp	Leu	Val	Thr	Asn	Glu	Ile	Ile	Thr	Gln	Gly	Pro	Pro	Val	Asp
		100						105					110		
Trp	Asn	Asp	Ile	Ala	Gly	Leu	Asp	Leu	Val	Lys	Ala	Val	Ile	Lys	Glu

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<210> 881
<211> 313
<212> DNA
<213> Homo sapiens
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<210> 882
<211> 57
<212> PRT
<213> Homo sapiens
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900

1	5	10	15
Asp Ser Thr Gly Arg Gly Leu Gln Gly Met Arg Glu Arg Ala Arg Ile			
	20	25	30
His Gly Gly Thr Ala Arg Trp Gly Asp Ser Gln Tyr Tyr Glu Gly Gly			
	35	40	45
Phe Asn Val Thr Val Glu Ile Pro Thr			
50	55		

<210> 883

<211> 576

<212> DNA

<213> Homo sapiens

<400> 883

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naattaagat ctgggggtccc agtgtcattg gtgaaggcct tgggattcga ggcagctgag
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tcctcactga ccaaggcaag ccatgcttct gagtgcttga ggccaccgaa atgaacaaat
120
ggaaaacact cccatctttt tcaagcctac ctttttagcag aagaggcaga tacacaagcc
180
ctaaagatgt aacatcaggc tgagtggagg aaggctgaga agaaaaataa agcaggctca
240
ggaggagaga gtgatgtcag gatgcccttg tgcttactcc agcctccttg tgaaaacca
300
gctctcctgt ctcccagtga agacttggat ggcagccatc agggaaggct ggggtcccagc
360
tgaggagtatg ggtgtgagct ctatagacca tccctctctg caatcaataa acacttgcct
420
gtgaaagagg cccaagccac catccgcatg gacaccagtg caagtggccc caccgcctg
480
gtcctcagtg actgtgccac cagccatggg agcctgcgca tccaactgct gcataagctc
540
tccttcttgg tgaacgcctt agctaagcag gtcatg
576

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<210> 884

<211> 105

<212> PRT

<213> Homo sapiens

<400> 884

Met Pro Leu Cys Leu Leu Gln Pro Pro Cys Glu Asn Pro Ala Leu Leu			
1	5	10	15
Ser Pro Ser Glu Asp Leu Asp Gly Ser His Gln Gly Arg Leu Gly Pro			
	20	25	30
Ser Trp Glu Tyr Gly Cys Glu Leu Tyr Arg Pro Ser Leu Ser Ala Ile			
	35	40	45
Asn Lys His Leu Pro Val Lys Glu Ala Gln Ala Thr Ile Arg Met Asp			
50	55	60	
Thr Ser Ala Ser Gly Pro Thr Arg Leu Val Leu Ser Asp Cys Ala Thr			
65	70	75	80
Ser His Gly Ser Leu Arg Ile Gln Leu Leu His Lys Leu Ser Phe Leu			
	85	90	95
Val Asn Ala Leu Ala Lys Gln Val Met			

100

105

<210> 885
<211> 370
<212> DNA
<213> Homo sapiens

<400> 885
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ggtgaggcga tgctgacgaa cgacacaccg gtgacttggg atggcgggaa agtacggggc
120
aggcgggtgt cgcgccctcgg tgcgatcgag ttgtcgtcga ccccggtccg cccagatccg
180
gtacggggtc gccacgtggc gctggaagca gtgaggtctg ggggacttga cgtagcgagc
240
ctgacgaaga acggtgaatc tttgcgacgc cgtcttgccc tggcccatcg ggtgtttggt
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gatecctggc ccgatgtcag cgatgaggct ctgctagcct gcgccgagga gtggcttgac
360
ctcgacgcgt
370

<210> 886
<211> 123
<212> PRT
<213> Homo sapiens

<400> 886
Thr Ser Gly Ala Leu Ile Arg Ala Ala Val Pro Leu Ser Glu Ser Ala
1 5 10 15
Ala Leu Glu Ser Gly Glu Ala Met Leu Thr Asn Asp Thr Pro Val Thr
20 25 30
Trp Asp Gly Gly Lys Val Arg Gly Arg Arg Val Ser Arg Leu Gly Ala
35 40 45
Ile Glu Leu Ser Ser Thr Pro Val Arg Pro Asp Pro Val Arg Ala Arg
50 55 60
His Val Ala Leu Glu Ala Val Arg Ser Gly Gly Leu Asp Val Ala Ser
65 70 75 80
Leu Thr Lys Asn Gly Glu Ser Leu Arg Arg Arg Leu Ala Leu Ala His
85 90 95
Arg Val Phe Gly Asp Pro Trp Pro Asp Val Ser Asp Glu Ala Leu Leu
100 105 110
Ala Cys Ala Glu Glu Trp Leu Asp Leu Asp Ala
115 120

<210> 887
<211> 447
<212> DNA
<213> Homo sapiens

<400> 887
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attatctccg gctgcctgaa ccagcttggt aaacgctatc cgcattctgac cggcgaaggc
 120
 caactgatgc caaacgtgc taatgctgat accacggctt cccaaccggc gttctccggt
 180
 aaagcggacg tgaccacat tgcctccggc gcgttgctgg ccgtgctgct ttacatggtg
 240
 ggtaggttgg ttcacaagt gattggcctg cctgctccgg ttggcatgtt gtttgtggcg
 300
 gtgctggtca aactgtgcaa cggcgcttct ccccgctgc tcgaaggctc gcaggtggtt
 360
 tacaaattct tccagacctc cgtcacctat ccgattctgt tcgccgttgg cgtggcgatt
 420
 acgccgtggc aggaactggt caacgcg
 447

<210> 888
 <211> 149
 <212> PRT
 <213> Homo sapiens

<400> 888
 Gln Gly Val Ala Leu Gly Arg Val Leu Pro Met Val Met Leu Gly Gly
 1 5 10 15
 Leu Thr Ala Ile Ile Ile Ser Gly Cys Leu Asn Gln Leu Gly Lys Arg
 20 25 30
 Tyr Pro His Leu Thr Gly Glu Gly Gln Leu Met Pro Asn Arg Ala Asn
 35 40 45
 Ala Asp Thr Thr Ala Ser Gln Pro Ala Phe Ser Gly Lys Ala Asp Val
 50 55 60
 Thr Thr Ile Ala Ser Gly Ala Leu Leu Ala Val Leu Leu Tyr Met Val
 65 70 75 80
 Gly Arg Leu Val His Lys Leu Ile Gly Leu Pro Ala Pro Val Gly Met
 85 90 95
 Leu Phe Val Ala Val Leu Val Lys Leu Cys Asn Gly Ala Ser Pro Arg
 100 105 110
 Leu Leu Glu Gly Ser Gln Val Val Tyr Lys Phe Phe Gln Thr Ser Val
 115 120 125
 Thr Tyr Pro Ile Leu Phe Ala Val Gly Val Ala Ile Thr Pro Trp Gln
 130 135 140
 Glu Leu Val Asn Ala
 145

<210> 889
 <211> 450
 <212> DNA
 <213> Homo sapiens

<400> 889
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 atctcccctc agtaaaattc aggatgccca gtgaagtttg aatgtcagat aaacaatttg
 120
 ttagtataag gatgtacctc gcattgaaat gatgccttgt aatttactaa atctgcaact
 180

atgcagcctt atttcatggc gggcagtggc ggtgatccca ggtttcaggg gcggggaagg
 240
 gtgctgggga gacctgagg tcaggaaccc gtacacctct gcttctgccc tctcttcct
 300
 gtgccggcca caaggcaatg actcctgtgt gggcgcagag gcagaaatgg gtctggaagg
 360
 ggattcccag tgtctggcaa gttctggtaa attctgcatt ggaggttctc tctgtagtaa
 420
 ggggagttgg cctggccgcc cttcacgcgt
 450

<210> 890
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 890
 Met Met Pro Cys Asn Leu Leu Asn Leu Gln Leu Cys Ser Leu Ile Ser
 1 5 10 15
 Trp Arg Ala Val Ala Val Ile Pro Gly Phe Arg Gly Gly Glu Gly Cys
 20 25 30
 Trp Gly Asp Pro Glu Val Arg Asn Pro Tyr Thr Ser Ala Ser Ala Leu
 35 40 45
 Ser Ser Leu Cys Arg Pro Gln Gly Asn Asp Ser Cys Val Gly Ala Glu
 50 55 60
 Ala Glu Met Gly Leu Glu Gly Asp Ser Gln Cys Leu Ala Ser Ser Gly
 65 70 75 80
 Lys Phe Cys Ile Gly Gly Ser Leu Cys Ser Lys Gly Ser Trp Pro Gly
 85 90 95
 Arg Pro Ser Arg
 100

<210> 891
 <211> 318
 <212> DNA
 <213> Homo sapiens

<400> 891
 nncaccgtcc ccgtactgga tccgcgcgag gatttcgccg actgcatgca cattgacgta
 60
 ctggatccct tccacactga caacaccagt gagcacagtg acctggccac agatggccag
 120
 actaacggcc cggctgatag cgggactggc acccactctg agcagggaaa ctccgacata
 180
 tctagccccg tcagctctag tgacgtgct aacaccaccg acagcactgc tggcaatacc
 240
 ggtgaaggta ctgccgcgaa tatgcctggt gacatggctc attcttcgac ggctaccac
 300
 ccctatgcaa gcaccggt
 318

<210> 892
 <211> 106
 <212> PRT

<213> Homo sapiens

<400> 892

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Xaa Thr Val Pro Val Leu Asp Pro Arg Glu Asp Phe Ala Asp Cys Met
 1           5           10           15
His Ile Asp Val Leu Asp Pro Phe His Thr Asp Asn Thr Ser Glu His
      20           25           30
Ser Asp Leu Ala Thr Asp Gly Gln Thr Asn Gly Pro Ala Asp Ser Gly
      35           40           45
Thr Gly Thr His Ser Glu Gln Gly Asn Ser Asp Ile Ser Ser Pro Val
      50           55           60
Ser Ser Ser Asp Ala Ala Asn Thr Thr Asp Ser Thr Ala Gly Asn Thr
65           70           75           80
Gly Glu Gly Thr Ala Ala Asn Met Pro Gly Asp Met Ala His Ser Ser
      85           90           95
Thr Ala Thr His Pro Tyr Ala Ser Thr Gly
      100           105

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<210> 893

<211> 510

<212> DNA

<213> Homo sapiens

<400> 893

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nnggataccta tccctgaatc taaggttggt gacacatgtg tttgggatag caaggtagag
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aagtcacaga aaaagcctgt ggaaaacagg atgaaggagg acaaaagcag catcagggaa
120
gcaatcagca aagccaagag tacagcaaata ataaagacag aacaggaagg tgaggcatct
180
gagaagagct tgcattctgag cccacagcat atcacacacc agactatgcc tataggacag
240
agaggcagtg agcaaggcaa acgtgtggag aacattaatg gaacctccta ccctagtcta
300
cagcagaaaa ccaatgctgt taagaaatta cataaatgtg atgaatgtgg gaaatccttc
360
aaatataatt cccgccttgt tcaacataaa attatgcaca ctgggggaaaa gcgctatgaa
420
tgtgatgact gtggagggac tttccggagc agctcgagcc ttcgggtcca caaacggatc
480
cacactgggt acggagagaa gacaacgcgt
510

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<210> 894

<211> 170

<212> PRT

<213> Homo sapiens

<400> 894

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Xaa Asp Pro Ile Pro Glu Ser Lys Val Gly Asp Thr Cys Val Trp Asp
 1           5           10           15
Ser Lys Val Glu Lys Ser Gln Lys Lys Pro Val Glu Asn Arg Met Lys
      20           25           30
Glu Asp Lys Ser Ser Ile Arg Glu Ala Ile Ser Lys Ala Lys Ser Thr

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<400> 895
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120
ccgcaccgga atcggggcttt tcttgggggt gccttcctaa atgcggtgtc ctcccttgctg
180
aggcctggcc tggcggcggt ggagcagacc gtcgatcggg ggatggcaat cctggccttg
240
gtccgatcag tgcgggatgg gggccgggca gttatcgtcg ggccttcgga ggacgccgcc
300
ttgcaggcca tgggttcgaaa tgatccagtc ggggtgggca cacgtgaact cgccgatcgt
360
cgggaggcac atttcccgcc cgcggtgccg tgcggaattg tcgacggtga cccgaaagcg
420
gtggctacag cggcacagcg actacgcgag tgggttcggaa ccgaccttga gatgcttggc
480
ccagctccac aaccacgccg tgccagcgaa tcggaacggg atcgaattat cgtgcgtcct
540
cgtagcacga tgctctctgc cgagctttcc cagggtctat ttcggctacg ttccaaacac
600
actatgagcc gcgaaccagg aagcttacgc gtggtcatcg acccggccaa cttgttgtga
660
ggtcggtagg cttgcggtgt gagacttctt tttgctggta ccccggacgt ggccgtccca
720
acgcttaccg ccttggttagc cgatccccgt cacgaggtag ctgccgtcct gacgcgtccg
780
gatgcagcag taggacggca ccgtactcca cgtccatgcc cggtcgccaa ggctgccgag
840
gaactcggtg tccccgccat taaggcgacc agcgtgaagt ccggcgaggg tcacgatgcc
900

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gtcacttccc tcgatgtcga cgtagccgtc gtcgtagcct acggaggtct cattcccgcc
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 gatctgctgg cagtaccacg acacggctgg attaaettac acttttctct cctaccgcga
 1020
 tggcgcggcg ctgctcccat acaacgggccc atcatggcgg gggatgagga gacgggcgct
 1080
 tgtgtctttc agctagttga aagcctcgat gccggaccg
 1119

<210> 896
 <211> 147
 <212> PRT
 <213> Homo sapiens

<400> 896
 Val Arg Leu Leu Phe Ala Gly Thr Pro Asp Val Ala Val Pro Thr Leu
 1 5 10 15
 Thr Ala Leu Val Ala Asp Pro Arg His Glu Val Ala Ala Val Leu Thr
 20 25 30
 Arg Pro Asp Ala Ala Val Gly Arg His Arg Thr Pro Arg Pro Cys Pro
 35 40 45
 Val Ala Lys Ala Ala Glu Glu Leu Gly Ile Pro Ala Ile Lys Ala Thr
 50 55 60
 Ser Val Lys Ser Gly Glu Gly His Asp Ala Val Thr Ser Leu Asp Val
 65 70 75 80
 Asp Val Ala Val Val Val Ala Tyr Gly Gly Leu Ile Pro Ala Asp Leu
 85 90 95
 Leu Ala Val Pro Arg His Gly Trp Ile Asn Leu His Phe Ser Leu Leu
 100 105 110
 Pro Arg Trp Arg Gly Ala Ala Pro Ile Gln Arg Ala Ile Met Ala Gly
 115 120 125
 Asp Glu Glu Thr Gly Ala Cys Val Phe Gln Leu Val Glu Ser Leu Asp
 130 135 140
 Ala Gly Pro
 145

<210> 897
 <211> 384
 <212> DNA
 <213> Homo sapiens

<400> 897
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 gacgactacc tcgtccagct gtcgaaggaa gggctcgaga cccgtctcgc gcagctgtat
 120
 ccggtcgaag cccgacgcga cgcgcagcgc gacacctact acaagcgcct cgaattcgag
 180
 tgcgggacca tcacgaagat gggctttccc ggctacttcc tgatcgtcgc ggacttcac
 240
 aactgggcaa agaacaacgg cgtgccggtc ggcccgggccc gcggctcggg cgccgggttcg
 300
 ctggtcgcgt atgcgctcgg cattaccgat ctogaagtac tgcgctacga cctgctgttc
 360

gagcgcttcc tgaacccgga acgc
384

<210> 898
<211> 128
<212> PRT
<213> Homo sapiens

<400> 898
Glu Leu Glu Ala Gly Lys Pro Glu Val Pro Leu Phe Pro Thr Pro Asp
1 5 10 15
Gly Met Ser Leu Asp Asp Tyr Leu Val Gln Leu Ser Lys Glu Gly Leu
20 25 30
Glu Thr Arg Leu Ala Gln Leu Tyr Pro Val Glu Ala Arg Arg Asp Ala
35 40 45
Gln Arg Asp Thr Tyr Tyr Lys Arg Leu Glu Phe Glu Cys Gly Thr Ile
50 55 60
Thr Lys Met Gly Phe Pro Gly Tyr Phe Leu Ile Val Ala Asp Phe Ile
65 70 75 80
Asn Trp Ala Lys Asn Asn Gly Val Pro Val Gly Pro Gly Arg Gly Ser
85 90 95
Gly Ala Gly Ser Leu Val Ala Tyr Ala Leu Gly Ile Thr Asp Leu Glu
100 105 110
Val Leu Arg Tyr Asp Leu Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg
115 120 125

<210> 899
<211> 6171
<212> DNA
<213> Homo sapiens

<400> 899
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ccatccgcct gcactggaga ggagagtttg agtatgctgc agctgcttta tctgaccaac
120
aatctcctga cggatcagtg catacctgtc ctggtagggc acctgcacct gcgaatcttg
180
caccttgcaa acaatcagtt acagaccttt cctgcaagca aactaaataa attggagcaa
240
ttggaggaac tgaacctaa gggcaacaag cttaaaacca tccccacaac catagcaaac
300
tgtaaaaggc tgcacaccct tggtgcacac tccaacaaca tcagcatttt cccagaaata
360
ctgcagttgc ctcagatcca gttttagtag ctaagttgca acgacttgac agaaatcctg
420
attccagagg ctttgctgc tacattacaa gaccttgacc tgactggaaa tacaaatctg
480
gttctggaac acaagacact ggacatattt agccatatca caaccctgaa aattgatcag
540
aaacctttgc caaccacaga ttctacagtt acgtcaacct tctggagcca tggactggct
600
gagatggcag ggcagagaaa taagctgtgt gtctcagcac ttgctatgga tagctttgca
660

gagggggtgg gagctgtgta tggcatgttt gatggagacc gaaatgagga gctcccgcgc
720
ctgctgcagt gtacgatggc agatgtgctt ttagaagagg tacagcagtc aactaatgac
780
acagttttca tggctaacac cttcttggtta tctcacagga aattaggaat ggctggccag
840
aagttgggct cctccgctct cctgtgctac atccgccctg acactgccga tccagcaagt
900
agcttttagct tgactgtagc caatgttggc acgtgccaaag cagtcctgtg ccgaggtggg
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aagccagtgc ccctctctaa agtcttcagc ctggagcagg acccagagga ggctcaaagg
1020
gtgaaggacc aaaaagccat catcacagag gacaacaaag tgaatgggggt aacctgctgt
1080
acccgatgc tgggctgtac atacctctac ccttgatcc tcccaagcc ccacatatct
1140
tccactccgc tgaccattca agatgagttg ctgattctgg gaaacaaagc attgtgggaa
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1260
gctaagaagc tgtgcacatt agcgcagagc tatggctgtc aggacagtgt aggggcgatg
1320
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1380
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<211> 734

<212> PRT

<213> Homo sapiens

<400> 900

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			20					25					30		
Leu	Gln	Leu	Leu	Tyr	Leu	Thr	Asn	Asn	Leu	Leu	Thr	Asp	Gln	Cys	Ile
		35				40					45				
Pro	Val	Leu	Val	Gly	His	Leu	His	Leu	Arg	Ile	Leu	His	Leu	Ala	Asn
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Asn	Gln	Leu	Gln	Thr	Phe	Pro	Ala	Ser	Lys	Leu	Asn	Lys	Leu	Glu	Gln
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Leu	Glu	Glu	Leu	Asn	Leu	Ser	Gly	Asn	Lys	Leu	Lys	Thr	Ile	Pro	Thr
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Thr	Ile	Ala	Asn	Cys	Lys	Arg	Leu	His	Thr	Leu	Val	Ala	His	Ser	Asn
			100					105					110		
Asn	Ile	Ser	Ile	Phe	Pro	Glu	Ile	Leu	Gln	Leu	Pro	Gln	Ile	Gln	Phe
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Leu	Pro	Ala	Thr	Leu	Gln	Asp	Leu	Asp	Leu	Thr	Gly	Asn	Thr	Asn	Leu
145				150						155				160	
Val	Leu	Glu	His	Lys	Thr	Leu	Asp	Ile	Phe	Ser	His	Ile	Thr	Thr	Leu
			165					170					175		
Lys	Ile	Asp	Gln	Lys	Pro	Leu	Pro	Thr	Thr	Asp	Ser	Thr	Val	Thr	Ser
		180						185					190		
Thr	Phe	Trp	Ser	His	Gly	Leu	Ala	Glu	Met	Ala	Gly	Gln	Arg	Asn	Lys

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Leu Cys Val Ser Ala Leu	Ala Met Asp Ser Phe	Ala Glu Gly Val Gly
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Ala Val Tyr Gly Met Phe	Asp Gly Asp Arg Asn	Glu Glu Leu Pro Arg
225	230	235
Leu Leu Gln Cys Thr Met	Ala Asp Val Leu Leu	Glu Glu Val Gln Gln
245	250	255
Ser Thr Asn Asp Thr Val	Phe Met Ala Asn Thr	Phe Leu Val Ser His
260	265	270
Arg Lys Leu Gly Met Ala	Gly Gln Lys Leu Gly	Ser Ser Ala Leu Leu
275	280	285
Cys Tyr Ile Arg Pro Asp	Thr Ala Asp Pro Ala	Ser Ser Phe Ser Leu
290	295	300
Thr Val Ala Asn Val Gly	Thr Cys Gln Ala Val	Leu Cys Arg Gly Gly
305	310	315
Lys Pro Val Pro Leu Ser	Lys Val Phe Ser Leu	Glu Gln Asp Pro Glu
325	330	335
Glu Ala Gln Arg Val Lys	Asp Gln Lys Ala Ile	Ile Thr Glu Asp Asn
340	345	350
Lys Val Asn Gly Val Thr	Cys Cys Thr Arg Met	Leu Gly Cys Thr Tyr
355	360	365
Leu Tyr Pro Trp Ile Leu	Pro Lys Pro His Ile	Ser Ser Thr Pro Leu
370	375	380
Thr Ile Gln Asp Glu Leu	Leu Ile Leu Gly Asn	Lys Ala Leu Trp Glu
385	390	395
His Leu Ser Tyr Thr Glu	Ala Val Asn Ala Val	Arg His Val Gln Asp
405	410	415
Pro Leu Ala Ala Ala Lys	Lys Leu Cys Thr Leu	Ala Gln Ser Tyr Gly
420	425	430
Cys Gln Asp Ser Val Gly	Ala Met Val Val Tyr	Leu Asn Ile Gly Glu
435	440	445
Glu Gly Cys Thr Cys Glu	Met Asn Gly Leu Thr	Leu Pro Gly Pro Val
450	455	460
Gly Phe Ala Ser Thr Thr	Thr Ile Lys Asp Ala	Pro Lys Pro Ala Thr
465	470	475
Pro Ser Ser Ser Ser Gly	Ile Ala Ser Glu Phe	Ser Ser Glu Met Ser
485	490	495
Thr Ser Glu Val Ser Ser	Glu Val Gly Ser Thr	Ala Ser Asp Glu His
500	505	510
Asn Ala Gly Gly Leu Asp	Thr Ala Leu Leu Pro	Arg Pro Glu Arg Arg
515	520	525
Cys Ser Leu His Pro Thr	Pro Thr Ser Gly Leu	Phe Gln Arg Gln Pro
530	535	540
Ser Ser Ala Thr Phe Ser	Ser Asn Gln Ser Asp	Asn Gly Leu Asp Ser
545	550	555
Asp Asp Asp Gln Pro Val	Glu Gly Val Ile Thr	Asn Gly Ser Lys Val
565	570	575
Glu Val Glu Val Asp Ile	His Cys Cys Arg Gly	Arg Asp Leu Glu Asn
580	585	590
Ser Pro Pro Leu Ile Glu	Ser Ser Pro Thr Leu	Cys Ser Glu Glu His
595	600	605
Ala Arg Gly Ser Cys Phe	Gly Ile Arg Arg Gln	Asn Ser Val Asn Ser
610	615	620
Gly Met Leu Leu Pro Met	Ser Lys Asp Arg Met	Glu Leu Gln Lys Ser

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Pro	Ser	Thr	Ser	Cys	Leu	Tyr	Gly	Lys	Lys	Leu	Ser	Asn	Gly	Ser	Ile
			645						650					655	
Val	Pro	Leu	Glu	Asp	Ser	Leu	Asn	Leu	Ile	Glu	Val	Ala	Thr	Glu	Val
		660						665					670		
Pro	Lys	Arg	Lys	Thr	Gly	Tyr	Phe	Ala	Ala	Pro	Thr	Gln	Met	Glu	Pro
	675					680						685			
Glu	Asp	Gln	Phe	Val	Val	Pro	His	Asp	Leu	Glu	Glu	Glu	Val	Lys	Glu
	690				695					700					
Gln	Met	Lys	Gln	His	Gln	Asp	Ser	Arg	Leu	Glu	Pro	Glu	Pro	His	Glu
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 <211> 309
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 <213> Homo sapiens

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<210> 902
 <211> 102
 <212> PRT
 <213> Homo sapiens

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 Met Ile His Leu Pro Arg Pro Pro Lys Val Leu Gly Leu His Thr Asp
 1 5 10 15
 Gly Lys Leu His Phe Leu Phe Leu Leu Met Gln Gln Gly His Pro Lys
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 Ile Arg Leu Pro Ser Val Ser Val Val Ser Ser Asp Gly His Leu Trp
 35 40 45
 Ser Phe Gln Arg Leu Met His Trp Val Thr Arg His Cys Lys Arg Pro
 50 55 60
 Gln Ile Ala Gln His His Leu Thr Phe Thr Pro His His Ile Asn Ile
 65 70 75 80
 Asp Ala Arg Arg Ser Lys Ala Asp Ala Thr Phe Arg Ala Ala Ser Ile
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 Gln Lys Thr Pro Leu Met
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 <211> 349
 <212> DNA
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 <213> Homo sapiens

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 Arg Lys Pro Phe Leu His Lys Ala Thr Met Gly Leu Pro Lys Ile Lys
 35 40 45
 Pro Cys His Pro Arg Asp Cys Ser Pro Ile Leu Tyr His His Glu Val
 50 55 60
 Gln Lys Ile Pro Ser Cys Glu Phe Ser Phe Lys Trp Pro Trp Ser Pro
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 Ile Phe Ile Leu Arg Leu
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 <211> 377
 <212> DNA
 <213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 His Gly Val Thr Ser Thr Val Val Pro Asn Ile Val Asp Val Glu Leu
 50 55 60
 Phe Asp Arg Pro Asp Arg Arg His Glu Gly Thr Ile Val Val Ser Val
 65 70 75 80
 Ala Thr Leu Asn Pro Gly Lys Gly Met Ile Glu Leu Ala Gln Ala Val
 85 90 95
 Glu Arg Leu Pro Glu Val Gln Leu Arg Ile Ile Gly Asp Gly Pro Gln
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 Arg His Gln Leu Glu Ala Ile Ala Ala Asp Asn Pro Arg
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<210> 907
 <211> 332
 <212> DNA
 <213> Homo sapiens

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<210> 908
 <211> 106
 <212> PRT
 <213> Homo sapiens

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Arg Glu Val Gly Asp Gln Phe Phe Asn Gly Glu Val Gln Leu Asn Leu
          20           25           30
Val Pro Gln Gly Thr Phe Ala Glu Arg Ile Arg Ala Gly Ala Ala Gly
          35           40           45
Ile Ala Ala Phe Phe Thr Pro Thr Gly Tyr Gly Thr Ala Val Gln Lys
          50           55           60
Gly Glu Leu Val Leu Lys Tyr Glu Lys Lys Asp Gly Lys Ala Val Pro
65           70           75           80
Val Met Thr Ser Lys Pro Arg Glu Val Arg Ser Phe Asp Gly Arg Asp
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Tyr Ile Ile Glu Glu Val Ile Lys Asp Glu
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<210> 909

<211> 318

<212> DNA

<213> Homo sapiens

<400> 909

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<210> 910

<211> 102

<212> PRT

<213> Homo sapiens

<400> 910

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Met Pro Gln Gly His Arg Arg Cys Arg His Gln Lys Ser Arg Leu Ala
          20           25           30
Pro Ala Ala Pro Pro Arg Asp Gly Asp Ser Arg Gly Ser Thr Arg Ala
          35           40           45
Arg Glu Ser Arg Gly Cys Val Thr Pro Leu Phe Phe Pro Pro Gln His
          50           55           60
Arg Thr Gly Gly Pro Trp Leu Arg Ile Arg Thr Pro Phe Ala Pro Ala
65           70           75           80
Cys Ala Cys Ser Ser Ala Pro Gly Ala Arg Met Arg Met Tyr Arg Arg
          85           90           95
His Lys Ala Arg Arg Arg

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<210> 911
 <211> 506
 <212> DNA
 <213> Homo sapiens

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<210> 912
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 912
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 His Leu His His Ser Met Leu Ser Pro Gln Thr Asp Gln Thr Met Asn
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 Pro Gly Trp Trp Lys Ala Asp Leu Arg Thr Leu Asp Phe Phe Phe
 35 40 45
 Leu Ala Leu His His Leu Gln Gly Ser Glu Met Ala Gly Leu Gly Gly
 50 55 60
 Gly Gln Gly Val Pro Gln Gly Leu Leu Gln Arg Pro Gly Cys Ser Val
 65 70 75 80
 Val Pro Gly Pro Ser Arg Leu Arg Phe His Pro Leu Ala His Ser Ser
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 His Gly Arg Thr Pro Ala Pro Val Pro Thr Pro Glu Val Ser Arg Pro
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 Ala Thr Lys Pro Asp Met His Phe Thr Pro Thr Ser His Ala Ala Ser
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<210> 913
 <211> 339

<212> DNA

<213> Homo sapiens

<400> 913

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<210> 914

<211> 113

<212> PRT

<213> Homo sapiens

<400> 914

Arg	Phe	Met	Ala	Trp	Phe	Arg	Arg	Thr	Val	Pro	Ala	Thr	Gly	Asp	Tyr
1				5					10					15	
Arg	Gly	Thr	Lys	Phe	Phe	Val	Arg	Glu	Asn	Gly	Lys	Thr	Leu	Ala	Thr
			20					25					30		
Ser	Met	Phe	Met	Val	Cys	Val	Ala	Leu	Gly	Ala	Thr	Asp	Leu	Leu	Phe
		35					40					45			
Ala	Leu	Asp	Ser	Ile	Pro	Ala	Ser	Tyr	Gly	Phe	Thr	Asn	Glu	Gly	Tyr
	50					55					60				
Leu	Ile	Leu	Thr	Ala	Asn	Val	Phe	Ala	Leu	Met	Gly	Leu	Arg	Gln	Leu
65					70				75					80	
Tyr	Phe	Leu	Ile	Gly	Ser	Leu	Leu	Glu	Arg	Leu	Val	Tyr	Leu	Ser	Leu
			85					90					95		
Gly	Leu	Val	Val	Ile	Leu	Gly	Phe	Ile	Ala	Leu	Lys	Leu	Ile	Gly	His
			100					105					110		

Ala

<210> 915

<211> 663

<212> DNA

<213> Homo sapiens

<400> 915

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 gacagtgaag atcctgttgt ggacattggt gctgctaccc ctgtcatcaa tggacagtca
 120
 ttaaccaagg gagagacttg catgaatcct caggatttta agccaggagc aatggttctg
 180
 gagcagaatg gaaaatcggg acacactttg actgggtgatg gtctcaatgg accatcagat
 240

gcaagtgagc agagagtatc catggcatcg tcaggcagct cccagcctga actagtgact
 300
 atccctttga ttaagggccc taaaggggtt gggtttgcaa ttgctgacag ccctactgga
 360
 cagaaggtga aaatgatact ggatagtcag tgggtgtcaag gccttcagaa aggagatata
 420
 attaaggaaa tataccatca aaatgtgcag aatttaacac atctccaagt ggtagaggtg
 480
 ctaaagcagt ttccagtagg tgctgatgta ccattgctta tcttaagagg aggtccccct
 540
 tcaccaacca aaagtgccaa aatgaaaaca gataaaaagg aaaatgcagg aagtttggag
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 gccataaatg agcctattcc tcagcctatg ccttttccac cgagcattat caggtcagga
 660
 tcc
 663

<210> 916
 <211> 221
 <212> PRT
 <213> Homo sapiens

<400> 916
 Xaa Val Pro Val Asn Gln Tyr Val Asn Leu Thr Leu Cys Arg Gly Tyr
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 Pro Leu Pro Asp Asp Ser Glu Asp Pro Val Val Asp Ile Val Ala Ala
 20 25 30
 Thr Pro Val Ile Asn Gly Gln Ser Leu Thr Lys Gly Glu Thr Cys Met
 35 40 45
 Asn Pro Gln Asp Phe Lys Pro Gly Ala Met Val Leu Glu Gln Asn Gly
 50 55 60
 Lys Ser Gly His Thr Leu Thr Gly Asp Gly Leu Asn Gly Pro Ser Asp
 65 70 75 80
 Ala Ser Glu Gln Arg Val Ser Met Ala Ser Ser Gly Ser Ser Gln Pro
 85 90 95
 Glu Leu Val Thr Ile Pro Leu Ile Lys Gly Pro Lys Gly Phe Gly Phe
 100 105 110
 Ala Ile Ala Asp Ser Pro Thr Gly Gln Lys Val Lys Met Ile Leu Asp
 115 120 125
 Ser Gln Trp Cys Gln Gly Leu Gln Lys Gly Asp Ile Ile Lys Glu Ile
 130 135 140
 Tyr His Gln Asn Val Gln Asn Leu Thr His Leu Gln Val Val Glu Val
 145 150 155 160
 Leu Lys Gln Phe Pro Val Gly Ala Asp Val Pro Leu Leu Ile Leu Arg
 165 170 175
 Gly Gly Pro Pro Ser Pro Thr Lys Ser Ala Lys Met Lys Thr Asp Lys
 180 185 190
 Lys Glu Asn Ala Gly Ser Leu Glu Ala Ile Asn Glu Pro Ile Pro Gln
 195 200 205
 Pro Met Pro Phe Pro Pro Ser Ile Ile Arg Ser Gly Ser
 210 215 220

<210> 917
 <211> 615

<212> DNA

<213> Homo sapiens

<400> 917

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 60
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 120
 caggagggcg acctggtgga ggtggtgctg tcggcctcgg ccaccttcga ggacttccag
 180
 atccgcccgc acgcccctcac ggtgcactcc tatcggggcg ctgccttctg tgatcactgc
 240
 ggggagatgc tcttcggcct agtgcgccag ggcctcaagt gcgatggctg cgggctgaac
 300
 taccacaagc gctgtgcctt cagcatcccc aacaactgta gtggggcccg caaacggcgc
 360
 ctgtcatcca cgtctctggc cagtggccac tcggtgcgcc tcggcacctc cgagtccttg
 420
 ccctgcacgg ctgaagagga gccgtagcac caccgaactc ctgcctcgcc gtccccgtca
 480
 tcctcttcct cctcttctgc ctcctcgtat acggggccgc ccattgagct ggacaagatg
 540
 ctgctctcca aggtcaaggt gccgcacacc ttcctcatcc acagctatac acggcccacc
 600
 gtttgccagg cttgc
 615

<210> 918

<211> 148

<212> PRT

<213> Homo sapiens

<400> 918

Ile	Val	Asp	Gln	Lys	Phe	Pro	Glu	Cys	Gly	Phe	Tyr	Gly	Leu	Tyr	Asp
1				5					10					15	
Lys	Ile	Leu	Leu	Phe	Lys	His	Asp	Pro	Thr	Ser	Ala	Asn	Leu	Leu	Gln
			20					25					30		
Leu	Val	Arg	Ser	Ser	Gly	Asp	Ile	Gln	Glu	Gly	Asp	Leu	Val	Glu	Val
		35				40					45				
Val	Leu	Ser	Ala	Ser	Ala	Thr	Phe	Glu	Asp	Phe	Gln	Ile	Arg	Pro	His
	50					55					60				
Ala	Leu	Thr	Val	His	Ser	Tyr	Arg	Ala	Pro	Ala	Phe	Cys	Asp	His	Cys
65					70					75				80	
Gly	Glu	Met	Leu	Phe	Gly	Leu	Val	Arg	Gln	Gly	Leu	Lys	Cys	Asp	Gly
				85					90					95	
Cys	Gly	Leu	Asn	Tyr	His	Lys	Arg	Cys	Ala	Phe	Ser	Ile	Pro	Asn	Asn
			100					105					110		
Cys	Ser	Gly	Ala	Arg	Lys	Arg	Arg	Leu	Ser	Ser	Thr	Ser	Leu	Ala	Ser
		115					120						125		
Gly	His	Ser	Val	Arg	Leu	Gly	Thr	Ser	Glu	Ser	Leu	Pro	Cys	Thr	Ala
	130					135						140			
Glu	Glu	Glu	Pro												
145															

<210> 919
 <211> 294
 <212> DNA
 <213> Homo sapiens

<400> 919
 accggtatgc gtccgctggc tgtgctcggc gacaacatca ccaccgacca tctatcgccg
 60
 acaaatgcga tcctgctcga tagcgcagcg ggtgagtacc tcgccaagat gggcccgcgcg
 120
 gaagaagact tcatttcgaa cgcgacccat cgtggcgatc acctgaccgc acagcgcgcc
 180
 accttcgcca acccgacctt gctcaacgag atggccgtag tcgatgggtga agtgaagaaa
 240
 ggctcgcttg cccgcgtgga accggaaggc catgtgatgc gcatgtggga agcc
 294

<210> 920
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 920
 Thr Gly Met Arg Pro Leu Ala Val Leu Gly Asp Asn Ile Thr Thr Asp
 1 5 10 15
 His Leu Ser Pro Thr Asn Ala Ile Leu Leu Asp Ser Ala Ala Gly Glu
 20 25 30
 Tyr Leu Ala Lys Met Gly Pro Pro Glu Glu Asp Phe Ile Ser Asn Ala
 35 40 45
 Thr His Arg Gly Asp His Leu Thr Ala Gln Arg Ala Thr Phe Ala Asn
 50 55 60
 Pro Thr Leu Leu Asn Glu Met Ala Val Val Asp Gly Glu Val Lys Lys
 65 70 75 80
 Gly Ser Leu Ala Arg Val Glu Pro Glu Gly His Val Met Arg Met Trp
 85 90 95
 Glu Ala

<210> 921
 <211> 378
 <212> DNA
 <213> Homo sapiens

<400> 921
 acgcgtttgc gcatcgcttt gaccggctctg acgatggctg agtacttccg cgatgttcag
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 aaccaggacg tgctgttggt catcgacaac atcttccggt tctcccaggc tggttctgag
 120
 gtttcaacct tgctaggtcg tatgccctcg gcggtgggct accagcccaa cttggccgac
 180
 gagatgggccc aattgcagga gcgaatcacc tcgacccgtg gtcactccat cacctcgatg
 240
 caggccgtct acgtccccgc tgacgattac accgacccgg ctccggcgac gaccttcgcc
 300

cacctggatg ccaccacgga gctttctcgt gagattgcct ctcgtaggcct gtacccggcc
 360
 gtggatccgc tggcgtcg
 378

<210> 922
 <211> 126
 <212> PRT
 <213> Homo sapiens

<400> 922
 Thr Arg Leu Arg Ile Ala Leu Thr Gly Leu Thr Met Ala Glu Tyr Phe
 1 5 10 15
 Arg Asp Val Gln Asn Gln Asp Val Leu Leu Phe Ile Asp Asn Ile Phe
 20 25 30
 Arg Phe Ser Gln Ala Gly Ser Glu Val Ser Thr Leu Leu Gly Arg Met
 35 40 45
 Pro Ser Ala Val Gly Tyr Gln Pro Asn Leu Ala Asp Glu Met Gly Gln
 50 55 60
 Leu Gln Glu Arg Ile Thr Ser Thr Arg Gly His Ser Ile Thr Ser Met
 65 70 75 80
 Gln Ala Val Tyr Val Pro Ala Asp Asp Tyr Thr Asp Pro Ala Pro Ala
 85 90 95
 Thr Thr Phe Ala His Leu Asp Ala Thr Thr Glu Leu Ser Arg Glu Ile
 100 105 110
 Ala Ser Arg Gly Leu Tyr Pro Ala Val Asp Pro Leu Ala Ser
 115 120 125

<210> 923
 <211> 571
 <212> DNA
 <213> Homo sapiens

<400> 923
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 ctggacaccg cgctggagca cgtgcgcgga gaaatccgca ttaccctgga gcatgcacgc
 120
 caacgcaaga atgtcgaaga agaagacatc ttcgccgccc accttgcgct attggaagac
 180
 cccacgctgc tggacgccgc cactggtgcc atcgaacacg gcagcgccgc caccacgcc
 240
 tggcgcgatg caatccaggc gcaatgcgcc gtggttgetgg ccctgggcaa accgctgttt
 300
 gccgagcgcg ccaacgacct gcgcgatctg caacagcgag tactgcgtgc gctgttgggg
 360
 gaagcctggc acttcgaatt gccggccggg ccgattttca ggnnggccat taacttacc
 420
 ccttccgcct tgttgcaact gagtgcccaa aacgccgtgg gtatttgcac ggccgaaggc
 480
 ggcgctacgt ctacgctgc gattttggcc cgaggcaaag gcttgccgtg cgtggtcgcg
 540
 ctgggcccgc aagtgctcga cgtgcccaca g
 571

<210> 924
 <211> 190
 <212> PRT
 <213> Homo sapiens

<400> 924
 Thr Gly Ile Glu Leu Pro Gln Asp Thr Gly Lys His Val Ala Asp Glu
 1 5 10 15
 Gln Leu Gln Arg Leu Asp Thr Ala Leu Glu His Val Arg Gly Glu Ile
 20 25 30
 Arg Ile Thr Leu Glu His Ala Arg Gln Arg Lys Asn Val Glu Glu Glu
 35 40 45
 Asp Ile Phe Ala Ala His Leu Ala Leu Leu Glu Asp Pro Thr Leu Leu
 50 55 60
 Asp Ala Ala Thr Gly Ala Ile Glu His Gly Ser Ala Ala Thr His Ala
 65 70 75 80
 Trp Arg Asp Ala Ile Gln Ala Gln Cys Ala Val Leu Leu Ala Leu Gly
 85 90 95
 Lys Pro Leu Phe Ala Glu Arg Ala Asn Asp Leu Arg Asp Leu Gln Gln
 100 105 110
 Arg Val Leu Arg Ala Leu Leu Gly Glu Ala Trp His Phe Glu Leu Pro
 115 120 125
 Ala Gly Pro Ile Phe Arg Xaa Ala Ile Asn Leu Pro Pro Ser Ala Leu
 130 135 140
 Leu Gln Leu Ser Ala Gln Asn Ala Val Gly Ile Cys Met Ala Glu Gly
 145 150 155 160
 Gly Ala Thr Ser His Val Ala Ile Leu Ala Arg Gly Lys Gly Leu Pro
 165 170 175
 Cys Val Val Ala Leu Gly Ala Glu Val Leu Asp Val Pro Gln
 180 185 190

<210> 925
 <211> 620
 <212> DNA
 <213> Homo sapiens

<400> 925
 acgcgtgcac tgtgtgtatg catggtaacg tacacgtgtg cactgtgtgt ggtgtgcatg
 60
 ncatgggtgtg tgcacgtgtg cnactgtgta tgcattgtaa tgtgcacgtg tgcactgtgt
 120
 gtgggtgtgta tgcattggtgt gtgcacgtgt gcactgtgtg tgtgtgtatg catgtgtgtg
 180
 cacgtgtgcc tgtgtgtatg catggtaatg tgcgtgtgca ctgtgtggtg tgtatgcatg
 240
 tgtgtgcacg tgtgcactgt gtatgcatag tgtgtgcacg tgtgcactgt gtgtggatgc
 300
 atggtaatgt gcacgtgtgc actgtgtgtg gtgtgtatga tgggtgtgtgc acgtgtgcac
 360
 ggtgtgtggt gtgtatgcat gtgtgtgcac gtgtgcactg tgtggcaggg gtgtttggtg
 420
 tgtgtgcatg tatgcatggt gtgtgcatac gtgtgcagca gcacctgggc ccatctccag
 480

tgcccagcag catcacacgc actttggtgc tttataaatg catggtcagt gaggctgcca
 540
 gcaccaagct gtccctttac cataacacct ggaatagtc cctgtgataa gctatcacat
 600
 aggaaacatt tttaaaattt
 620

<210> 926
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 926
 Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys
 1 5 10 15
 Val Val Cys Met Xaa Trp Cys Val His Val Cys Xaa Cys Val Cys Met
 20 25 30
 Val Met Cys Thr Cys Ala Leu Cys Val Val Cys Met His Gly Val Cys
 35 40 45
 Thr Cys Ala Leu Cys Val Cys Val Cys Met Cys Val His Val Cys Leu
 50 55 60
 Cys Val Cys Met Val Met Cys Val Cys Thr Val Trp Cys Val Cys Met
 65 70 75 80
 Cys Val His Val Cys Thr Val Tyr Ala
 85

<210> 927
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 927
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 aagaggcatt tggggctctg ttcagatcat tccaacagca aaccgggcat ggagacccca
 120
 tctcaggtct gtgcttctct gggggccacc cagccatcct gcccaccagc tcagaggcag
 180
 ggacaaagcc ctccaagag gcagcaggca gcaagggtea gccagcgcag tggggacagg
 240
 caggtacaac ctggaaaccc caaaggaccc cagatggcaa tgtgacacgg cccatccacc
 300
 aagcacctgt aatgccggct tcccacagag gcgagccaga tcctggcact attctttaag
 360

<210> 928
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 928
 Met Glu Leu Leu Glu Ile Val Arg His Asp Gln Arg Glu Glu Ala Phe
 1 5 10 15
 Gly Val Leu Phe Arg Ser Phe Gln Gln Gln Thr Gly His Gly Asp Pro

	20		25		30										
Ile	Ser	Gly	Leu	Cys	Phe	Ser	Gly	Gly	His	Pro	Ala	Ile	Leu	Pro	Thr
	35		40		45										
Ser	Ser	Glu	Ala	Gly	Thr	Lys	Pro	Ser	Gln	Glu	Ala	Ala	Gly	Ser	Lys
	50		55		60										
Gly	Gln	Pro	Ala	Gln	Trp	Gly	Gln	Ala	Gly	Thr	Thr	Trp	Lys	Pro	Gln
65			70		75				80						
Arg	Thr	Pro	Asp	Gly	Asn	Val	Thr	Arg	Pro	Ile	His	Gln	Ala	Pro	Val
			85		90				95						
Met	Pro	Ala	Ser	His	Arg	Gly	Glu	Pro	Asp	Pro	Gly	Thr	Ile	Leu	
	100		105		110										

<210> 929

<211> 2340

<212> DNA

<213> Homo sapiens

<400> 929

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nnctccccag ggccgagtct tccggagtca gcagagagcc tggatggatc acaggaggat
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aagcctcggg gctcatgtgc ggagcccact ttactgata cgggaatggg ggctcacata
120
aacaacagcc ggctcaaggc caagggcgtg ggccagcacg acaacgcca gaactttggg
180
aaccagagct ttgaggagct gcgagcagcc tgtctaagaa agggggagct cttcgaggac
240
cccttattcc ctgctgaacc cagctcactg ggcttcaagg acctgggccc caactccaaa
300
aatgtgcaga acatctcctg gcagcggccc aaggatatca taaacaaccc tctattcatc
360
atggatggga tttctccaac agacatctgc caggggatcc tcggggactg ctggtgctg
420
gctgccatcg gctcccttac cacctgcccc aaactgctat accgcgtggg gccagagga
480
cagagcttca agaaaaacta tgctggcatc ttccattttc agatttggca gtttggacag
540
tggtggaacg tggtggtaga tgaccggctg cccacaaaga atgacaagct ggtgtttgtg
600
cactcaaccg aacgcagtga gttctggagt gccctgctgg agaaggcgta tgccaagctg
660
agtgggtcct atgaagcatt gtcagggggc agtaccatgg agggccttga ggacttcaca
720
ggaggcgtgg cccagagctt ccaactccag agggccccctc agaacctgct caggctcctt
780
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840
gaactggaat ccatgactga caagatgctg gtgagagggc acgcttactc tgtgactggc
900
cttcaggatg tccactacag aggcaaaatg gaaacactga ttcgggtccg gaatccctgg
960
ggccggattg agtggaatgg agcttggagt gacagtgcc aaggagtggga agaggtggcc
1020
tcagacatcc agatgcagct gctgcacaag acggaggacg gggagtctct gatgtcctac
1080

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caagatttcc tgaacaactt cacgctcctg gagatctgca acctcacgcc tgatacactc
1140
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1200
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1260
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1320
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1380
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1440
gtccacttga agaaggaatt cttcacgaag tatcaggacc acggcttctc agagatcttc
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accaactcac gggaggtgag cagccaactc cggctgcctc cgggggaata tatcattatt
1560
ccctccacct ttgagccaca cagagatgct gacttcctgc ttcgggtctt caccgagaag
1620
cacagcgagt catgggaatt ggatgaagtc aactatgctg agcaactcca agaggaaaag
1680
gtctctgagg atgacatgga ccaggacttc ctacatttgt ttaagatagt ggcaggagag
1740
ggcaaggaga taggggtgta tgagctccag aggctgctca acaggatggc catcaaattc
1800
aaaagcttca agaccaaggg ctttggcctg gatgcttgcc gctgcatgat caacctcatg
1860
gataaagatg gctctggcaa gctggggctt ctagagttca agatcctgtg gaaaaaactc
1920
aagaaatgga tggacatctt cagagagtgt gaccaggacc attcaggcac cttgaactcc
1980
tatgagatgc gcctggttat tgagaaagca ggcataagc tgaacaacaa ggtaatgcag
2040
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2100
tgtttcctga ggctaaagac catgttcaca ttctttctaa ccatggacce caagaatact
2160
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2220
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2280
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2340

<210> 930

<211> 702

<212> PRT

<213> Homo sapiens

<400> 930

Met	Val	Ala	His	Ile	Asn	Asn	Ser	Arg	Leu	Lys	Ala	Lys	Gly	Val	Gly
1				5					10					15	
Gln	His	Asp	Asn	Ala	Gln	Asn	Phe	Gly	Asn	Gln	Ser	Phe	Glu	Glu	Leu
			20					25					30		
Arg	Ala	Ala	Cys	Leu	Arg	Lys	Gly	Glu	Leu	Phe	Glu	Asp	Pro	Leu	Phe

928

```

465          470          475          480
Glu Tyr Ile Ile Ile Pro Ser Thr Phe Glu Pro His Arg Asp Ala Asp
          485          490          495
Phe Leu Leu Arg Val Phe Thr Glu Lys His Ser Glu Ser Trp Glu Leu
          500          505          510
Asp Glu Val Asn Tyr Ala Glu Gln Leu Gln Glu Glu Lys Val Ser Glu
          515          520          525
Asp Asp Met Asp Gln Asp Phe Leu His Leu Phe Lys Ile Val Ala Gly
          530          535          540
Glu Gly Lys Glu Ile Gly Val Tyr Glu Leu Gln Arg Leu Leu Asn Arg
545          550          555          560
Met Ala Ile Lys Phe Lys Ser Phe Lys Thr Lys Gly Phe Gly Leu Asp
          565          570          575
Ala Cys Arg Cys Met Ile Asn Leu Met Asp Lys Asp Gly Ser Gly Lys
          580          585          590
Leu Gly Leu Leu Glu Phe Lys Ile Leu Trp Lys Lys Leu Lys Lys Trp
          595          600          605
Met Asp Ile Phe Arg Glu Cys Asp Gln Asp His Ser Gly Thr Leu Asn
          610          615          620
Ser Tyr Glu Met Arg Leu Val Ile Glu Lys Ala Gly Ile Lys Leu Asn
625          630          635          640
Asn Lys Val Met Gln Val Leu Val Ala Arg Tyr Ala Asp Asp Gly Leu
          645          650          655
Ile Ile Asp Phe Asp Ser Phe Ile Ser Cys Phe Leu Arg Leu Lys Thr
          660          665          670
Met Phe Thr Phe Phe Leu Thr Met Asp Pro Lys Asn Thr Gly His Ile
          675          680          685
Cys Leu Ser Leu Glu Gln Trp Leu Gln Met Thr Met Trp Gly
          690          695          700

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<210> 931
 <211> 297
 <212> DNA
 <213> Homo sapiens

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<400> 931
tcgcaaggagg agcctgacat gggccagaaa atcaatcccc atggtttccg tctcgggtgtg
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acgaccgatac acaagacccg ctggtacgcc gagaagcagt acgccgagct cgtgggtgag
120
gatgtcaaga tccgagagtg gctccacaag aatctggagc gcgccggtct ttcgtccatc
180
gagatcgagc gtcgctccga gcgcgtgacc attttccttt acgccgctcg cccggggcatc
240
gttatcgggc gcaatggccg ggaggccgag cgcggtgcgtn ntgagctcga aaagctt
297

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<210> 932
 <211> 93
 <212> PRT
 <213> Homo sapiens

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<400> 932
Met Gly Gln Lys Ile Asn Pro His Gly Phe Arg Leu Gly Val Thr Thr

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```

      1             5             10             15
Asp His Lys Thr Arg Trp Tyr Ala Glu Lys Gln Tyr Ala Glu Leu Val
      20             25             30
Gly Glu Asp Val Lys Ile Arg Glu Trp Leu His Lys Asn Leu Glu Arg
      35             40             45
Ala Gly Leu Ser Ser Ile Glu Ile Glu Arg Arg Ser Glu Arg Val Thr
      50             55             60
Ile Phe Leu Tyr Ala Ala Arg Pro Gly Ile Val Ile Gly Arg Asn Gly
65             70             75             80
Arg Glu Ala Glu Arg Val Arg Xaa Glu Leu Glu Lys Leu
      85             90

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<210> 933
 <211> 305
 <212> DNA
 <213> Homo sapiens

<400> 933
 nnacgcgtcg ccaagctggt gatggccgaa tacaaggggc tcaacgtcat cgtcaaaacc
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 tccgccgatc cggcaagcca agccaatgcc gtgcaggatc tggcgggggc aggcacgcac
 120
 gcgctggcca tcttgccgac cgaccgggat cagctggttt cggcgatcca gcaggtcaag
 180
 gacgacggca agttcgtggc gctggtcgac cgtgcgcctt ccgtcaacga caacacgatc
 240
 cgcgatctct acgtggccgg caacaacccg gcgctcggcg aagtggcggg caaattcatg
 300
 ggcga
 305

<210> 934
 <211> 101
 <212> PRT
 <213> Homo sapiens

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<400> 934
Xaa Arg Val Ala Lys Leu Leu Met Ala Glu Tyr Lys Gly Leu Asn Val
  1             5             10             15
Ile Val Lys Thr Ser Ala Asp Pro Ala Ser Gln Ala Asn Ala Val Gln
      20             25             30
Asp Leu Ala Gly Ala Gly Ile Asp Ala Leu Ala Ile Leu Pro Thr Asp
      35             40             45
Pro Asp Gln Leu Val Ser Ala Ile Gln Gln Val Lys Asp Asp Gly Lys
      50             55             60
Phe Val Ala Leu Val Asp Arg Ala Pro Ser Val Asn Asp Asn Thr Ile
65             70             75             80
Arg Asp Leu Tyr Val Ala Gly Asn Asn Pro Ala Leu Gly Glu Val Ala
      85             90             95
Gly Lys Phe Met Gly
      100

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<210> 935
 <211> 333

<212> DNA

<213> Homo sapiens

<400> 935

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 caggctcccc tggggaagtc ctcttagaac tgagggatca acactggagg agactgcaag
 120
 gggtacggga taaatgttcc tgggtgaagga aacagcaggg gcaaaggccc tgcagcagaa
 180
 aggagcgagg ccctttggag taacagaaag accatggtga caggagctca gaaagaccac
 240
 tgggtgtaag actataagcc agtggaggcc agattgggga atgggatggg aggggtgctt
 300
 gaagaccatg gtgaggctct cttggtcttt act
 333

<210> 936

<211> 103

<212> PRT

<213> Homo sapiens

<400> 936

Met	Val	Phe	Lys	His	Pro	Ser	His	Pro	Ile	Pro	Gln	Ser	Gly	Leu	His
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Trp	Leu	Ile	Val	Leu	Thr	Pro	Val	Val	Phe	Leu	Ser	Ser	Cys	His	His
			20					25					30		
Gly	Leu	Ser	Val	Thr	Pro	Lys	Gly	Leu	Ala	Pro	Phe	Cys	Cys	Arg	Ala
		35					40					45			
Phe	Ala	Pro	Ala	Val	Ser	Phe	Thr	Arg	Asn	Ile	Tyr	Pro	Val	Pro	Leu
	50					55					60				
Ala	Val	Ser	Ser	Ser	Val	Asp	Pro	Ser	Val	Leu	Arg	Gly	Leu	Pro	Gln
65					70					75					80
Gly	Ser	Leu	Ser	Thr	Pro	Val	Ser	Ser	Gly	Pro	Trp	Leu	Phe	His	Ser
				85					90					95	
Thr	His	Gln	Pro	Phe	Thr	Arg									
															100

<210> 937

<211> 464

<212> DNA

<213> Homo sapiens

<400> 937

nnnttatctg cggaggggggt ggccaccctg cccacactca tgctgcaggc ctccaccgac
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 120
 gaccgtgccc tggcagggtt gcgtgccagt cacgtcatcg acgaagctcg cgccgaggtg
 180
 cagcggcgtg ccgatctcgc ccgtggccat ctcgccatcc ttcccgcagg cgatgcccg
 240
 acggcggttg agaccctgtg cgacgaggtg ggttcccggg cggcctgaac cccgaccctg
 300

ccagnctgcg tcccatctcc tggccgggac cgctccagcg tctgctctct gacagctcat
 360
 cgttcttccg acaccaagga gtttctcgtg gcccgtcac tcgatctcat cggcattggg
 420
 cccggcaacc cggactggat caccctggct gccgtcaagg ccan
 464

<210> 938
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 938
 Xaa Leu Ser Ala Glu Gly Val Ala Thr Leu Pro Thr Leu Met Leu Gln
 1 5 10 15
 Ala Ser Thr Asp Pro Ala Asp Asp Glu Leu Lys Asp Leu Leu Thr Ala
 20 25 30
 Asp Leu Met Asp Gln His Asn Leu Asp Arg Ala Leu Ala Gly Leu Arg
 35 40 45
 Ala Ser His Val Ile Asp Glu Ala Arg Ala Glu Val Gln Arg Arg Ala
 50 55 60
 Asp Leu Ala Arg Gly His Leu Ala Ile Leu Pro Ala Gly Asp Ala Arg
 65 70 75 80
 Thr Ala Leu Glu Thr Leu Cys Asp Glu Val Gly Ser Arg Ala Ala
 85 90 95

<210> 939
 <211> 385
 <212> DNA
 <213> Homo sapiens

<400> 939
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 ggactgctgc cggtcgaggt ggacttcgcc gccacgaaga cccttgccctt gtcgcacggg
 120
 acatggcggg ggatcgaggt tggctggctat gaaatccatc acgggcgtct gtcgttcgct
 180
 gaggacgctg aagccttctt cgacggcgta cacgtcggtc cggtatgggg gacgatgtgg
 240
 cacggggcat tcgagcacga cgaattccgt cgcacgtggc tggctgacgc ggcccgtcac
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 360
 atgatcgaaa ccctcgccga cgcgt
 385

<210> 940
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 940
 Xaa Thr Ile Leu Asp Pro Asp Gly Gln Glu Thr Thr Pro Gly Ser Val


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      1           5           10           15
Ile Glu Gly Leu Gly Leu Leu Pro Val Glu Val Asp Phe Ala Ala Thr
      20           25           30
Lys Thr Leu Ala Leu Ser His Gly Thr Trp Arg Gly Ile Glu Val Gly
      35           40           45
Gly Tyr Glu Ile His His Gly Arg Leu Ser Phe Ala Glu Asp Ala Glu
      50           55           60
Ala Phe Leu Asp Gly Val His Val Gly Pro Val Trp Gly Thr Met Trp
      65           70           75           80
His Gly Ala Phe Glu His Asp Glu Phe Arg Arg Thr Trp Leu Ala Asp
      85           90           95
Ala Ala Arg His Ala Gly Ser Ser Trp Arg Pro His Ser Asp Glu Leu
      100          105          110
Gly Tyr Gln Ala Arg Arg Glu Ala Met Ile Glu Thr Leu Ala Asp Ala
      115          120          125

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<210> 941

<211> 348

<212> DNA

<213> Homo sapiens

<400> 941

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gaagccatgc aaaccatggt cgtgctggcc gggctgccgt tctcggtggt gctgattttc
120
ttcatgttcg gtttgcacaa ggcgatgcgc caggacgtgg ccatggagca ggagcaggca
180
caattggctg aacgtggctg ccgtggtttc agcgagcgcc tgaccgcgct ggacctgcaa
240
ccgagccagg gcaccgtgca acgctttatg gacaaacatg tgacgccggc gttggaacaa
300
gcggcgactg cgttgcgtga tcaagggctg gaagtgcaga ccctgctt
348

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<210> 942

<211> 116

<212> PRT

<213> Homo sapiens

<400> 942

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Ile Phe Trp Ser Ala Val Ile Thr Leu Val Thr Ile Gly Leu Leu Phe
  1           5           10           15
Ala Gly Asn Phe Glu Ala Met Gln Thr Met Val Val Leu Ala Gly Leu
      20           25           30
Pro Phe Ser Val Val Leu Ile Phe Phe Met Phe Gly Leu His Lys Ala
      35           40           45
Met Arg Gln Asp Val Ala Met Glu Gln Glu Gln Ala Gln Leu Ala Glu
      50           55           60
Arg Gly Arg Arg Gly Phe Ser Glu Arg Leu Thr Ala Leu Asp Leu Gln
      65           70           75           80
Pro Ser Gln Gly Thr Val Gln Arg Phe Met Asp Lys His Val Thr Pro
      85           90           95
Ala Leu Glu Gln Ala Ala Thr Ala Leu Arg Asp Gln Gly Leu Glu Val

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100
Gln Thr Leu Leu
115

105

110

<210> 943
<211> 439
<212> DNA
<213> Homo sapiens

<400> 943
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ctcctctaata gcatcctggg ctccctgctaa ccctgtggga aacaccgtct cttctctcct
120
ttgccctctt ctgtgatcac atcctcactt ctgagcctat ctgcccatcc agtcaatccc
180
ccttggttct gggatgctat ttccctggcc gcctccctct aggagtgttt agaaccctca
240
ctgtgggcag aaggaggga agatggctga ggtacctgga aaggacgtg tggatccccg
300
ggcatggaag gaaggaggca ggagagctag aaaaagggat gagatctaata gttccctaag
360
gaacctggct tagtgctggc ccttcacata ctgagacatg gaatccttac tactgttctc
420
tgaggaaaga ggctgttcc
439

<210> 944
<211> 118
<212> PRT
<213> Homo sapiens

<400> 944
Met Ala Gly Ala Glu Gln Ile Glu Gln Asp Leu Val Ser Phe Ser Leu
1 5 10 15
His Phe Val Pro Pro Leu Met His Pro Gly Leu Leu Leu Thr Leu Trp
20 25 30
Glu Thr Pro Ser Leu Leu Ser Phe Ala Leu Phe Cys Asp His Ile Leu
35 40 45
Thr Ser Glu Pro Ile Cys Pro Ser Ser Gln Ser Pro Leu Val Leu Gly
50 55 60
Cys Tyr Phe Pro Gly Arg Leu Pro Leu Gly Val Phe Arg Thr Leu Thr
65 70 75 80
Val Gly Arg Arg Glu Gly Arg Trp Leu Arg Tyr Leu Glu Arg Asp Val
85 90 95
Trp Ile Pro Gly His Gly Arg Lys Glu Ala Gly Glu Leu Glu Lys Gly
100 105 110
Met Arg Ser Asn Val Pro
115

<210> 945
<211> 339
<212> DNA
<213> Homo sapiens

<400> 945

ngaattcgtg aagcgttcca tatttttttc cttttaataa tttcaattgc actttatgtc
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 gagatggtga tatatatata tactcacaca catatatatg tgtgtgtgtg tatatatgta
 120
 tatatatata gcgtgtacaa caaaacatgc actgtttact cagcaccccg tgtttgtctc
 180
 agcaatagct tttctaaaga actgctacta tttgaaatgg agggggaggg gggtcctgga
 240
 cagagtattg tgcaagttga aagtctctgg atggggctat gtatatacta ccagccaatt
 300
 tgggtgcaaa ttggatttga aggcctgcct ctgtccacn
 339

<210> 946

<211> 113

<212> PRT

<213> Homo sapiens

<400> 946

Xaa	Ile	Arg	Glu	Ala	Phe	His	Ile	Phe	Phe	Leu	Leu	Ile	Ile	Ser	Ile
1				5				10						15	
Ala	Leu	Tyr	Val	Glu	Met	Val	Ile	Tyr	Ile	Tyr	Thr	His	Thr	His	Ile
			20					25					30		
Tyr	Val	Cys	Val	Cys	Ile	Tyr	Val	Tyr	Ile	Tyr	Ser	Val	Tyr	Asn	Lys
		35					40				45				
Thr	Cys	Thr	Val	Tyr	Ser	Ala	Pro	Arg	Val	Cys	Leu	Ser	Asn	Ser	Phe
	50					55				60					
Ser	Lys	Glu	Leu	Leu	Leu	Phe	Glu	Met	Glu	Gly	Glu	Gly	Gly	Pro	Gly
65				70					75					80	
Gln	Ser	Ile	Val	Gln	Val	Glu	Ser	Leu	Trp	Met	Gly	Leu	Cys	Ile	Ser
			85					90					95		
Tyr	Gln	Pro	Ile	Trp	Val	Gln	Ile	Gly	Phe	Glu	Gly	Leu	Pro	Leu	Ser
			100					105					110		

Thr

<210> 947

<211> 648

<212> DNA

<213> Homo sapiens

<400> 947

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 120
 agtagtgctg ccggctcaag cgatgcctca gcctttctgc tgtgtgcgaa gctttgcaga
 180
 ggagatgatg cttcaaagtt gtccctgttg gggatgagca gccaggcctt tatacactgg
 240
 gacagtcagt catggatacg tggatactct ggaaaccctc atccctggag gtctgagccc
 300

ctggatacca tgcccttctt aggcctggagt tgctgccctt gtccatttac cataaaaatt
 360
 ggacaagaga ataccaggac acacctgagt ttctcatcgt atgctaaacc tgttcttcca
 420
 cgtacatccc caatgtgtac agccctactt ttttctgctg atcaagttca attacttctg
 480
 ctaagatggg gactattctt gcctgctggg ccttggatgc aaggacccca atgttcaggc
 540
 agcctttggg gccttctagc atacgaatca gagcattatc tttaggtgtg gaataagctg
 600
 ccccaaaacc tgttgaagcc agccaggcac tgtgctccct tcacgcgt
 648

<210> 948
 <211> 154
 <212> PRT
 <213> Homo sapiens

<400> 948
 Met Glu Met Ser Gly Gln Gln Val Tyr Gly Val Leu Val Ala Ser His
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 Leu Cys Thr Gly Val Gly Lys Glu Trp Thr Gly Val Asp Lys Ser Ser
 20 25 30
 Ser Ala Ala Gly Ser Ser Asp Ala Ser Ala Phe Leu Leu Cys Ala Lys
 35 40 45
 Leu Cys Arg Gly Asp Asp Ala Ser Lys Leu Ser Leu Leu Gly Met Ser
 50 55 60
 Ser Gln Ala Phe Ile His Trp Asp Ser Gln Ser Trp Ile Arg Gly Tyr
 65 70 75 80
 Ser Gly Asn Pro His Pro Trp Arg Ser Glu Pro Leu Asp Thr Met Pro
 85 90 95
 Phe Leu Gly Trp Ser Cys Cys Pro Cys Pro Phe Thr Ile Lys Ile Gly
 100 105 110
 Gln Glu Asn Thr Arg Thr His Leu Ser Phe Ser Ser Tyr Ala Lys Pro
 115 120 125
 Val Leu Pro Arg Thr Ser Pro Met Cys Thr Ala Leu Leu Phe Ser Ala
 130 135 140
 Asp Gln Val Gln Leu Leu Leu Arg Trp
 145 150

<210> 949
 <211> 661
 <212> DNA
 <213> Homo sapiens

<400> 949
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 aagtaatgtg gaattttatc acagtgggtca agaaggcttc agggatagca cagatccaag
 120
 atatgctgta acgtttctta acctaggaca gattcaagaa catggctcat cttatattcg
 180
 aggcgtgtgct tttcaccatg gcttctctcc agcaattggg gtatttgga cagatggatt
 240

ggacatagat gacaacatca ttcactttac agtgggggaa ggcataagaa tatgggggaa
 300
 tgccaaccga gtccgaggga atttgattgc actttcggtt tggccaggaa cctatcagaa
 360
 cagaaaagat ttaagttcaa ctctctggca tgcagcaatt gagataaata gagggaccaa
 420
 tacagtttta cagaataatg tagtggctgg atttggaaga gcaggatacc gcattgatgg
 480
 tgaaccttgc ccaggccagt ttaatcctgt ggaaaagtgg tttgacaatg aagcccatgg
 540
 aggtttatat gggatctata tgaaccaaga tggccttcct ggatgttctc ttatacaagg
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 atttaccatt tggacatgct gggattatgg aatttatattt cagaccacag agagtgtgca
 660
 c
 661

<210> 950
 <211> 210
 <212> PRT
 <213> Homo sapiens

<400> 950
 Met Met Thr Phe Lys Gly Asn Ala Arg Ile Ser Asn Val Glu Phe Tyr
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 His Ser Gly Gln Glu Gly Phe Arg Asp Ser Thr Asp Pro Arg Tyr Ala
 20 25 30
 Val Thr Phe Leu Asn Leu Gly Gln Ile Gln Glu His Gly Ser Ser Tyr
 35 40 45
 Ile Arg Gly Cys Ala Phe His His Gly Phe Ser Pro Ala Ile Gly Val
 50 55 60
 Phe Gly Thr Asp Gly Leu Asp Ile Asp Asp Asn Ile Ile His Phe Thr
 65 70 75 80
 Val Gly Glu Gly Ile Arg Ile Trp Gly Asn Ala Asn Arg Val Arg Gly
 85 90 95
 Asn Leu Ile Ala Leu Ser Val Trp Pro Gly Thr Tyr Gln Asn Arg Lys
 100 105 110
 Asp Leu Ser Ser Thr Leu Trp His Ala Ala Ile Glu Ile Asn Arg Gly
 115 120 125
 Thr Asn Thr Val Leu Gln Asn Asn Val Val Ala Gly Phe Gly Arg Ala
 130 135 140
 Gly Tyr Arg Ile Asp Gly Glu Pro Cys Pro Gly Gln Phe Asn Pro Val
 145 150 155 160
 Glu Lys Trp Phe Asp Asn Glu Ala His Gly Gly Leu Tyr Gly Ile Tyr
 165 170 175
 Met Asn Gln Asp Gly Leu Pro Gly Cys Ser Leu Ile Gln Gly Phe Thr
 180 185 190
 Ile Trp Thr Cys Trp Asp Tyr Gly Ile Tyr Phe Gln Thr Thr Glu Ser
 195 200 205
 Val His
 210

<210> 951
 <211> 2615

<212> DNA

<213> Homo sapiens

<400> 951

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120
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780
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960
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 1680
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 1740
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 1980
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 2520
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 2580
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<210> 952

<211> 357

<212> PRT

<213> Homo sapiens

<400> 952

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Ser	Gly	Ala	Gln	Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys	Glu
			20					25					30		
Val	Glu	Thr	Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val	Asp
		35					40					45			
Cys	Ser	Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu	Asp
	50					55					60				
Thr	Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn	Glu

65					70					75				80
Ser	Val	Leu	Ala	Gly	Pro	Gly	Tyr	Thr	Thr	Leu	Ala	Gly	Leu	Asp Leu
				85					90					95
Ser	His	Asn	Leu	Leu	Thr	Ser	Ile	Ser	Pro	Thr	Ala	Phe	Ser	Arg Leu
			100					105					110	
Arg	Tyr	Leu	Glu	Ser	Leu	Asp	Leu	Ser	His	Asn	Gly	Leu	Thr	Ala Leu
		115				120					125			
Pro	Ala	Glu	Ser	Phe	Thr	Ser	Ser	Pro	Leu	Ser	Asp	Val	Asn	Leu Ser
		130				135					140			
His	Asn	Gln	Leu	Arg	Glu	Val	Ser	Val	Ser	Ala	Phe	Thr	Thr	His Ser
145					150					155				160
Gln	Gly	Arg	Ala	Leu	His	Val	Asp	Leu	Ser	His	Asn	Leu	Ser	Pro Pro
			165					170						175
Arg	Ala	Pro	Pro	His	Glu	Gly	Arg	Pro	Ala	Cys	Ala	His	His	Ser Glu
			180					185					190	
Pro	Glu	Pro	Gly	Leu	Glu	Pro	Ala	Pro	Cys	Arg	Ala	Gln	Pro	Arg Asp
		195					200					205		
Leu	Pro	Leu	Arg	Tyr	Leu	Ser	Leu	Asp	Gly	Asn	Pro	Leu	Ala	Val Ile
	210					215					220			
Gly	Pro	Gly	Ala	Phe	Ala	Gly	Leu	Gly	Gly	Leu	Thr	His	Leu	Ser Leu
225					230					235				240
Ala	Ser	Leu	Gln	Arg	Leu	Pro	Glu	Leu	Ala	Pro	Ser	Gly	Phe	Arg Glu
			245						250					255
Leu	Pro	Gly	Leu	Gln	Val	Leu	Asp	Leu	Ser	Gly	Asn	Pro	Lys	Leu Asn
		260						265					270	
Trp	Ala	Gly	Ala	Glu	Val	Phe	Ser	Gly	Leu	Ser	Ser	Leu	Gln	Glu Leu
		275					280					285		
Asp	Leu	Ser	Gly	Thr	Asn	Leu	Val	Pro	Leu	Pro	Glu	Ala	Leu	Leu Leu
	290					295					300			
His	Leu	Pro	Ala	Leu	Gln	Ser	Val	Ser	Val	Gly	Gln	Asp	Val	Arg Cys
305					310					315				320
Arg	Arg	Leu	Val	Arg	Glu	Gly	Thr	Tyr	Pro	Arg	Arg	Pro	Gly	Ser Ser
			325						330					335
Pro	Lys	Val	Ala	Leu	His	Cys	Val	Asp	Thr	Arg	Glu	Ser	Ala	Ala Arg
		340						345					350	
Gly	Pro	Thr	Ile	Leu										
			355											

<210> 953

<211> 347

<212> DNA

<213> Homo sapiens

<400> 953

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accacacttt ccccatccct tgatccatca ttgggcgttg aggttttccc atgtcttgac
120
tgttgtacct ggcggctctg cggagtaacc gctgcggaca cacagtagga cgggagggag
180
aagccattgc gtttcaccct ttcattggccc ttcctttccc cttccaagtg agctctttga
240
ggtagtcat ggagggcagt gtccctctgc atcctgtctg gggttgtcaa atatggccaa
300

gtgggctcca tcggggcagc ggggtggggtg ggggggtgtct gtcagag
347

<210> 954
<211> 103
<212> PRT
<213> Homo sapiens

<400> 954
Met Glu Pro Thr Trp Pro Tyr Leu Thr Thr Pro Asp Arg Met Gln Arg
1 5 10 15
Asp Thr Ala Leu His Asp Ser Pro Gln Arg Ala His Leu Glu Gly Glu
20 25 30
Arg Lys Gly His Glu Arg Val Lys Arg Asn Gly Phe Ser Leu Pro Ser
35 40 45
Tyr Cys Val Ser Ala Ala Val Thr Pro Gln Ser Arg Gln Val Gln Gln
50 55 60
Ser Arg His Gly Lys Thr Ser Thr Pro Asn Asp Gly Ser Arg Asp Gly
65 70 75 80
Glu Ser Val Val His Thr Leu Arg Gly Asp Pro Arg Glu Thr Gly Leu
85 90 95
Arg Thr Gly Met Ala Ser Arg
100

<210> 955
<211> 634
<212> DNA
<213> Homo sapiens

<400> 955
acgcgtgaag ggctctgcag gtgagcggct ctgcaggtga agggttctgc aggtgagcgg
60
ctctgcaggt gaatgggttct gcaggtgaag ggctctgcag gtgaacgggt ctgcaggtga
120
agggctctgc aggtgaacgg ttctgcaggt gagcggctct gcaggtgagc ggctctgcat
180
gtgagtgcct ctgtgactgg ctcgcaagca gcatttgtgc acacttgact ggccacaaca
240
gaatgttctt ctctgttgtc agcactgagg aggaagctcc tgcctaagcg accacagcca
300
ggcacccgct ccatggagac attgctctct ccagactcca ttcagactca ggaaacctga
360
gtctctggaa tgcaggtga ggcagctccc acacaaaagc tatctactct ggcagttatc
420
agaggcctcc gttgcacaaa tcacacacct actgtgcctg acgtggctgg gcctccagca
480
ggacccgctc ctgagaacac acgggtgcta gtccaagttc acagcacggc tcaagtcact
540
cccacaaacc tctctataca aacacacaaa gctctgggag gctaccctgc atccaagagt
600
caccatctca cacctggaac aagggttacg gccg
634

<210> 956

<211> 113
 <212> PRT
 <213> Homo sapiens

<400> 956
 Met Glu Ser Gly Glu Ser Asn Val Ser Met Glu Arg Val Pro Gly Cys
 1 5 10 15
 Gly Arg Leu Gly Arg Ser Phe Leu Leu Ser Ala Asp Asn Arg Glu Glu
 20 25 30
 His Ser Val Val Ala Ser Gln Val Cys Thr Asn Ala Ala Cys Glu Pro
 35 40 45
 Val Thr Glu Ala Leu Thr Cys Arg Ala Ala His Leu Gln Ser Arg Ser
 50 55 60
 Pro Ala Glu Pro Phe Thr Cys Arg Ala Leu His Leu Gln Asn Arg Ser
 65 70 75 80
 Pro Ala Glu Pro Phe Thr Cys Arg Thr Ile His Leu Gln Ser Arg Ser
 85 90 95
 Pro Ala Glu Pro Phe Thr Cys Arg Ala Ala His Leu Gln Ser Pro Ser
 100 105 110
 Arg

<210> 957
 <211> 823
 <212> DNA
 <213> Homo sapiens

<400> 957
 acgcgtggcc tgaccaccgt gtcccgccca tctacaggtg cccgagatcg tgagcgtcct
 60
 gcgctccaag cttcaggagg cccagggaga gcacgtcctg ccggccaccc agcacagcgt
 120
 gtacctcctg gccacccagc actgcgcagc cgtggtgtcc agcctcctgg gcagcccctt
 180
 gcccttggac aggtacccag ctcagactcc aggcttaggg gtccctctgg aatgatgctc
 240
 cccttggaat gatgctcccc gagccctcca cccggctctg caccocgact ttctgcatga
 300
 gttcccatgg ctgtaggcca cgtgggacag aaagtgcacat ggagccaggc cccagtctct
 360
 caggtaccca cggggacctc tcctctccag gcgttttggg atcctcactg gctccggtgg
 420
 gccctgcaca gcacccccac agggaaagctg ctgtttctgc ctctctctaa ggtcccaaaa
 480
 ctgcctgggt gctctgttgg cccagggctc cagcacacac tggaggctgc ccctcaccct
 540
 gtgtcttgggt tccggctact ccaagccttg tcctctgcag ggcattccact gctgcctgtg
 600
 agcagacccc tgggaactgc ctgatctgag cccctcagg agcccaagga caaccttgtc
 660
 tgtaccatac atcactatgt cttcccaagc tcacacctcc cagctcccag caaagggcag
 720
 ggcgtgtcta ccaccacca gccactggg gtcccccttc ctgcgcgagg cctccggagc
 780

atgggtctgc tggcccttcc tttctttgcc tcttagtctg gaa
823

<210> 958
<211> 105
<212> PRT
<213> Homo sapiens

<400> 958
Met Ala Val Gly His Val Gly Gln Lys Val Thr Trp Ser Gln Ala Pro
1 5 10 15
Val Ser Gln Val Pro Thr Gly Thr Ser Pro Leu Gln Ala Phe Trp Asp
20 25 30
Pro His Trp Leu Arg Trp Ala Leu His Ser Thr Pro Thr Gly Lys Leu
35 40 45
Leu Phe Leu Pro Ser Ser Lys Val Pro Lys Leu Pro Gly Cys Ser Val
50 55 60
Gly Pro Arg Leu Gln His Thr Leu Glu Ala Ala Pro His Pro Val Ser
65 70 75 80
Trp Phe Arg Leu Leu Gln Ala Leu Ser Ser Ala Gly His Pro Leu Leu
85 90 95
Pro Val Ser Arg Pro Leu Gly Thr Ala
100 105

<210> 959
<211> 586
<212> DNA
<213> Homo sapiens

<400> 959
ngtcatgact gcatggccaa gcatgactcc aacaccatca ttaagtttgc cgacgacaca
60
acagtggtag gcctgatcac cgacaacgat gaggcagcct atagggagga ggtcagagac
120
ctggcagtgt ggtgccagga taacaacctc tccctcaacg tgatcaagac cacgaagatg
180
atcgtggact acaggaaaag gagggtcgag caccgccccca ttctcattga tggggctgta
240
tgggagccag ttgagagctt caagtccctt ggtgtccaca tcaccatcga actatcatgg
300
tccaaacaca ccaagacagt agtgaagagg gtgcgacaat gcctattcca cctcggtaga
360
caaaaaagat ttggaatgga tcctcagacc ctcaaaaagt ttgacatcta caccatcgag
420
agcatcatga ctggttgcat caccgcctgg tatggcaact gctcggcctc cgaccgcaag
480
gcactacaga gggtagtgcg tacggcccag tacatcactg gggctaagct tcctgccatc
540
caggacctct ataccaggcg gtgtcagcgg aagaccctga caattg
586

<210> 960
<211> 195
<212> PRT

<213> Homo sapiens

<400> 960

Xaa His Asp Cys Met Ala Lys His Asp Ser Asn Thr Ile Ile Lys Phe
 1 5 10 15
 Ala Asp Asp Thr Thr Val Val Gly Leu Ile Thr Asp Asn Asp Glu Ala
 20 25 30
 Ala Tyr Arg Glu Glu Val Arg Asp Leu Ala Val Trp Cys Gln Asp Asn
 35 40 45
 Asn Leu Ser Leu Asn Val Ile Lys Thr Thr Lys Met Ile Val Asp Tyr
 50 55 60
 Arg Lys Arg Arg Val Glu His Ala Pro Ile Leu Ile Asp Gly Ala Val
 65 70 75 80
 Trp Glu Pro Val Glu Ser Phe Lys Phe Leu Gly Val His Ile Thr Ile
 85 90 95
 Glu Leu Ser Trp Ser Lys His Thr Lys Thr Val Val Lys Arg Val Arg
 100 105 110
 Gln Cys Leu Phe His Leu Gly Arg Gln Lys Arg Phe Gly Met Asp Pro
 115 120 125
 Gln Thr Leu Lys Lys Phe Asp Ile Tyr Thr Ile Glu Ser Ile Met Thr
 130 135 140
 Gly Cys Ile Thr Ala Trp Tyr Gly Asn Cys Ser Ala Ser Asp Arg Lys
 145 150 155 160
 Ala Leu Gln Arg Val Val Arg Thr Ala Gln Tyr Ile Thr Gly Ala Lys
 165 170 175
 Leu Pro Ala Ile Gln Asp Leu Tyr Thr Arg Arg Cys Gln Arg Lys Thr
 180 185 190
 Leu Thr Ile
 195

<210> 961

<211> 502

<212> DNA

<213> Homo sapiens

<400> 961

acgcgttgtc gtctctccgt agaccattca gtttggcaaa acttccactg gagtctgtgc
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 atgactggat ggtctctttg acagccctgt caaggaatac caacagaata ttgattctcc
 120
 taaactgtat agtaacctgc taaccagtcg gaaagagcta ccacccaatg gagatactaa
 180
 atccatggta atggaccatc gagggcaacc tccagagttg gctgctcttc ccactcctga
 240
 gtctacaccc gtgcttcacc agaagaccct gcaggccatg aagagccact cagaaaaggc
 300
 ccatggccat ggagcttcaa ggaaagaaac ccctcagttt tttccgtcta gtccgccacc
 360
 tcattcccca ataagtcatg ggcatatccc cagtgccatt gttcttccaa atgctaccca
 420
 tgactacaac acgtctttct caaactccaa tgctcacaaa gctgaaaaga agcttcaaaa
 480
 cattgatcac cccttcacgc gt
 502

<210> 962
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 962
 Met Val Met Asp His Arg Gly Gln Pro Pro Glu Leu Ala Ala Leu Pro
 1 5 10 15
 Thr Pro Glu Ser Thr Pro Val Leu His Gln Lys Thr Leu Gln Ala Met
 20 25 30
 Lys Ser His Ser Glu Lys Ala His Gly His Gly Ala Ser Arg Lys Glu
 35 40 45
 Thr Pro Gln Phe Phe Pro Ser Ser Pro Pro Pro His Ser Pro Ile Ser
 50 55 60
 His Gly His Ile Pro Ser Ala Ile Val Leu Pro Asn Ala Thr His Asp
 65 70 75 80
 Tyr Asn Thr Ser Phe Ser Asn Ser Asn Ala His Lys Ala Glu Lys Lys
 85 90 95
 Leu Gln Asn Ile Asp His Pro Phe Thr Arg
 100 105

<210> 963
 <211> 1298
 <212> DNA
 <213> Homo sapiens

<400> 963
 nntcgcgagc acactccagc ctctggggag caggccacag aacgcagggt gaaacccaag
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 gcgctctaga ggagatgaat tatggatccg ccctcccgga atcctggctc ggccctcccc
 120
 acgccaccca gggccagtcg ggtctgctca cagcccagag aggccgcgtg tccagccgcg
 180
 ggcaagagac agagcaggtc cctgtgtatc caagtccctg agcccgtgac accggcccca
 240
 ggccctgtag agagccagca gccaccatgg cgaaggagga agatgaggag aagaaagcca
 300
 agaaagggaa gaaggggaag aaggcaccgg acccgagaaa gcccaaacgg agcctgaagg
 360
 ggacgtcgcg ggtgttcatt ggcttccgcg accgaacacc caagatctac aagaagggcc
 420
 agttccgcag cgctcgggcc ttcttctggg gcctccacac cggccccac aagaccaagc
 480
 gcacgaggaa ggcccgcacc gtgctcgggt acacgtcaga gcttatgacg cacatgcgca
 540
 tgggcaagaa gaagcgggag atgaagggca agaagccgtc cttcatggtg atccgcttcc
 600
 caggccgccc tggctacggc cgcttcgggc cgcgcgcccg gtcactcagc aaagcgtcca
 660
 cggccatcaa ctggctcaca aaaaagttcc tcctcaagaa ggccgaggag tcgggcagcg
 720
 aacaggccac agtggacgcc tggctgcagc gctcgagctc ccgcatgggc tcccgcaaac
 780

tccccctccc gtcgggtgcc gagatcctgc ggcctggggg ccggtcccg aggttcccc
 840
 gcagccgcag catctacgcg tcaggcgagc ccctgggctt cctgcccttc gaggacgagg
 900
 cccattcca tcactcgggc tcccgcaagt cgctgtacgg gcttgagggc ttccaggacc
 960
 tgggcgagta ttatgactat caccgcgacg gcgacgacta ctacgaccgg cagtcactcc
 1020
 accgctacga ggagcaggaa ccctacctgg cgggcctcgg cccctacagc ccggcctggc
 1080
 caccctacgg cgaccactac tacgggtacc cgcccaggga tccctacgac tactaccacc
 1140
 ccgactatta cggtagggccc gttgatccgg ggtacaccta cggctacggc tacgacgatt
 1200
 acgaaccccc atatgcgcc ccgtcgggggt actcgtctcc ttacagctac cacgatgggt
 1260
 acgagggcga ggcgcaccct tatggctact acctggat
 1298

<210> 964

<211> 235

<212> PRT

<213> Homo sapiens

<400> 964

Ser	Ala	Ser	Gln	Ala	Ala	Val	Ala	Thr	Ala	Ala	Cys	Gly	Arg	Ala	Pro
1				5					10					15	
Gly	His	Ser	Ala	Lys	Arg	Pro	Arg	Pro	Ser	Thr	Gly	Ser	Gln	Lys	Ser
			20					25					30		
Ser	Ser	Ser	Arg	Arg	Pro	Arg	Ser	Arg	Ala	Ala	Asn	Arg	Pro	Gln	Trp
		35					40				45				
Thr	Pro	Gly	Cys	Ser	Ala	Arg	Ala	Pro	Ala	Trp	Ala	Pro	Ala	Asn	Ser
	50					55					60				
Pro	Ser	Arg	Arg	Val	Pro	Arg	Ser	Cys	Gly	Leu	Gly	Ala	Gly	Ser	Gly
65				70					75					80	
Gly	Ser	Pro	Ala	Ala	Ala	Ala	Ser	Thr	Arg	Gln	Ala	Ser	Pro	Trp	Ala
			85						90					95	
Ser	Cys	Pro	Ser	Arg	Thr	Arg	Pro	His	Ser	Ile	Thr	Arg	Ala	Pro	Ala
		100					105						110		
Ser	Arg	Cys	Thr	Gly	Leu	Arg	Ala	Ser	Arg	Thr	Trp	Ala	Ser	Ile	Met
		115					120					125			
Thr	Ile	Thr	Ala	Thr	Ala	Thr	Thr	Thr	Thr	Thr	Gly	Ser	His	Ser	Thr
	130					135					140				
Ala	Thr	Arg	Ser	Arg	Asn	Pro	Thr	Trp	Arg	Ala	Ser	Ala	Pro	Thr	Ala
145					150					155				160	
Arg	Pro	Gly	His	Pro	Thr	Ala	Thr	Thr	Thr	Thr	Gly	Thr	Arg	Pro	Arg
			165						170					175	
Ile	Pro	Thr	Thr	Thr	Thr	Thr	Pro	Thr	Ile	Thr	Val	Ala	Pro	Leu	Ile
		180						185					190		
Arg	Gly	Thr	Pro	Thr	Ala	Thr	Ala	Thr	Thr	Ile	Thr	Asn	Pro	His	Met
	195						200					205			
Arg	Pro	Arg	Arg	Gly	Thr	Arg	Leu	Leu	Thr	Ala	Thr	Thr	Met	Gly	Thr
	210					215					220				
Arg	Ala	Arg	Arg	Thr	Leu	Met	Ala	Thr	Thr	Trp					

225

230

235

<210> 965

<211> 336

<212> DNA

<213> Homo sapiens

<400> 965

nnngtgacca ttatgggtgg tgcccggtacc cgtgaagtgg aaggcggtga ttttggtggc
60

cggtgcagcg atgccgaaaa ggctgaaatc ctgggccgcg ccgatgtgta tgtcgcccc
120

aataccggcg gtgagagctt tggcattgtc ttggtggaag ccatggcggc aggcgcagcc
180

gttggtgctt cagacttggg ggccttcgc gcagtgtgca acgccgattc cgatgatgtt
240

gccggcgcg tatatcgcaa tgaggatagt aatgaccttg ctctgtgtact caacgaggtg
300

ctcgaggatc ctgagtatcg tgcccgctta gtgcac
336

<210> 966

<211> 112

<212> PRT

<213> Homo sapiens

<400> 966

Xaa Val Thr Ile Met Gly Gly Ala Arg Thr Arg Glu Val Glu Gly Val
1 5 10 15

Asp Phe Val Gly Arg Val Ser Asp Ala Glu Lys Ala Glu Ile Leu Gly
20 25 30

Arg Ala Asp Val Tyr Val Ala Pro Asn Thr Gly Gly Glu Ser Phe Gly
35 40 45

Ile Val Leu Val Glu Ala Met Ala Ala Gly Ala Ala Val Val Ala Ser
50 55 60

Asp Leu Glu Ala Phe Arg Ala Val Cys Asn Ala Asp Ser Asp Asp Val
65 70 75 80

Ala Gly Ala Leu Tyr Arg Asn Glu Asp Ser Asn Asp Leu Ala Arg Val
85 90 95

Leu Asn Glu Val Leu Glu Asp Pro Glu Tyr Arg Ala Arg Leu Val His
100 105 110

<210> 967

<211> 393

<212> DNA

<213> Homo sapiens

<400> 967

ncaaattggca attcatagcc cgccagatcg gacacggagc tgggtggtatc cacggattcg
60

ggcgcgagg cgtcgggctc aagctccgct tcggcaccgg tcggcactga ggaatctccg
120

tcggcctccg cttcggccgc agcctgggct gcgccagact ctgcgggagg caccttctcc
180

cgggttcgcc agccaaatgg cgttgcaggc tccagcatcc agtccggtgc cttcggcacc
 240
 cccgcactgc gcagagaggc cgccagaaac gatggcaccg gcggcgcggg aggtgataca
 300
 ggcgcttcgg ccggagcgct cacggactcc ggcactacag gtgcagcttg cgcttcctgc
 360
 ggcggagcaa cagggtcact tcgaggcggg gat
 393

<210> 968
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 968
 Pro Ala Arg Ser Asp Thr Glu Leu Val Val Ser Thr Asp Ser Gly Ala
 1 5 10 15
 Glu Ala Ser Gly Ser Ser Ser Ala Ser Ala Pro Val Gly Thr Glu Glu
 20 25 30
 Ser Pro Ser Ala Ser Ala Ser Ala Ala Trp Ala Ala Pro Asp Ser
 35 40 45
 Ala Gly Gly Thr Phe Ser Arg Val Arg Gln Pro Asn Gly Val Ala Gly
 50 55 60
 Ser Ser Ile Gln Ser Gly Ala Phe Gly Thr Pro Ala Leu Arg Arg Glu
 65 70 75 80
 Ala Ala Arg Asn Asp Gly Thr Gly Gly Ala Gly Gly Asp Thr Gly Ala
 85 90 95
 Ser Ala Gly Ala Leu Thr Asp Ser Gly Thr Thr Gly Ala Ala Cys Ala
 100 105 110
 Ser Cys Gly Gly Ala Thr Gly Ser Leu Arg Gly Gly Asp
 115 120 125

<210> 969
 <211> 880
 <212> DNA
 <213> Homo sapiens

<400> 969
 caattgtcat gcaggacacc aaagatgaac acaggcttca cagtggcaaa ctctgtctga
 60
 ttatccttac atgtattgca gaggatcaat atgaccatgc atttttgcat gatgatcaac
 120
 atgaattttc gagtaaaactt acatagaatg cctatgagac acaggaagaa ggcagcagac
 180
 aagaatctta ccctgccgtc tttagtatgt gaagtactgg acctgatggg agagtttatt
 240
 gtaacacaca tgatgaagga gtttcctatg gatctctata tacgctgcat ccaggtagta
 300
 cacaaactgc tctgctacca gaagaagtgt cgggtacgcc tgcattacac ctggcgggag
 360
 ctctggtcag ccttgataaa tttgctgaag ttccttatgt caaatgagac tgtacttttg
 420
 gccaaacaca acattttttac attagccctt atgattgtga acctatttaa tatgtttatc
 480

acatatggcg acacatttct gccaaccccc agcagctatg atgaacttta ctatgagatt
 540
 atccgcgatgc accagagctt tgacaacctc tactccatgg tcctgaggct ttctaccaat
 600
 gcaggccagt ggaaggaagc agctagcaag gtgacccatg cattgggttaa tatcagagcc
 660
 atcatcaacc actttaaccc caaaattgag tcctacgctg ctgtgaatca catatcccaa
 720
 ctgtcagagg agcaggtgct ggaggtggtg agagccaact atgacacgct cacgctgaag
 780
 ctgcaggatg gcctggacca gtatgagcgc tactcagagc agcacaagga agctgccttc
 840
 ttcaaagagc tggttcgatc cattagcacc aacgtccgga
 880

<210> 970

<211> 263

<212> PRT

<213> Homo sapiens

<400> 970

Met	Thr	Met	His	Phe	Cys	Met	Met	Ile	Asn	Met	Asn	Phe	Arg	Val	Asn
1				5					10					15	
Leu	His	Arg	Met	Pro	Met	Arg	His	Arg	Lys	Lys	Ala	Ala	Asp	Lys	Asn
			20					25					30		
Leu	Thr	Leu	Pro	Ser	Leu	Val	Cys	Glu	Val	Leu	Asp	Leu	Met	Val	Glu
		35					40					45			
Phe	Ile	Val	Thr	His	Met	Met	Lys	Glu	Phe	Pro	Met	Asp	Leu	Tyr	Ile
	50					55					60				
Arg	Cys	Ile	Gln	Val	Val	His	Lys	Leu	Leu	Cys	Tyr	Gln	Lys	Lys	Cys
65					70					75					80
Arg	Val	Arg	Leu	His	Tyr	Thr	Trp	Arg	Glu	Leu	Trp	Ser	Ala	Leu	Ile
			85					90						95	
Asn	Leu	Leu	Lys	Phe	Leu	Met	Ser	Asn	Glu	Thr	Val	Leu	Leu	Ala	Lys
			100					105						110	
His	Asn	Ile	Phe	Thr	Leu	Ala	Leu	Met	Ile	Val	Asn	Leu	Phe	Asn	Met
		115						120					125		
Phe	Ile	Thr	Tyr	Gly	Asp	Thr	Phe	Leu	Pro	Thr	Pro	Ser	Ser	Tyr	Asp
	130					135					140				
Glu	Leu	Tyr	Tyr	Glu	Ile	Ile	Arg	Met	His	Gln	Ser	Phe	Asp	Asn	Leu
145					150					155					160
Tyr	Ser	Met	Val	Leu	Arg	Leu	Ser	Thr	Asn	Ala	Gly	Gln	Trp	Lys	Glu
			165						170					175	
Ala	Ala	Ser	Lys	Val	Thr	His	Ala	Leu	Val	Asn	Ile	Arg	Ala	Ile	Ile
			180					185						190	
Asn	His	Phe	Asn	Pro	Lys	Ile	Glu	Ser	Tyr	Ala	Ala	Val	Asn	His	Ile
		195					200					205			
Ser	Gln	Leu	Ser	Glu	Glu	Gln	Val	Leu	Glu	Val	Val	Arg	Ala	Asn	Tyr
	210					215						220			
Asp	Thr	Leu	Thr	Leu	Lys	Leu	Gln	Asp	Gly	Leu	Asp	Gln	Tyr	Glu	Arg
225					230					235					240
Tyr	Ser	Glu	Gln	His	Lys	Glu	Ala	Ala	Phe	Phe	Lys	Glu	Leu	Val	Arg
			245						250					255	
Ser	Ile	Ser	Thr	Asn	Val	Arg									

260

<210> 971
 <211> 337
 <212> DNA
 <213> Homo sapiens

<400> 971
 tcgcgaggcc tcactatgga gccttctgag gtgctcaacc ttattaaaga ctccggacta
 60
 cgcggtcgtg gtggtgcagg cttccccact ggggtgaaat ggtcctttgt tccccaaaac
 120
 aatcccaacc ccaaatacct ggttggttaac ggagacgaat ccgaaccgag cacgtgcaag
 180
 gacatgccgc tcattatggc aagcccgac acgcttgctg aaggtgctct tatctccgag
 240
 tacgctttcg gatccgagca ggctttcctc tacctccgtg gagaagttgt tcaggtagcc
 300
 cggcgccttg aagaaaaaaaa aaaaatgcga nnnnnnn
 337

<210> 972
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 972
 Ser Arg Gly Leu Thr Met Glu Pro Ser Glu Val Leu Asn Leu Ile Lys
 1 5 10 15
 Asp Ser Gly Leu Arg Gly Arg Gly Gly Ala Gly Phe Pro Thr Gly Val
 20 25 30
 Lys Trp Ser Phe Val Pro Gln Asn Asn Pro Asn Pro Lys Tyr Leu Val
 35 40 45
 Val Asn Gly Asp Glu Ser Glu Pro Gly Thr Cys Lys Asp Met Pro Leu
 50 55 60
 Ile Met Ala Ser Pro His Thr Leu Val Glu Gly Ala Leu Ile Ser Arg
 65 70 75 80
 Tyr Ala Phe Gly Ser Glu Gln Ala Phe Ile Tyr Leu Arg Gly Glu Val
 85 90 95
 Val Gln Val Ala Arg Arg Leu Glu Glu Lys Lys Lys Met Arg Xaa Xaa
 100 105 110

<210> 973
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 973
 acgcgtgaag gggaaagggg gagtcgtctc cttggttcct aagtgcgccc tctccaggtt
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 ccagcagggc ggcacagcca aggaaatggc atggctcctgc tgcattggtc tcagtggggt
 120
 ccgggacctt ctgtataggc atcacttagg aaccagtcag accatcagat tctcaggacc
 180

cactggatca actgagtcag gaactcaggg ttttcaacac atcctccggg gggattccag
240
tggctgtgta actttgagga ccactggcaa agtggctctg gggtcagaga tccgagttca
300
tattctgggt ctgcctctga ctgactgcaa cggtgggcaa gtcacttgcc gtgcccagcc
360

<210> 974

<211> 91

<212> PRT

<213> Homo sapiens

<400> 974

Met	Ala	Trp	Ser	Cys	Cys	Met	Val	Leu	Ser	Gly	Val	Arg	Asp	Leu	Leu
1				5					10					15	
Tyr	Arg	His	His	Leu	Gly	Thr	Ser	Gln	Thr	Ile	Arg	Phe	Ser	Gly	Pro
			20					25					30		
Thr	Gly	Ser	Thr	Glu	Ser	Gly	Thr	Gln	Gly	Phe	Gln	His	Ile	Leu	Arg
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<211> 2604

<212> DNA

<213> Homo sapiens

<400> 975

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<211> 411

<212> PRT

<213> Homo sapiens

<400> 976

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<211> 378
<212> DNA
<213> Homo sapiens
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<212> PRT
<213> Homo sapiens
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<211> 73

<212> PRT

<213> Homo sapiens

<400> 980

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		20						25				30			
Cys	Phe	Gln	Val	Leu	Thr	Ala	Ser	Gly	Trp	Ser	Leu	Glu	Ala	Thr	Glu
	35						40				45				
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<211> 404

<212> DNA

<213> Homo sapiens

<400> 981

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<210> 982
 <211> 134
 <212> PRT
 <213> Homo sapiens

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 Asp Asp Glu Asp Val Asp Asp Glu Asn Thr Asp Ile Thr Ala Leu Ala
 50 55 60
 Glu Ala Gly Ala Arg Gly Gly Ala Gly Asn His Arg Phe Gly Gly Asp
 65 70 75 80
 Arg Pro Gly Ser Asp Arg Val Leu Gly Arg Gln Arg Leu Gln Gln Pro
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<210> 983
 <211> 579
 <212> DNA
 <213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Leu Phe Pro Lys Arg Ala Arg Tyr Pro Ser Phe Ser Gly Pro Leu Tyr
 50 55 60
 Leu Phe Phe Ser Leu Pro Glu Thr Pro Phe Leu Leu Asn Asn Leu Met
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<210> 985
 <211> 313
 <212> DNA
 <213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

<400> 986
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Ala Asn Phe Lys Ala His Asp Leu Lys Leu Val Thr Glu Ile Asn His			
35	40	45	
Leu Asp Asn Gln Ile Phe Ile Asp Tyr Ala Lys Leu Ile Lys Glu Ser			
50	55	60	
Asp Ala Leu Pro Val Asp Gln Gln Val Ala Phe Phe Leu Asn Asn Met			
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<210> 987

<211> 4224

<212> DNA

<213> Homo sapiens

<400> 987

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<210> 988

<211> 873

<212> PRT

<213> Homo sapiens

<400> 988

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			20					25					30		
Met	Leu	Leu	Arg	Gly	Leu	Thr	Gln	Ile	Gln	Ser	Arg	Ile	Leu	Gly	Pro
			35				40					45			
Gly	Arg	Lys	Cys	Cys	Ala	Leu	Ala	Asn	Leu	Ala	Asp	Met	Leu	Thr	Val
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Phe	Ala	Leu	Thr	Glu	Asp	Asp	Pro	Gln	Glu	Val	Ser	Ala	Thr	Val	Tyr
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Leu	Asp	Lys	Leu	Ala	Thr	Val	Ile	Ser	Val	Trp	Asn	Ser	Asp	Thr	Gln
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Asn	Pro	Tyr	His	Gln	Gln	Ala	Leu	Ala	Glu	Lys	Val	Lys	Glu	Ala	Glu
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Phe	Val	Gly	Cys	Glu	Phe	Leu	His	His	Leu	Leu	Arg	Glu	Trp	Gly	Glu
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Glu	Leu	Gln	Ala	Val	Leu	Arg	Ser	Ser	Gln	Gly	Thr	Ser	Tyr	Asp	Ser
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Tyr	Arg	Leu	Cys	Asp	Ser	Leu	Thr	Ser	Phe	Ser	Gln	Asn	Ala	Thr	Leu
			165						170					175	
Tyr	Leu	Asn	Arg	Thr	Ser	Leu	Ser	Lys	Glu	Asp	Arg	Gln	Val	Val	Ser
		180						185					190		
Glu	Leu	Ala	Glu	Cys	Val	Arg	Asp	Phe	Leu	Arg	Lys	Thr	Ser	Thr	Val
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Leu	Lys	Asn	Arg	Ala	Leu	Glu	Asp	Ile	Thr	Ala	Ser	Ile	Ala	Met	Ala
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Val	Ile	Gln	Gln	Lys	Met	Asp	Arg	His	Met	Glu	Val	Cys	Tyr	Ile	Phe
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Ala	Ser	Glu	Lys	Lys	Trp	Ala	Phe	Ser	Asp	Glu	Trp	Val	Ala	Cys	Leu
			245						250					255	
Gly	Ser	Asn	Arg	Ala	Leu	Phe	Arg	Glu	Pro	Asp	Leu	Val	Leu	Arg	Leu
		260						265					270		
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Ser	Gln	Ile	Arg	Gln	Val	Ile	His	Leu	Ile	Leu	Glu	Cys	Tyr	Ala	Asp
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Phe	Gln	Glu	Asp	Leu	Asn	Thr	Thr	Phe	Asn	Gln	Leu	Thr	Gln	Ser	Ala
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Ile	Val	His	Pro	Glu	Val	Thr	Val	Lys	Lys	Met	Cys	Ser	Leu	Ala	Val

370	375	380
Val Asn Leu Gly Thr His	Lys Phe Leu Ala Gln Ile Leu Thr Ala Phe	
385	390	395
Pro Ala Leu Arg Phe Val	Glu Val Gln Gly Pro Asn Ser Ser Ala Thr	400
	405	410
Phe Met Val Ser Cys Leu Lys	Glu Thr Val Trp Met Lys Phe Ser Thr	415
	420	425
Pro Lys Glu Glu Lys Gln Phe	Leu Glu Leu Leu Asn Cys Leu Met Ser	430
	435	440
Pro Val Lys Pro Gln Gly Ile	Pro Val Ala Ala Leu Leu Glu Pro Asp	445
	450	455
Glu Val Leu Lys Glu Phe Val	Leu Pro Phe Leu Arg Leu Asp Val Glu	460
465	470	475
Glu Val Asp Leu Ser Leu Arg	Ile Phe Ile Gln Thr Leu Glu Ala Asn	480
	485	490
Ala Cys Arg Glu Glu Tyr Trp	Leu Gln Thr Cys Ser Pro Phe Pro Leu	495
	500	505
Leu Phe Ser Leu Cys Gln Leu	Leu Asp Arg Phe Ser Lys Tyr Trp Gln	510
	515	520
Leu Pro Lys Glu Lys Arg Cys	Leu Ser Leu Asp Arg Lys Asp Leu Ala	525
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Ile His Ile Leu Glu Leu Leu	Cys Glu Ile Val Ser Ala Asn Ala Glu	540
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Thr Phe Ser Pro Asp Val Trp	Ile Lys Ser Leu Ser Trp Leu His Arg	560
	565	570
Lys Leu Glu Gln Leu Asp Trp	Thr Val Gly Leu Arg Leu Lys Ser Phe	575
	580	585
Phe Glu Gly His Phe Lys Cys	Glu Val Pro Ala Thr Leu Phe Glu Ile	590
	595	600
Cys Lys Leu Ser Glu Asp Glu	Trp Thr Ser Gln Ala His Pro Gly Tyr	605
	610	615
Gly Ala Gly Thr Gly Leu Leu	Ala Trp Met Glu Cys Cys Cys Val Ser	620
625	630	635
Ser Gly Ile Ser Glu Arg Met	Leu Ser Leu Leu Val Val Asp Val Gly	640
	645	650
Asn Pro Glu Glu Val Arg Leu	Phe Ser Lys Gly Phe Leu Val Ala Leu	655
	660	665
Val Gln Val Met Pro Trp Cys	Ser Pro Gln Glu Trp Gln Arg Leu His	670
	675	680
Gln Leu Thr Arg Arg Leu Leu	Glu Lys Gln Leu Leu His Val Pro Tyr	685
	690	695
Ser Leu Glu Tyr Ile Gln Phe	Val Pro Leu Leu Asn Leu Lys Pro Phe	700
705	710	715
Ala Gln Glu Leu Gln Leu Ser	Val Leu Phe Leu Arg Thr Phe Gln Phe	720
	725	730
Leu Cys Ser His Ser Cys Arg	Asn Trp Leu Pro Leu Glu Gly Trp Asn	735
	740	745
His Val Val Lys Leu Leu Cys	Gly Ser Leu Thr Arg Leu Leu Asp Ser	750
	755	760
Val Arg Ala Ile Gln Ala Ala	Gly Pro Trp Val Gln Gly Pro Glu Gln	765
	770	775
Asp Leu Thr Gln Glu Ala Leu	Phe Val Tyr Thr Gln Val Phe Cys His	780
785	790	795
Ala Leu His Ile Met Ala Met	Leu His Pro Glu Val Cys Glu Pro Leu	800

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Tyr	Val	Leu	Ala	Leu	Glu	Thr	Leu	Thr	Cys	Tyr	Glu	Thr	Leu	Ser	Lys		
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Thr	Asn	Pro	Ser	Val	Ser	Ser	Leu	Leu	Gln	Arg	Ala	His	Glu	Gln	Cys		
		835						840					845				
Phe	Leu	Lys	Ser	Ile	Ala	Glu	Gly	Ile	Gly	Pro	Glu	Glu	Arg	Arg	Gln		
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Thr	Leu	Leu	Gln	Lys	Met	Ser	Ser	Phe									
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<210> 989

<211> 402

<212> DNA

<213> Homo sapiens

<400> 989

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<210> 990

<211> 134

<212> PRT

<213> Homo sapiens

<400> 990

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			20					25					30				
Arg	Arg	Val	Ala	Leu	Cys	Lys	Leu	Leu	Ile	Glu	Gln	Pro	Asp	Leu	Leu		
		35					40					45					
Leu	Leu	Asp	Glu	Pro	Thr	Asn	His	Leu	Asp	Ala	Glu	Ser	Val	Asn	Trp		
	50					55				60							
Leu	Glu	Gly	His	Leu	Lys	Ser	Tyr	Pro	Gly	Ala	Val	Leu	Ala	Val	Thr		
65					70					75					80		
His	Asp	Arg	Tyr	Phe	Leu	Asp	His	Val	Ala	Glu	Trp	Ile	Cys	Glu	Val		
			85					90					95				
Asp	Arg	Gly	Gln	Leu	His	Pro	Tyr	Glu	Gly	Asn	Tyr	Ser	Thr	Tyr	Leu		
		100						105					110				
Asp	Thr	Lys	Arg	Lys	Arg	Leu	Gln	Ile	Glu	Gly	Lys	Lys	Asp	Ala	Lys		
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Arg	Ala	Lys	Ile	Leu	Glu												

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<210> 991
 <211> 359
 <212> DNA
 <213> Homo sapiens

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<210> 992
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 992
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 20 25 30
 Lys Ser Ala Phe Leu Pro Leu Ile Ala Gln Phe Leu Gly Val Asp Gly
 35 40 45
 Tyr Trp Leu Thr Thr Gly Asn Thr Glu Asp Ser Phe Arg Glu Ser Asp
 50 55 60
 Val Phe Ser Pro Thr Val Val Ser Ala Glu Ser Thr Asp Gln Tyr Val
 65 70 75 80
 Trp Ile Glu Val Val Glu Ala Asn Phe Ser Cys Gly Thr Gly Glu Ser
 85 90 95
 Ile Glu Phe His Phe Asp Ala Ile Asn Gly Lys Ile Pro Phe Pro Ala
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 Ser Phe Phe Lys Glu Lys Arg
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<210> 993
 <211> 450
 <212> DNA
 <213> Homo sapiens

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<210> 994
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 994
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 20 25 30
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 35 40 45
 Leu Gly Lys Phe Asp Pro Asp Asn Ile Pro Ala Asp Pro Asn Glu Leu
 50 55 60
 Phe Ala Thr Trp Phe Lys Glu Ala Val Glu Asn Glu Val Gly Asp Pro
 65 70 75 80
 Thr Ala Val Thr Val Ala Thr Val Asp Asp Asn Gly Gln Pro Asp Ala
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 Arg Val Val Asp Leu Leu Tyr Leu Asn Ser Asp Gly Phe His
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<210> 995
 <211> 924
 <212> DNA
 <213> Homo sapiens

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<210> 996

<211> 308

<212> PRT

<213> Homo sapiens

<400> 996

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Phe	Gly	Pro	Val	Val	Asp	Gly	Asp	Val	Val	Pro	Asp	Asp	Pro	Glu	Ile
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Leu	Met	Gln	Gln	Gly	Glu	Phe	Leu	Asn	Tyr	Asp	Met	Leu	Ile	Gly	Val
	35						40					45			
Asn	Gln	Gly	Glu	Gly	Leu	Lys	Phe	Val	Glu	Asp	Ser	Ala	Glu	Ser	Glu
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Asp	Gly	Val	Ser	Ala	Ser	Ala	Phe	Asp	Phe	Thr	Val	Ser	Asn	Phe	Val
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Asp	Asn	Leu	Tyr	Gly	Tyr	Pro	Glu	Gly	Lys	Asp	Val	Leu	Arg	Glu	Thr
			85						90					95	
Ile	Lys	Phe	Met	Tyr	Thr	Asp	Trp	Ala	Asp	Arg	Asp	Asn	Gly	Glu	Met
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Arg	Arg	Lys	Thr	Leu	Leu	Ala	Leu	Phe	Thr	Asp	His	Gln	Trp	Val	Ala
		115					120					125			
Pro	Ala	Val	Ala	Thr	Ala	Lys	Leu	His	Ala	Asp	Tyr	Gln	Ser	Pro	Val
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Tyr	Phe	Tyr	Thr	Phe	Tyr	His	His	Cys	Gln	Ala	Glu	Gly	Arg	Pro	Glu
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Trp	Ala	Asp	Ala	Ala	His	Gly	Asp	Glu	Leu	Pro	Tyr	Val	Phe	Gly	Val
			165					170					175		
Pro	Met	Val	Gly	Ala	Thr	Asp	Leu	Phe	Pro	Cys	Asn	Phe	Ser	Lys	Asn
		180						185					190		
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	195						200					205			
Lys	Thr	Gly	Asp	Pro	Asn	Gln	Pro	Val	Pro	Gln	Asp	Thr	Lys	Phe	Ile
	210					215					220				
His	Thr	Lys	Pro	Asn	Arg	Phe	Glu	Glu	Val	Val	Trp	Ser	Lys	Phe	Asn

225 230 235 240
 Ser Lys Glu Lys Gln Tyr Leu His Ile Gly Leu Lys Pro Arg Val Arg
 245 250 255
 Asp Asn Tyr Arg Ala Asn Lys Val Ala Phe Trp Leu Glu Leu Val Pro
 260 265 270
 His Leu His Asn Leu His Thr Glu Leu Phe Thr Thr Thr Thr Arg Leu
 275 280 285
 Pro Pro Tyr Ala Thr Arg Trp Pro Pro Arg Pro Pro Ala Gly Ala Pro
 290 295 300
 Gly Thr Arg Arg
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<210> 997
 <211> 320
 <212> DNA
 <213> Homo sapiens

<400> 997
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 180
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<210> 998
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 998
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 Ala Val Pro Lys Arg Val Ser Arg Ala Leu Ser Leu Phe Gly Ala Phe
 35 40 45
 Ala Ala Ile Met Tyr Gly Leu Ile Leu Leu Asp Ser Thr Trp Leu Ala
 50 55 60
 Leu Leu Gly Ile Asp Val Arg Gly Gly Ala Ile Glu Tyr Trp Ala Lys
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 Met Gln Asp Met Phe Asp Leu Arg Pro Arg
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<210> 999
 <211> 401

<212> DNA

<213> Homo sapiens

<400> 999

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caactatctc aatcgtggct acaaggacat tctgagctat gcagacgatg ctagtctttt
180
gcaaaagcct ccagcagtgg cttcagatga tctggataca ggtctcttga agagggcctt
240
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gtcaaccggg ctcaacattg acagtttcta cgtctttggg gaccaagaca tctgctggca
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401

<210> 1000

<211> 115

<212> PRT

<213> Homo sapiens

<400> 1000

Met	Val	His	Leu	Ser	Lys	Ser	Phe	Ile	Gly	Val	Tyr	Leu	Tyr	Ser	Glu
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Gly	Lys	Phe	Val	Thr	Ser	Asn	Tyr	Leu	Asn	Arg	Gly	Tyr	Lys	Asp	Ile
			20					25					30		
Leu	Ser	Tyr	Ala	Asp	Asp	Ala	Ser	Leu	Leu	Gln	Lys	Pro	Pro	Ala	Val
		35				40					45				
Ala	Ser	Asp	Asp	Leu	Asp	Thr	Gly	Leu	Leu	Lys	Arg	Ala	Leu	Asp	Glu
	50					55					60				
Trp	Val	Ala	Asp	Ala	Lys	Asn	His	Ile	Leu	Asn	Thr	Glu	Asn	Phe	Phe
65					70				75					80	
Ser	Gly	Ser	Thr	Gly	Leu	Asn	Ile	Asp	Ser	Phe	Tyr	Val	Phe	Gly	Asp
			85					90					95		
Gln	Asp	Ile	Cys	Trp	Gln	Leu	Ala	Ala	Ile	Leu	Lys	Gln	Ser	Met	Asn
			100					105					110		
Arg	Glu	Leu													
			115												

<210> 1001

<211> 351

<212> DNA

<213> Homo sapiens

<400> 1001

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120
atcggtatga ttgtcttccc gctgtttggt ctggcgatga tccttcggg tctgctaact
180

aacttcttcg ctggtggtgc cgctggagtc tttggcaacg cgatgggagg acgtaaaggg
 240
 gcaattattg gcggcgtagt gcacgggctg tttatcaccc tgttaccagc gatgctaatac
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 cccttactgg aaaccttcgg cttcaaaggc gtcaccttca gtgattccga t
 351

<210> 1002
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 1002
 Arg Gly Ile Ala Met Arg Leu Val Pro Asn Ala Lys Pro Ala Leu Asp
 1 5 10 15
 Cys Pro Val Leu Phe Pro Tyr Ala Pro Asn Ala Val Ile Val Gly Phe
 20 25 30
 Leu Ala Thr Thr Val Gly Ser Ile Ile Gly Met Ile Val Phe Pro Leu
 35 40 45
 Phe Gly Leu Ala Met Ile Leu Pro Gly Leu Leu Thr Asn Phe Phe Ala
 50 55 60
 Gly Gly Ala Ala Gly Val Phe Gly Asn Ala Met Gly Gly Arg Lys Gly
 65 70 75 80
 Ala Ile Ile Gly Gly Val Val His Gly Leu Phe Ile Thr Leu Leu Pro
 85 90 95
 Ala Met Leu Ile Pro Leu Leu Glu Thr Phe Gly Phe Lys Gly Val Thr
 100 105 110
 Phe Ser Asp Ser Asp
 115

<210> 1003
 <211> 444
 <212> DNA
 <213> Homo sapiens

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 acgagcactg ccccatctcc taggcttagg gttatgcaga ctcccatcga cgctacctcc
 120
 acccccgcacat ggggcacact ctccggccta aagtcccgcct tcgctgacgg gccacataaa
 180
 ctgcgccggtt tgttcgacgc cgaccctcac cgcgctgagc gctacacctt tgacgtcgcg
 240
 gatttgcacg tcgatttatc gaagaacctc cttaccgacg agattcgtga cgctctcctc
 300
 gaactggctg cgcagatgcg cgtcaccgag cgtcgtgacg cgatgtatgc cggtgagcac
 360
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 420
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 444

<210> 1004

<211> 117
 <212> PRT
 <213> Homo sapiens

<400> 1004
 Met Gln Thr Pro Ile Asp Ala Thr Ser Thr Pro Ala Trp Gly Thr Leu
 1 5 10 15
 Ser Gly Leu Lys Ser Arg Phe Ala Asp Gly Pro His Lys Leu Arg Arg
 20 25 30
 Leu Phe Asp Ala Asp Pro His Arg Ala Glu Arg Tyr Thr Phe Asp Val
 35 40 45
 Ala Asp Leu His Val Asp Leu Ser Lys Asn Leu Leu Thr Asp Glu Ile
 50 55 60
 Arg Asp Ala Leu Leu Glu Leu Ala Ala Gln Met Arg Val Thr Glu Arg
 65 70 75 80
 Arg Asp Ala Met Tyr Ala Gly Glu His Ile Asn Val Thr Glu Asp Arg
 85 90 95
 Ala Val Leu His Thr Ala Leu Cys Arg Pro Arg Thr Asp Glu Leu His
 100 105 110
 Val Asp Gly Gln Asp
 115

<210> 1005
 <211> 299
 <212> DNA
 <213> Homo sapiens

<400> 1005
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 120
 tatctatctg ccttagccac tcgtgtctga cgagcacctc acacctccag aggctcctca
 180
 tttcttccca tgctgcttc tcccacactc ctccctctca catgagggca acttcacct
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 cccagttgct caggccccaac acctccatca gttttgactc ttctctcgca cactactcg
 299

<210> 1006
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 1006
 Met Ala Ile Pro Leu Val Thr Ala Ser Ser Pro Met Asp Leu Asn Thr
 1 5 10 15
 Pro Asn Val Leu Val Thr Pro Lys Phe Thr Pro Pro Ala Arg Ala Ser
 20 25 30
 Leu Leu Gly Leu His Thr His Leu Ser Ile Cys Leu Ser His Ser Cys
 35 40 45
 Leu Thr Ser Thr Ser His Leu Gln Arg Leu Leu Ile Ser Ser His Ala
 50 55 60
 Cys Phe Ser His Thr Pro Pro Ser His Met Arg Ala Thr Ser Ser Ser

65 70 75 80
 Gln Leu Leu Arg Pro Gln Thr Ser Ile Ser Phe Asp Ser Ser Leu Ala
 85 90 95
 His Tyr Ser

<210> 1007
 <211> 389
 <212> DNA
 <213> Homo sapiens

<400> 1007
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 tcaacgacgc caccgaggca cccagaggtg tgacgttgag tgatggccga cgacagggca
 180
 acgccggagc aatcggtgac ttcttcgcat cgaaggacta caagccgtcc gcggcgagcc
 240
 tccgaggtcc ggcgagggat ccgaaatgga tgcacgttca acgctcattc cagagaacg
 300
 aagaaggccc gtacagctgg tacacctggc gcgggcaggc ttttgacacg ggcgctggat
 360
 ggcgtaaata cgtccatgcc gcgacaacg
 389

<210> 1008
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 1008
 Met Asp Ser Ile Phe Gly Pro Gly Pro Gly Val Thr Val Ser Glu Ile.
 1 5 10 15
 Asn Asp Ala Thr Glu Ala Pro Arg Gly Val Thr Leu Ser Asp Gly Arg
 20 25 30
 Arg Gln Gly Asn Ala Gly Ala Ile Gly Asp Phe Phe Ala Ser Lys Asp
 35 40 45
 Tyr Lys Pro Ser Ala Ala Ser Leu Arg Gly Pro Ala Arg Asp Pro Lys
 50 55 60
 Trp Ile Asp Val Gln Arg Ser Phe His Glu Asn Glu Glu Gly Pro Tyr
 65 70 75 80
 Ser Trp Tyr Thr Trp Arg Gly Gln Ala Phe Asp Thr Gly Ala Gly Trp
 85 90 95
 Arg Lys Tyr Val His Ala Ala Thr Thr
 100 105

<210> 1009
 <211> 324
 <212> DNA
 <213> Homo sapiens

<400> 1009

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 cattccactg gtgtttcccc aggaaagcca accctacctg catctcagca gagcttccac
 120
 ggagttggaa ccccgctccg agaggggtgtg ggctcagggg ccaggggtca cacaaactcc
 180
 agaaggagga cgtagttggt ttgcaaggct gtcctttgcc ctggttgaat aaccttcggt
 240
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 300
 aaacttggcc catggtgcag atct
 324

<210> 1010
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 1010
 Met Gly Gln Val Ser Gln Lys Ile His Gly Phe Leu Arg Val Gln Pro
 1 5 10 15
 Asn Ala His Val Pro Leu Gly Ala Asp Arg Arg Leu Phe Asn Gln Gly
 20 25 30
 Lys Gly Gln Pro Cys Lys Pro Thr Thr Ser Ser Phe Trp Ser Leu Cys
 35 40 45
 Asp Pro Trp Pro Leu Ser Pro His Pro Leu Gly Ala Gly Phe Gln Leu
 50 55 60
 Arg Gly Ser Ser Ala Glu Met Gln Val Gly Leu Ala Phe Leu Gly Lys
 65 70 75 80
 His Gln Trp Asn Val Ala Ile Val Thr Gly Ala Arg Asp Gly Asp Glu
 85 90 95
 Ala Arg His Xaa Ser His Glu Gly
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<210> 1011
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 1011
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 120
 gtgggcagca gctcggaggg tccgagaggt gcaggagacg caggcatggc cggtagagctg
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 actcctgagg aggaggccca gtacaaaaag gctttctccg cggttgacac ggatggaaac
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 ggcaccatca atgcccagga gctgggcgcg gcgctgaagg ccacgggcaa gaacctctcg
 300
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 330

<210> 1012

<211> 55
 <212> PRT
 <213> Homo sapiens

<400> 1012
 Met Ala Gly Glu Leu Thr Pro Glu Glu Glu Ala Gln Tyr Lys Lys Ala
 1 5 10 15
 Phe Ser Ala Val Asp Thr Asp Gly Asn Gly Thr Ile Asn Ala Gln Glu
 20 25 30
 Leu Gly Ala Ala Leu Lys Ala Thr Gly Lys Asn Leu Ser Glu Ala Gln
 35 40 45
 Leu Lys Lys Leu Ile Ser Glu
 50 55

<210> 1013
 <211> 432
 <212> DNA
 <213> Homo sapiens

<400> 1013
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 cccgggattg gctcgaacgc cgccactttg gcgcgttccc aggctcgcag tgacaaggctc
 180
 gaggctgatt tggcgggtcca tcccgcacaag tggcgcattc tggggggggga ccgtcctact
 240
 ggcagcctgc acatcggtca ctacttcggg tcgctggcga atcggggtacg cgtgcagaac
 300
 aagggcattg agtctttcct tgctcgctgc gactaccagg ttatctatga ccgcggggggg
 360
 ggtggtgacc tgcaggccaa tgttatgtcg aatgtcgccg attacctggc aatcggcatt
 420
 gacccaacgc gt
 432

<210> 1014
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 1014
 Met Thr Ser Asp Val Pro Gly Ile Gly Ser Asn Ala Ala Thr Leu Ala
 1 5 10 15
 Arg Ser Gln Ala Arg Ser Asp Lys Val Glu Ala Asp Leu Ala Val His
 20 25 30
 Pro Asp Lys Trp Arg Ile Leu Gly Gly Asp Arg Pro Thr Gly Ser Leu
 35 40 45
 His Ile Gly His Tyr Phe Gly Ser Leu Ala Asn Arg Val Arg Val Gln
 50 55 60
 Asn Lys Gly Ile Glu Ser Phe Leu Val Val Ala Asp Tyr Gln Val Ile
 65 70 75 80
 Tyr Asp Arg Gly Gly Gly Gly Asp Leu Gln Ala Asn Val Met Ser Asn

85 90 95
Val Ala Asp Tyr Leu Ala Ile Gly Ile Asp Pro Thr Arg
100 105

<210> 1015
<211> 467
<212> DNA
<213> Homo sapiens

<400> 1015
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gaaaacttcc cgatgaaagc gcgcacgggt gaagagctga aagaattgga aagagtttta
120
cagcaaaaga agattgaagc agagtgtctt aaactacgga aggaaattgt agaggctcag
180
tctggagtta agttgattaa acagcgtcat gaagaggatg atgaagaaga ggaagaggaa
240
gacaagacag taaaatatag caatttgccc aattacctgc ttggtagtct gagtactgat
300
tttggggtag atacctcttt attgtcaagc caattggagc ttcattccag agaagagaaa
360
atcaaccaa ttatattatt gaaagatatc atttacaagg taaaaactgt tttcaataat
420
gagtttgacg ctgcatataa acaaaaagag tttgaaattg cacgcgt
467

<210> 1016
<211> 155
<212> PRT
<213> Homo sapiens

<400> 1016
Xaa Asn Ser Met Ala Val Lys Gly Arg Ala Leu Lys Cys Phe His Ile
1 5 10 15
Pro Cys Val Val Glu Asn Phe Pro Met Lys Ala Arg Thr Val Glu Glu
20 25 30
Leu Lys Glu Leu Glu Arg Val Leu Gln Gln Lys Lys Ile Glu Ala Glu
35 40 45
Cys Leu Lys Leu Arg Lys Glu Ile Val Glu Ala Gln Ser Gly Val Lys
50 55 60
Leu Ile Lys Gln Arg His Glu Glu Asp Asp Glu Glu Glu Glu Glu
65 70 75 80
Asp Lys Thr Val Lys Tyr Ser Asn Leu Pro Asn Tyr Leu Leu Gly Ser
85 90 95
Leu Ser Thr Asp Phe Gly Val Asp Thr Ser Leu Leu Ser Ser Gln Leu
100 105 110
Glu Leu His Ser Arg Glu Glu Lys Ile Asn Gln Ile Ile Leu Leu Lys
115 120 125
Asp Ile Ile Tyr Lys Val Lys Thr Val Phe Asn Asn Glu Phe Asp Ala
130 135 140
Ala Tyr Lys Gln Lys Glu Phe Glu Ile Ala Arg
145 150 155

<210> 1017
<211> 335
<212> DNA
<213> Homo sapiens

<400> 1017
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aacattaaag tgggtcgccc cggtactttt gcggaggtca tggatttcta tgcgcattat
120
ctgaagggtg cggttaccgc tttccgtccg aattttattg tgcaggataa tacggggccgt
180
tggcgtgttc agtcgtcgtg gccgcagccg aatcgcaactg ttacttttgc gggaccccg
240
ggcattgtcc gctacggtac gacgttggcg gcccgcacgc atgggaatgg tcaggctatt
300
ccgcaggcgg atgcacagtc tcttaaccgc gagaa
335

<210> 1018
<211> 105
<212> PRT
<213> Homo sapiens

<400> 1018
Met Trp Asn His Val Arg Ala Asn Glu Lys Asp Ala Lys Gly Asn Ile
1 5 10 15
Lys Val Gly Arg Pro Gly Tyr Phe Ala Glu Val Met Asp Phe Tyr Ala
20 25 30
His Tyr Leu Lys Gly Ala Val Thr Arg Phe Arg Pro Asn Phe Ile Val
35 40 45
Gln Asp Asn Thr Gly Arg Trp Arg Val Gln Ser Ser Trp Pro Gln Pro
50 55 60
Asn Arg Thr Val Thr Phe Ala Gly Pro Arg Gly Ile Val Arg Tyr Gly
65 70 75 80
Thr Thr Leu Ala Ala Arg Thr His Gly Asn Gly Gln Ala Ile Pro Gln
85 90 95
Ala Asp Ala Gln Ser Leu Asn Arg Glu
100 105

<210> 1019
<211> 454
<212> DNA
<213> Homo sapiens

<400> 1019
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ctctggagcc tctctctcaa tggcgttgcc catggtgcct ggcttgggtg atgaggcggg
120
tgaagggcgt ggggccaggt ggtgcgggat gaagtcagcc tcgttgaaga gctcgtggct
180
ggaggagccg ctgcctgagc cttcagggcc cagtgtgccc agggggccacc gacagagtgg
240

cagagagcag gtgacttcct ggcactgcgg agcgaggacc cggagaagta cttcctcaat
300
ggtggctgga ccatccagtg gaacggggac taccaggtgg cagggaccac cttcacatac
360
gcacgcaggg gcaactggga gaacctcacg tccccgggtc ccaccaagga gcctgtctgg
420
atccagctgc tgttccagga gagcaaccct gggg
454

<210> 1020
<211> 125
<212> PRT
<213> Homo sapiens

<400> 1020
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1 5 10 15
Arg Gly Ala Arg Trp Cys Gly Met Lys Ser Ala Ser Leu Lys Ser Ser
20 25 30
Trp Leu Glu Glu Pro Leu Pro Glu Pro Ser Gly Pro Ser Val Pro Arg
35 40 45
Gly His Arg Gln Ser Gly Arg Glu Gln Val Thr Ser Trp His Cys Gly
50 55 60
Ala Arg Thr Arg Arg Ser Thr Ser Ser Met Val Ala Gly Pro Ser Ser
65 70 75 80
Gly Thr Gly Thr Thr Arg Trp Gln Gly Pro Pro Ser His Thr His Ala
85 90 95
Gly Ala Thr Gly Arg Thr Ser Arg Pro Arg Val Pro Pro Arg Ser Leu
100 105 110
Ser Gly Ser Ser Cys Cys Ser Arg Arg Ala Thr Leu Gly
115 120 125

<210> 1021
<211> 366
<212> DNA
<213> Homo sapiens

<400> 1021
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gccgagatta tctgacagga ccaaagcata taaagttgac tgaagcagga gcaaacacgc
120
tggttgaggg tcaagtgtg gggcagcagc aacaacaaac caaaaaaag ccctttgaac
180
tcccttaatg ttgccccaaag gttctggtag agaacaagtc acatgcctaa gaaggtcttt
240
taaagggcac tcttgcaagt tcagcatttg gtccggggaa ttgcacaagg ctctgcttaa
300
atgcagagct ctttctagca tcttcatatt caaggcggaa aaactgagct tggcgaggaa
360
ccctgt
366

<210> 1022

<211> 109
 <212> PRT
 <213> Homo sapiens

<400> 1022
 Met Lys Met Leu Glu Arg Ala Leu His Leu Ser Arg Ala Leu Cys Asn
 1 5 10 15
 Ser Pro Asp Gln Met Leu Lys Leu Gln Glu Cys Pro Leu Lys Asp Leu
 20 25 30
 Leu Arg His Val Thr Cys Ser Leu Pro Glu Pro Leu Gly Asn Ile Lys
 35 40 45
 Gly Val Gln Arg Ala Phe Phe Trp Phe Val Val Ala Ala Ala Pro Ala
 50 55 60
 Leu Asp Pro Gln Pro Ala Cys Leu Leu Leu Leu Gln Ser Thr Leu Tyr
 65 70 75 80
 Ala Leu Val Leu Ser Asp Asn Leu Gly Ser Met Ser Ile Phe His Ala
 85 90 95
 Leu Pro Leu Ser Gly Leu Gln Glu Val Thr Thr Gln Leu
 100 105

<210> 1023
 <211> 426
 <212> DNA
 <213> Homo sapiens

<400> 1023
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 ggcattcctga ccatacagca gaccaagttt ggcaagtccc gcatgggtgcc gctacacccc
 120
 agcgtgatcg gtccgatggc agcctaccgg gccttgccgc gccagtacgt gcctgcgaag
 180
 ccgcagatga cattcttcgt gggctcgcgt ggcggtgcacc ggggtgaacc gctgggagat
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 aggcaggtgc atcgagtgtt ctgtcagctg cgcgagcaat tgggttgat cgatcgcggc
 300
 ggccatggcc gaccgcgggt gcatgacctg cgccatagct tcgccgtgag acggatgatc
 360
 ctgtggcacc agcagggagc gaaccttgac caacgaatgc tggccctgtc cacgtacatg
 420
 ggccac
 426

<210> 1024
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 1024
 Ala Gly Leu Arg Val Ser Glu Ala Ile Asn Leu Ala Asp Ser Asp Ala
 1 5 10 15
 Asp Leu Asp Gly Gly Ile Leu Thr Ile Gln Gln Thr Lys Phe Gly Lys
 20 25 30
 Ser Arg Met Val Pro Leu His Pro Ser Val Ile Gly Pro Met Ala Ala

	35		40		45	
Tyr	Arg	Ala	Leu	Arg	Arg	Gln
	50		55		60	
Phe	Phe	Val	Gly	Ser	Arg	Gly
65			70		75	
Arg	Gln	Val	His	Arg	Val	Phe
	85		90		95	
Ile	Asp	Arg	Gly	Gly	His	Gly
	100		105		110	
Ser	Phe	Ala	Val	Arg	Arg	Met
	115		120		125	
Leu	Asp	Gln	Arg	Met	Leu	Ala
	130		135		140	

<210> 1025
 <211> 518
 <212> DNA
 <213> Homo sapiens

<400> 1025
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 120
 gatagcggcg ctgcgtacgc gatgatggat gagccgtggg gggaagggcg cgtcgccctcg
 180
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 240
 ccactcctga agagccgccg gttcttcgtg gacatcctga ccctgctgag cagccactgc
 300
 cagctctgcc ctgcagcccg gcacctggcc gtctacctgc tggaccactt catggatcgc
 360
 tacaacgtca ccacctccaa gcagctctac accgtggccg tctcctgcct cctgcttgca
 420
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 480
 atcctgagca gccagaactt caccctcacc aagaagga
 518

<210> 1026
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 1026
 Met Met Asp Glu Pro Trp Trp Glu Gly Arg Val Ala Ser Asp Val His
 1 5 10 15
 Cys Thr Leu Arg Glu Lys Glu Leu Lys Leu Pro Thr Phe Arg Ala His
 20 25 30
 Ser Pro Leu Leu Lys Ser Arg Arg Phe Phe Val Asp Ile Leu Thr Leu
 35 40 45
 Leu Ser Ser His Cys Gln Leu Cys Pro Ala Ala Arg His Leu Ala Val
 50 55 60
 Tyr Leu Leu Asp His Phe Met Asp Arg Tyr Asn Val Thr Thr Ser Lys

65					70					75					80
Gln	Leu	Tyr	Thr	Val	Ala	Val	Ser	Cys	Leu	Leu	Leu	Ala	Ser	Lys	Phe
				85					90					95	
Glu	Asp	Arg	Glu	Asp	His	Val	Pro	Lys	Leu	Glu	Gln	Ile	Asn	Ser	Thr
			100					105					110		
Arg	Ile	Leu	Ser	Ser	Gln	Asn	Phe	Thr	Leu	Thr	Lys	Lys			
		115					120					125			

<210> 1027

<211> 465

<212> DNA

<213> Homo sapiens

<400> 1027

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ggcccaaaag tcatcaaaga aaagctgaca caggagctga aggaccacaa cgccaccagc
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120
gtgctgggca gcctggtgaa caccngtcct gaagcacatc atnnctggct gaaggtcac
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aagatcccc tggacatggt ggctggattc aacacgcccc tggcacaagac catcgtggag
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ttccacatga cgactgaggc ccaagccacc atccgcatgg acaccagtgc aagtggcccc
360
accgcctgg tcctcagtga ctgtgccacc agccatggga gcctgcgcac ccaactgctg
420
cataagctct ccttcaagct gaacgcctca gctaagcagg tcatg
465

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<210> 1028

<211> 155

<212> PRT

<213> Homo sapiens

<400> 1028

Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys	Asp	His
1				5					10					15	
Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Lys	Ala	Met	Arg
			20					25					30		
Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser	Leu	Val	Asn	Thr
		35					40					45			
Xaa	Pro	Glu	Ala	His	His	Xaa	Trp	Leu	Lys	Val	Ile	Thr	Ala	Asn	Ile
	50					55					60				
Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp	Gln	Glu	Leu	Leu	Val
65				70					75					80	
Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe	Asn	Thr	Pro	Leu	Val	Lys
			85					90					95		
Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr	Glu	Ala	Gln	Ala	Thr	Ile	Arg
		100						105					110		
Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro	Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys
		115					120					125			
Ala	Thr	Ser	His	Gly	Ser	Leu	Arg	Ile	Gln	Leu	Leu	His	Lys	Leu	Ser

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 Ala Asn Arg Trp Gly Lys Ser Phe Thr Gly Gly Asn Pro Leu Gly Ser
 35 40 45
 Pro Cys Asp Ser Cys Thr Arg Ser Ser Gly Pro Ala Arg Asp Asn Phe
 50 55 60
 Pro His Leu Val Ser Asn Asn Asn Asn Asn Tyr Thr Leu Met Ser Ser
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 35 40 45
 Asp Pro Ala Ser Arg Ala Gln Ala Asn Asp Val His Gly Trp Ser Val
 50 55 60
 Val Val Asp Pro Leu Ala Tyr Gln Trp Arg His Pro Asn Trp Gln Gly
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 Arg Pro Trp His Glu Ala Val Ile Tyr Glu Leu His Val Gly Val Leu
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 180
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 300
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 360
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 420

aaagccgata gaggaatctt tttctgcggc accgggatgg gcatggccat cacggccaac
 480
 aaggtgccag gcattcgcgc ctgcaccgcc cagcactcct tctccgtaga gcggctcatc
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 <212> PRT
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 Val Ile Asp Val Gly Val Gln Ala Gly Asp Asp Thr Leu Tyr Pro Arg
 35 40 45
 Ile Gly Ile Lys Gly Ala His Val Ile Lys Asp Gly Lys Ala Asp Arg
 50 55 60
 Gly Ile Phe Phe Cys Gly Thr Gly Met Gly Met Ala Ile Thr Ala Asn
 65 70 75 80
 Lys Val Pro Gly Ile Arg Ala Cys Thr Ala His Asp Ser Phe Ser Val
 85 90 95
 Glu Arg Leu Ile Met Ser Asn Asp Ala His Val Leu Cys Leu Gly Gln
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 Arg

<210> 1035
 <211> 363
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 363

<210> 1036
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<213> Homo sapiens

<400> 1036

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Val	Cys	Val	Xaa	Glu	Ala	Val	Cys	Ile	Cys	Xaa	Cys	Leu	Cys	Ala	Cys
		35					40					45			
Thr	Xaa	Met	Cys	Ala	Cys	Met	Glu	Cys	Ile	Cys	Val	Cys	Val	Trp	Thr
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Val	Cys	Val	Ile	Met	Gln	Tyr	Val	Arg	Val	Cys	Val	Trp	Ser	Val	Ser
65					70					75				80	
Val	Trp	His	Val	Cys	Val	Tyr	Leu	Leu	Cys	Val	Ser	Val	Cys	Val	Xaa
			85						90				95		
Thr	Cys	Ile	Cys	Ile	Glu	Ser	Val	Cys	Ala	Val	Cys	Met	Cys	Val	Ser
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<210> 1037

<211> 5832

<212> DNA

<213> Homo sapiens

<400> 1037

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<210> 1038
 <211> 1485
 <212> PRT
 <213> Homo sapiens

<400> 1038
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 35 40 45
 Ser Tyr Ser Gly Pro Gly Pro Gly Met Gly Ile Ser Ala Asn Asn Gln
 50 55 60
 Met His Gly Gln Gly Pro Ser Gln Pro Cys Gly Ala Val Pro Leu Gly
 65 70 75 80
 Arg Met Pro Ser Ala Gly Met Gln Asn Arg Pro Phe Pro Gly Asn Met
 85 90 95
 Ser Ser Met Thr Pro Ser Ser Pro Gly Met Ser Gln Gln Gly Gly Pro
 100 105 110
 Gly Met Gly Pro Pro Met Pro Thr Val Asn Arg Lys Ala Gln Glu Ala
 115 120 125
 Ala Ala Ala Val Met Gln Ala Ala Ala Asn Ser Ala Gln Ser Arg Gln
 130 135 140
 Gly Ser Phe Pro Gly Met Asn Gln Ser Gly Leu Met Ala Ser Ser Ser
 145 150 155 160
 Pro Tyr Ser Gln Pro Met Asn Asn Ser Ser Ser Leu Met Asn Thr Gln
 165 170 175
 Ala Pro Pro Tyr Ser Met Ala Pro Ala Met Val Asn Ser Ser Ala Ala
 180 185 190
 Ser Val Gly Leu Ala Asp Met Met Ser Pro Gly Glu Ser Lys Leu Pro
 195 200 205
 Leu Pro Leu Lys Ala Asp Gly Lys Glu Glu Gly Thr Pro Gln Pro Glu
 210 215 220
 Ser Lys Ser Lys Asp Ser Tyr Ser Ser Gln Gly Ile Ser Gln Pro Pro
 225 230 235 240
 Thr Pro Gly Asn Leu Pro Val Pro Ser Pro Met Ser Pro Ser Ser Ala
 245 250 255
 Ser Ile Ser Ser Phe His Gly Asp Glu Ser Asp Ser Ile Ser Ser Pro
 260 265 270
 Gly Trp Pro Lys Thr Pro Ser Ser Pro Lys Ser Ser Ser Thr Thr
 275 280 285
 Thr Gly Glu Lys Ile Thr Lys Val Tyr Glu Leu Gly Asn Glu Pro Glu
 290 295 300
 Arg Lys Leu Trp Val Asp Arg Tyr Leu Thr Phe Met Glu Glu Arg Gly
 305 310 315 320
 Ser Pro Val Ser Ser Leu Pro Ala Val Gly Lys Lys Pro Leu Asp Leu

990

991

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Leu His His Glu His Pro Glu Arg Lys Arg Ala Pro Gln Thr Tyr Glu
          1220          1225          1230
Lys Glu Glu Asp Glu Asp Lys Gly Val Ala Cys Ser Lys Asp Glu Trp
          1235          1240          1245
Trp Trp Asp Cys Leu Glu Val Leu Arg Asp Asn Thr Leu Val Thr Leu
          1250          1255          1260
Ala Asn Ile Ser Gly Gln Leu Asp Leu Ser Ala Tyr Thr Glu Ser Ile
1265          1270          1275          1280
Cys Leu Pro Ile Leu Asp Gly Leu Leu His Trp Met Val Cys Pro Ser
          1285          1290          1295
Ala Glu Ala Gln Asp Pro Phe Pro Thr Val Gly Pro Asn Ser Val Pro
          1300          1305          1310
Ser Pro Gln Arg Leu Val Leu Glu Thr Leu Cys Lys Leu Ser Ile Gln
          1315          1320          1325
Asp Asn Asn Val Asp Leu Ile Leu Ala Thr Pro Pro Phe Ser Arg Gln
          1330          1335          1340
Glu Lys Phe Tyr Ala Thr Leu Val Arg Tyr Val Gly Asp Arg Lys Asn
1345          1350          1355          1360
Pro Val Cys Arg Glu Met Ser Met Ala Leu Leu Ser Asn Leu Ala Gln
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Gly Asp Ala Leu Ala Ala Arg Ala Ile Ala Val Gln Lys Gly Ser Ile
          1380          1385          1390
Gly Asn Leu Ile Ser Phe Leu Glu Asp Gly Val Thr Met Ala Gln Tyr
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Gln Gln Ser Gln His Asn Leu Met His Met Gln Pro Pro Pro Leu Glu
          1410          1415          1420
Pro Pro Ser Val Asp Met Met Cys Arg Ala Ala Lys Ala Leu Leu Ala
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Arg Leu Leu Asp Ile Ser Ile Ser Ala Val Leu Asn Ser Leu Val Ala
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<211> 379

<212> DNA

<213> Homo sapiens

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120

cagaggggag agaggggagag agtgtgagag ctaaggtttc gggagaagac tttgtggaaa
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aagtcttttg ctgggtcctg caacatagcc aggattcagt gacaggtgag gaccactcca
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<210> 1040
 <211> 125
 <212> PRT
 <213> Homo sapiens

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 Ser Ser Pro Val Thr Glu Ser Trp Leu Cys Cys Arg Thr Gln Pro Lys
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 Thr Phe Ser Thr Lys Ser Ser Pro Glu Thr Leu Ala Leu Thr Leu Ser
 65 70 75 80
 Pro Ser Leu Pro Ser Ala Pro Arg Leu Tyr Leu Val Ser Leu Cys Ala
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<210> 1041
 <211> 388
 <212> DNA
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 accccggtgg tgttctgggg tgccctggccg ctgcaccacg ccgcgtggac caacctgcgg
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 cacggcgcg ccatcatgga caccctggtg tcgctcggcg tcctcacttc gtacctctgg
 300
 tcggtatgga tgctgaccac aggcggcgag cacctctacc tggaggtagc cgtccaccgt
 360
 cacgacgctg atcctggccg gcaaattt
 388

<210> 1042
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 1042

Leu Val Ala Val Glu Ala Ile Gly Tyr Ile Ala Ser Ile Asp Lys Ala
 1 5 10 15
 Asp Met Ser Ile Glu Thr Ala Tyr Leu Pro Arg Leu Leu Val Ser Leu
 20 25 30
 Ala Leu Thr Ile Pro Val Leu Ala Leu Ser Met Ile Pro Ala Leu His
 35 40 45
 Phe Pro His Trp Pro Leu Trp Ala Leu Ala Leu Thr Thr Pro Val Val
 50 55 60
 Phe Trp Gly Ala Trp Pro Leu His His Ala Ala Trp Thr Asn Leu Arg
 65 70 75 80
 His Gly Ala Ala Ile Met Asp Thr Leu Val Ser Leu Gly Val Leu Thr
 85 90 95
 Ser Tyr Leu Trp Ser Val Trp Met Leu Thr Thr Gly Gly Glu His Leu
 100 105 110
 Tyr Leu Glu Val Ala Val His Arg His Asp Ala Asp Pro Gly Arg Gln
 115 120 125
 Ile

<210> 1043

<211> 555

<212> DNA

<213> Homo sapiens

<400> 1043

accggtgaaa ccctgatcgg ccaatcgttt tccaccgttc ccggcggcaa gggcgcaaac
 60
 caggcggtcg cttcggcgcg tcttggggcc gaagtcgcga tggtcggttg cgtgggtacc
 120
 gatgcctacg gcgcgcaatt acgcgacgca ttgttggttg aaggcatcga ttgccaggcc
 180
 gtcagcaccg tcgacgggttc cagcgggtgtg gcgctgatcg tggtaggatga cagcagccag
 240
 aatgcgatcg ttatcgtcgc cggtagcaat ggcgagctga ctccggccaa gttacagacc
 300
 tttgacagcg tgctgcaggc tgccgacgtg attgtctgcc agcttgagac gccgatggac
 360
 actgtcggcc atgcgcctaa gcgcggtcgc gaactgggca agacgggtgat cctcaatccg
 420
 gcgcccggcca gcggcccgtt gcctgaggat tggtagcccg ccatcgatta cctgattccc
 480
 aacgaaagcg aagcctcggc cttgagtggc gtggtggttg attcactgga cagcgccaag
 540
 gtcgctgcta cgcgt
 555

<210> 1044

<211> 185

<212> PRT

<213> Homo sapiens

<400> 1044

Thr Gly Glu Thr Leu Ile Gly Gln Ser Phe Ser Thr Val Pro Gly Gly

1	5	10	15
Lys Gly Ala Asn Gln Ala Val Ala Ser Ala Arg Leu Gly Ala Glu Val			
20	25	30	
Ala Met Val Gly Cys Val Gly Thr Asp Ala Tyr Gly Ala Gln Leu Arg			
35	40	45	
Asp Ala Leu Leu Val Glu Gly Ile Asp Cys Gln Ala Val Ser Thr Val			
50	55	60	
Asp Gly Ser Ser Gly Val Ala Leu Ile Val Val Asp Asp Ser Ser Gln			
65	70	75	80
Asn Ala Ile Val Ile Val Ala Gly Ser Asn Gly Glu Leu Thr Pro Ala			
85	90	95	
Lys Leu Gln Thr Phe Asp Ser Val Leu Gln Ala Ala Asp Val Ile Val			
100	105	110	
Cys Gln Leu Glu Thr Pro Met Asp Thr Val Gly His Ala Pro Lys Arg			
115	120	125	
Gly Arg Glu Leu Gly Lys Thr Val Ile Leu Asn Pro Ala Pro Ala Ser			
130	135	140	
Gly Pro Leu Pro Glu Asp Trp Tyr Ala Ala Ile Asp Tyr Leu Ile Pro			
145	150	155	160
Asn Glu Ser Glu Ala Ser Ala Leu Ser Gly Val Val Val Asp Ser Leu			
165	170	175	
Asp Ser Ala Lys Val Ala Ala Thr Arg			
180	185		

<210> 1045
 <211> 371
 <212> DNA
 <213> Homo sapiens

<400> 1045
 ctattgccat actaccgccg cggcaaccta caggacatga tcaacgccaa cctcttcaat
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 cactccaaat tccccgagac gcaccttatg aatctatttc tcggcgtctg caaggccctg
 120
 cgcgccatgc acgattacca cgcaccgccg gcagagcgca tgccaattgg gcaccgaagg
 180
 cagaccacca cccaggtgca aagcaacagt ggtagagcgg tcgctcatcg acgaaacgta
 240
 cggaagaaga cgaagagacg gagcaggaaa gacctgttat ggaatcacag aaccacatcg
 300
 ggcagggcgg cgagcacaaa accatatgcg catcgcgaca ttaaaccagg tacgtgctgc
 360
 aagctcctcg g
 371

<210> 1046
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 1046
 Leu Leu Pro Tyr Tyr Arg Arg Gly Asn Leu Gln Asp Met Ile Asn Ala
 1 5 10 15
 Asn Leu Phe Asn His Ser Lys Phe Pro Glu Thr His Leu Met Asn Leu

		20						25					30				
Phe	Leu	Gly	Val	Cys	Lys	Ala	Leu	Arg	Ala	Met	His	Asp	Tyr	His	Ala		
		35						40					45				
Pro	Pro	Ala	Glu	Arg	Met	Pro	Ile	Gly	His	Arg	Arg	Gln	Thr	Thr	Thr		
		50						55				60					
Gln	Val	Gln	Ser	Asn	Ser	Gly	Arg	Ala	Val	Ala	His	Arg	Arg	Asn	Val		
65						70				75				80			
Arg	Lys	Lys	Thr	Lys	Arg	Arg	Ser	Arg	Lys	Asp	Leu	Leu	Trp	Asn	His		
				85				90						95			
Arg	Thr	Thr	Ser	Gly	Arg	Ala	Ala	Ser	Thr	Lys	Pro	Tyr	Ala	His	Arg		
			100					105					110				
Asp	Ile	Lys	Pro	Gly	Thr	Cys	Cys	Lys	Leu	Leu							
		115						120									

<210> 1047

<211> 754

<212> DNA

<213> Homo sapiens

<400> 1047

natgcccaga aggacctgga cgaggcggtg ccagccctgg atgcggctct ggccagccta
 60
 cgcaacctca acaagaacga agtgaccag gtacgtgcca tgcagcggcc acccccgggt
 120
 gtgaaactgg tcatagaagc tgtgtgcatt atgaaaggca tcaagcccaa gaagggtgcct
 180
 ggagaaaagc caggcaccaa ggtggatgac tactgggagc ctggcaaggg gctgctgcag
 240
 gaccggggcc acttccttga gagcctcttc aagtttgaca aggacaacat tggagatgtg
 300
 gtgatcaaag ccatccagcc gtacatcgat aatgaagagt tccagccagc caccattgcc
 360
 aagggtgtcca aggggtgccc cttcatttgg ccgtgggggg gggcaatgcc caagtacccc
 420
 tttgtggcca aggccgtgga gccaagcgg caagccctgc tggaggccca ggatgacctg
 480
 ggggtgacac agaggatcct ggatgaggca aaacagcgcc ttcgtgaggt ggaggacggc
 540
 atcgccacaa tgcaggctaa gtaccgggaa tgcattacca agaaggagga gctggagctg
 600
 aagtgtgagc agtgtgagca gcggctgggc cacgctggca aggtgcgcac cctcctcctg
 660
 caaggcctgc aagcggggccc ggcccagaca ggggccagaa aggaccaggg cgccgggtggg
 720
 tcctgggggtg gctgtccaac cccctccctg gcaa
 754

<210> 1048

<211> 251

<212> PRT

<213> Homo sapiens

<400> 1048

Xaa Ala Gln Lys Asp Leu Asp Glu Ala Leu Pro Ala Leu Asp Ala Ala

1	5	10	15
Leu Ala Ser Leu Arg Asn Leu Asn Lys Asn Glu Val Thr Gln Val Arg			
20	25	30	
Ala Met Gln Arg Pro Pro Pro Gly Val Lys Leu Val Ile Glu Ala Val			
35	40	45	
Cys Ile Met Lys Gly Ile Lys Pro Lys Lys Val Pro Gly Glu Lys Pro			
50	55	60	
Gly Thr Lys Val Asp Asp Tyr Trp Glu Pro Gly Lys Gly Leu Leu Gln			
65	70	75	80
Asp Pro Gly His Phe Leu Glu Ser Leu Phe Lys Phe Asp Lys Asp Asn			
85	90	95	
Ile Gly Asp Val Val Ile Lys Ala Ile Gln Pro Tyr Ile Asp Asn Glu			
100	105	110	
Glu Phe Gln Pro Ala Thr Ile Ala Lys Val Ser Lys Gly Cys Pro Phe			
115	120	125	
Ile Trp Pro Trp Gly Gly Ala Met Pro Lys Tyr Pro Phe Val Ala Lys			
130	135	140	
Ala Val Glu Pro Lys Arg Gln Ala Leu Leu Glu Ala Gln Asp Asp Leu			
145	150	155	160
Gly Val Thr Gln Arg Ile Leu Asp Glu Ala Lys Gln Arg Leu Arg Glu			
165	170	175	
Val Glu Asp Gly Ile Ala Thr Met Gln Ala Lys Tyr Arg Glu Cys Ile			
180	185	190	
Thr Lys Lys Glu Glu Leu Glu Leu Lys Cys Glu Gln Cys Glu Gln Arg			
195	200	205	
Leu Gly His Ala Gly Lys Val Arg Thr Leu Leu Leu Gln Gly Leu Gln			
210	215	220	
Ala Gly Pro Ala Gln Thr Gly Ala Arg Lys Asp Gln Gly Ala Gly Gly			
225	230	235	240
Ser Trp Gly Gly Cys Pro Thr Pro Ser Leu Ala			
245	250		

<210> 1049

<211> 558

<212> DNA

<213> Homo sapiens

<400> 1049

cgcagcaata gctgcacttg accagactgg gctttgcaat aagcgcattc cccgggctga
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 atgctgcaga tccttacagg ctgactgcag ggtgtttcag attctcctgg agtcacacgt
 120
 gccagcttga tttcaagaaa caactagaat aacagttttc tgataagaag tctatagcac
 180
 tttatggctt acataatcca gagatagatg ggctgggcat gattcccatt ttctgttggg
 240
 gaaaccgact cacagagaag ttaagggaca agtataaagt gatgaaactg tgtactgaac
 300
 ctcatgtctc ccagactccc gggteccccg gctttttctc ggggcggccc cattcacatt
 360
 gcaattcatg gccggggcaa atgctcaccc acagagatat taagcactcc aacactccat
 420
 ccaccagggt gcagccaaag gattcagaag acaatgatca ttccatcagc atgcactatg
 480

cagctaaaga aaggttttgg catgctctgc tttattgttt cacagaagat aagaaaataa
 540
 actgcaaagt aacttaag
 558

<210> 1050
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 1050
 Met Ile Pro Ile Phe Cys Trp Gly Asn Arg Leu Thr Glu Lys Leu Arg
 1 5 10 15
 Asp Lys Tyr Lys Val Met Lys Leu Cys Thr Glu Pro His Val Ser Gln
 20 25 30
 Thr Pro Gly Ser Pro Gly Phe Phe Ser Gly Arg Pro His Ser His Cys
 35 40 45
 Asn Ser Trp Pro Gly Gln Met Leu Thr His Arg Asp Ile Lys His Ser
 50 55 60
 Asn Thr Pro Ser Thr Arg Leu Gln Pro Lys Asp Ser Glu Asp Asn Asp
 65 70 75 80
 His Ser Ile Ser Met His Tyr Ala Ala Lys Glu Arg Phe Trp His Ala
 85 90 95
 Leu Leu Tyr Cys Phe Thr Glu Asp Lys Lys Ile Asn Cys Lys Val Thr
 100 105 110

<210> 1051
 <211> 317
 <212> DNA
 <213> Homo sapiens

<400> 1051
 gcgttgagtc gggatgtcgc attcatgccc ggcgaacctt tttttgccga accggagcgt
 60
 aatccgggta atcttcgtct caatttcagt cacatcgcac cggagcgtct ggacgaaggt
 120
 ctcaagcgcc tggctgctgt catccgtcac gcacaggctg cacaagcggc ttaaggggag
 180
 ggccatgtac aaggtttatg gcgattacca gtcgggcaat tgctacaaga tcaagctgat
 240
 gctgcacctg ctggggcagg aatatcgctg gcacccgggg gacatcctca aggtgacacc
 300
 gagaccccg aattttt
 317

<210> 1052
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 1052
 Ala Leu Ser Arg Asp Val Ala Phe Met Pro Gly Glu Pro Phe Phe Ala
 1 5 10 15
 Glu Pro Glu Arg Asn Pro Gly Asn Leu Arg Leu Asn Phe Ser His Ile

	20		25		30										
Ala	Pro	Glu	Arg	Leu	Asp	Glu	Gly	Leu	Lys	Arg	Leu	Ala	Ala	Val	Ile
	35		40		45										
Arg	His	Ala	Gln	Ala	Ala	Gln	Ala	Ala							
	50		55												

<210> 1053
 <211> 318
 <212> DNA
 <213> Homo sapiens

<400> 1053
 caattggcta cgcgatccga acgggcgcat gggctcttat gactggcaag ccgtcgctcg
 60
 cggggagtgg gccctcgact atgcctacgc gatgtcgggtg aacctgacca ccgagaaccg
 120
 gcgtgcctgg gaacgcgacc tgctcgagcg ttatctgtgg cgcctcgccg aagagggtgt
 180
 cgccaacccg ccctcgttcg agcaagcgtg gctacgctac cggcaacagc cgttccacgt
 240
 cgggatcttc tcactcttga ccatcggcgc cggacgcttt caaccggcca tgcaaccggc
 300
 ggactcnnnn ccccnenc
 318

<210> 1054
 <211> 96
 <212> PRT
 <213> Homo sapiens

Met	Gly	Leu	Tyr	Asp	Trp	Gln	Ala	Val	Ala	Arg	Gly	Glu	Trp	Ala	Leu
1				5					10					15	
Asp	Tyr	Ala	Tyr	Ala	Met	Ser	Val	Asn	Leu	Thr	Thr	Glu	Asn	Arg	Arg
		20						25				30			
Ala	Trp	Glu	Arg	Asp	Leu	Leu	Glu	Arg	Tyr	Leu	Trp	Arg	Leu	Ala	Glu
	35					40					45				
Glu	Gly	Val	Ala	Asn	Pro	Pro	Ser	Phe	Glu	Gln	Ala	Trp	Leu	Arg	Tyr
	50				55					60					
Arg	Gln	Gln	Pro	Phe	His	Val	Gly	Ile	Phe	Ser	Leu	Leu	Thr	Ile	Gly
65			70				75							80	
Ala	Gly	Arg	Phe	Gln	Pro	Ala	Met	Gln	Pro	Ala	Asp	Ser	Xaa	Pro	Xaa
		85					90						95		

<210> 1055
 <211> 391
 <212> DNA
 <213> Homo sapiens

<400> 1055
 tacaatgtat catcaaccag aaatacaatg agaaccacct gccagtctcc caaatactat
 60
 ctgcagccac tcattttaact ctcttggtga gctccacgtg ggccgtctga actctcttag
 120

aagaatcatc tctctgctca ggcaccggga gcaaggggca tctgtcgctc tgcagaacgg
 180
 aggggaccag gcctgatgaa caccatcctg ggcccagaaa cctgggaggg taaagagaac
 240
 tgccaggggt gaagtccaag gatgggaaaa aggcctccgg ggcagagtcc tgaaatgtca
 300
 gaagtacacc aaagaggaaa cagcatcacg ttattgctga ggcagggcct cattctgttg
 360
 ccaaggctgc agtgcagtgg tgacaccatg g
 391

<210> 1056
 <211> 83
 <212> PRT
 <213> Homo sapiens

<400> 1056
 Met Val Ser Pro Leu His Cys Ser Leu Gly Asn Arg Met Arg Pro Cys
 1 5 10 15
 Leu Ser Asn Asn Val Met Leu Phe Pro Leu Trp Cys Thr Ser Asp Ile
 20 25 30
 Ser Gly Leu Cys Pro Gly Gly Leu Phe Pro Ile Leu Gly Leu His Pro
 35 40 45
 Trp Gln Phe Ser Leu Pro Ser Gln Val Ser Gly Pro Arg Met Val Phe
 50 55 60
 Ile Arg Pro Gly Pro Leu Arg Ser Ala Glu Arg Gln Met Pro Leu Ala
 65 70 75 80
 Pro Gly Ala

<210> 1057
 <211> 341
 <212> DNA
 <213> Homo sapiens

<400> 1057
 gaattccctg cgcgtgtgac gccggtcgcc gagcaactcg gcgtgtcgct gacgctgcat
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 cccgatgatc cgccgcgtcc gctgttcggg ttgccgcgca ttgcgtccag cgccgaggac
 120
 tatcaggcgc tgttcgatgc ggtaccgtcc aaggcgaacg gcacatgcct gtgcacgggt
 180
 tcgctcggcg tgcgcgcgga gaacgatctg cctgaaatgg ccgaacgttt cggcccgcgt
 240
 atcgcctttg cgcacatctgcg cgcgaccaag cgcgacgccg atggcctgtc gtttcatgaa
 300
 tccgaccatc tcgacggcga tgtcgacatg gtcgcgtgct c
 341

<210> 1058
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 1058

Glu Phe Pro Ala Arg Val Thr Pro Val Ala Glu Gln Leu Gly Val Ser
 1 5 10 15
 Leu Thr Leu His Pro Asp Asp Pro Pro Arg Pro Leu Phe Gly Leu Pro
 20 25 30
 Arg Ile Ala Ser Ser Ala Glu Asp Tyr Gln Ala Leu Phe Asp Ala Val
 35 40 45
 Pro Ser Lys Ala Asn Gly Ile Cys Leu Cys Thr Gly Ser Leu Gly Val
 50 55 60
 Arg Ala Glu Asn Asp Leu Pro Glu Met Ala Glu Arg Phe Gly Pro Arg
 65 70 75 80
 Ile Ala Phe Ala His Leu Arg Ala Thr Lys Arg Asp Ala Asp Gly Leu
 85 90 95
 Ser Phe His Glu Ser Asp His Leu Asp Gly Asp Val Asp Met Val Ala
 100 105 110
 Cys

<210> 1059

<211> 372

<212> DNA

<213> Homo sapiens

<400> 1059

nagctgaccg gctggcagat caacatcatg acgccggaag aaagcgtgaa ccgccgggaa
 60
 gtcgagcgtt cgggcctgcg caccacgttc atgaacaagc tggacgtcga tgaggaagtc
 120
 gccgacatcc tgatcgacga aggtttcacc ggtatcgagg aaatcgccta cgtcccatg
 180
 caggaactgc tggagatcga ggcgttcgac gaagacacca tcaacgagtt gcgcgcccgt
 240
 gcccgcaatg cgctgctgac cgaggccatc gccaggaag agcgccttga gaccgcgcag
 300
 gatctgcttg aactcgaagg cgtgacgccg gaactggctg ccaagctggc cgagcgtcaa
 360
 gtgcgtacgc gt
 372

<210> 1060

<211> 124

<212> PRT

<213> Homo sapiens

<400> 1060

Xaa Leu Thr Gly Trp Gln Ile Asn Ile Met Thr Pro Glu Glu Ser Val
 1 5 10 15
 Asn Arg Arg Glu Val Glu Arg Ser Gly Leu Arg Thr Thr Phe Met Asn
 20 25 30
 Lys Leu Asp Val Asp Glu Glu Val Ala Asp Ile Leu Ile Asp Glu Gly
 35 40 45
 Phe Thr Gly Ile Glu Glu Ile Ala Tyr Val Pro Met Gln Glu Leu Leu
 50 55 60
 Glu Ile Glu Ala Phe Asp Glu Asp Thr Ile Asn Glu Leu Arg Ala Arg

65		70		75		80									
Ala	Arg	Asn	Ala	Leu	Leu	Thr	Glu	Ala	Ile	Ala	Gln	Glu	Glu	Arg	Leu
			85					90						95	
Glu	Thr	Ala	Gln	Asp	Leu	Leu	Glu	Leu	Glu	Gly	Val	Thr	Pro	Glu	Leu
		100					105						110		
Ala	Ala	Lys	Leu	Ala	Glu	Arg	Gln	Val	Arg	Thr	Arg				
		115					120								

<210> 1061
 <211> 456
 <212> DNA
 <213> Homo sapiens

<400> 1061
 tctagactcc atggcaccgg gctgagcggg taagtaagaa agataaaaag tgccttttgc
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 cccttcgagg aaaccctttt gcaggccaag caagggctgc aagtgtttgg gagctgagag
 120
 gagaaggagg attctggagc attgtatttg gcagccggag cgggcagtgg gcgggggggtt
 180
 gggacacgaa gggctcttcg gaccctgtg cctcttctgc cccaagggcg agaagacggg
 240
 cttegcagcg accctcgggg gtccatggag ccgcctgcct tcgccccctc gctcttccca
 300
 ggtctgaacc tggatgggga gaagaaattg aagtgccttg gagacggggg ggcttaaaac
 360
 actagggagc ctcategccc agccttgggc ccactttcct ttcgatcgtg aggattccgc
 420
 accccgaagc cgtcttctcg gggctccggg gcgcgc
 456

<210> 1062
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 1062
Met Arg Leu Pro Ser Val Leu Ser Pro Pro Val Ser Lys Ala Leu Gln
1 5 10 15
Phe Leu Leu Pro Ile Gln Val Gln Thr Trp Glu Glu Arg Gly Gly Glu
20 25 30
Gly Arg Arg Leu His Gly Pro Pro Arg Val Ala Ala Lys Pro Val Phe
35 40 45
Ser Pro Leu Gly Gln Lys Arg His Arg Gly Pro Lys Ser Pro Ser Cys
50 55 60
Pro Asn Pro Pro Pro Thr Ala Arg Ser Gly Cys Gln Ile Gln Cys Ser
65 70 75 80
Arg Ile Leu Leu Leu Leu Ser Ala Pro Lys His Leu Gln Pro Leu Leu
85 90 95
Gly Leu Gln Lys Gly Phe Leu Glu Gly Ala Lys Gly Thr Phe Tyr Leu
100 105 110
Ser Tyr Leu Pro Ala Gln Pro Gly Ala Met Glu Ser Arg
115 120 125

<210> 1063
<211> 3760
<212> DNA
<213> Homo sapiens

<400> 1063
ntagtagaga cagggtttca ccatgttggc caggctggtc ttgaactcct gagcttgtga
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tccacccgcc tcagcctccc aaagtgtggt gattacaggc gtgacgactg caccagcct
120
taaggtctta taactagtaa atatctgcat taaagaacga gttgaatgaa aattctgata
180
aattcctact taaagtgtat ccaaagaaaa cggaaaaagt ctaggagtta gtgatattag
240
attcagaaga atgagctttg taattcttaa aaattagtct cagaatagaa aggattttaa
300
aagtaattga gtaaagtcac aggaaatgtg accatataaa ggaatggctc taaatgtatt
360
aatccagaag gaagcaacag gttaaacagt aagaggtaag aaacaaaaaa taaggaacga
420
gagagagaga gtgacaggga gagagagaca gagcggggaa ggagagaatg agaaggaaaa
480
tcaggaaaac gaggagaaac agaattaagg aggtgatact ggaatagtat cagaccattc
540
tgaatcaatt taagaattgc catgtctaata tcttatatgg aagatttgaa atacaaggat
600
attgaaagga ataacaaatt ataatgaatg catagaaatc cttatgtaat ccaaggtcac
660
taatttgaag gaagacatca agaaaatgtg atctagaaat aaagggttgag attgctccat
720
ttacaaaatt attatgctct ataatcttcc catatgcaaa tatttcatat tccctctttt
780
gtcccatgga catatttcac agcaacaacg aatcaagtgc tgacctaaat ggggtatctg
840
ttaaaactta gtatattgat atccttcacc cactccagg aacgttcgct acgctaggac
900
tgcaccttgg gaacagaatt ttagagatga tcatctctta catcagaagc aggatctaaa
960
tgatccctgg atgcccaatt tctgaccct gctattgttg tgggtggcaa gataagagga
1020
gttgcacac agatgaaaaa gtaaggccga agaagaccag agaagagttg gttgaatgtg
1080
tagatataag atccatctgt gacattgtag aatgaaattt caccggcttc atagtccaag
1140
aaaatcccaa tgcagtgagg actttccagt tggagaagag gcactgatgg ggaggcaagg
1200
accatgtact cattcccttt cagcagccac agggcccaga cccattctc aggagatggc
1260
gtggtttccc cctttcttgg cagtgtgtct tgacagacc ctaaacccca ctctgctcct
1320
tctcccacca gaacctccca gtaatgcctc cctgatgaga agctctgcaa acccaggatg
1380
cagggccatg tgtcaaactg ctcagggttg ttggggacat ccctccatgg ttctccatcc
1440

tgcacactgc gcaggtcggc ggtcaagagc agactcgggt gcgccgtggc gggatccagc
1500
tttacatcca cttggaactt ccttaagagc tccctcctcc cagggatgca gcatgctgtc
1560
ttcagttcca tggggatgtt ctctgcttcc agccttgtga cagccttact tctgctcagg
1620
actcctctca caccctccag cagacccagg gctgggcgct ggcacctctc ctgcagctca
1680
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1740
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1800
atggctctgg aacttatgag gaaagagttg gaggacgcct tgactcagga ggccaacgtg
1860
gggaaaaaga ctgtcatttg gaaggagaaa gtggaaatgc agaggcagcg cttcagattg
1920
gagtttgaga agcatcgtgg ctttctggcc caggaggagc aacggcagct gaggcggctg
1980
gaggcggagg agcgagcgac gctgcagaga ctgcgggaga gcaagagccg gctgggtccag
2040
cagagcaagg ccctgaagga gctggcggat gagctgcagg agaggtgcc a gcgccagcc
2100
ctgggtctgc tggaggggtg gagaggagtc ctgagcagaa gtaaggctgt cacaaggctg
2160
gaagcagaga acatcccat ggaactgaag acagcatgct gcatccctgg gaggagggag
2220
ctcttaagga agttccaagt ggatgtaaag ctggatcccc ccacggcgca cccgagtctg
2280
ctcttgaccg ccgacctgcg cagtgtgcag gatggagaac catggaggga tgtccccaac
2340
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2400
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2580
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 3420
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 3480
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<210> 1064

<211> 483

<212> PRT

<213> Homo sapiens

<400> 1064

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His	Gly	Ser	Pro	Ser	Cys	Thr	Leu	Arg	Arg	Ser	Ala	Val	Lys	Ser	Arg
			20					25					30		
Leu	Gly	Cys	Ala	Val	Ala	Gly	Ser	Ser	Phe	Thr	Ser	Thr	Trp	Asn	Phe
		35					40					45			
Leu	Lys	Ser	Ser	Leu	Leu	Pro	Gly	Met	Gln	His	Ala	Val	Phe	Ser	Ser
	50					55					60				
Met	Gly	Met	Phe	Ser	Ala	Ser	Ser	Leu	Val	Thr	Ala	Leu	Leu	Leu	Leu
65					70				75					80	
Arg	Thr	Pro	Leu	Thr	Pro	Ser	Ser	Arg	Pro	Arg	Ala	Gly	Arg	Trp	His
				85				90					95		
Leu	Ser	Cys	Ser	Ser	Ser	Ala	Ser	Ser	Phe	Arg	Ala	Leu	Leu	Cys	Trp
			100					105					110		
Thr	Ser	Arg	Leu	Leu	Leu	Ser	Arg	Ser	Leu	Cys	Ser	Val	Ala	Arg	Ser
		115					120					125			
Ser	Ala	Ser	Ser	Arg	Leu	Ser	Tyr	Gln	Val	Lys	Leu	Gln	Met	Ala	Leu
	130					135					140				
Glu	Leu	Met	Arg	Lys	Glu	Leu	Glu	Asp	Ala	Leu	Thr	Gln	Glu	Ala	Asn
145				150						155				160	
Val	Gly	Lys	Lys	Thr	Val	Ile	Trp	Lys	Glu	Lys	Val	Glu	Met	Gln	Arg
			165					170					175		
Gln	Arg	Phe	Arg	Leu	Glu	Phe	Glu	Lys	His	Arg	Gly	Phe	Leu	Ala	Gln

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<210> 1065
<211> 892
<212> DNA
<213> Homo sapiens
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<400> 1065
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120
ttgtccagtc tggaaggggg gaagaagaga tgaggggaag gctgtccagg ggggtgcaag
180
gccctagaga cccagcagag aagggaactt ggccactgaa ggggccctcc cattgtggct
240
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ctggttcctt agagcagctc cagcttcttg gcctcccccg tctgatgctt agctcatccc
 300
 atcccctgga gtgctgtgga gcttagatga aacagcccag tgctcactct tcaatgagcc
 360
 caccagagc agcatcaaga tgcagttggc ggggtactgg aactggcttg gcaagggctg
 420
 cgcaggcaac aggtcccagc aagagtcagc tagcctagct cagccctgca cacctggaga
 480
 cctgggggtg ctccagacac ctcgccctt taggtccctt taattgaatg tgtgtggatc
 540
 agtgaagggt gaggaatcat ttctctatgg cccaagacgt ttctctctgc agttgtcatg
 600
 ttagtacctg ccagcttttc ctctcttaca taaatttcat gccagagcct ggaaatgtgt
 660
 gccctttgta ggaggggcat cacaggctgg ctcacctcag cagtgccagg cagagcccgt
 720
 ccctctcatt gcaggaggcg catgaagcgt gtctgggacc gagctgtgga gttcctggcc
 780
 tccaacgaat cccggatcca gacggagtcc caccgcgttg caggagagga catgctggtg
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 892

<210> 1066

<211> 76

<212> PRT

<213> Homo sapiens

<400> 1066

Met	Cys	Ala	Leu	Cys	Arg	Arg	Gly	Ile	Thr	Gly	Trp	Leu	Thr	Ser	Ala
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Val	Pro	Gly	Arg	Ala	Arg	Pro	Ser	His	Cys	Arg	Arg	Arg	Met	Lys	Arg
			20					25					30		
Val	Trp	Asp	Arg	Ala	Val	Glu	Phe	Leu	Ala	Ser	Asn	Glu	Ser	Arg	Ile
		35					40				45				
Gln	Thr	Glu	Ser	His	Arg	Val	Ala	Gly	Glu	Asp	Met	Leu	Val	Leu	Arg
	50					55				60					
Trp	Thr	Lys	Pro	Ser	Ser	Phe	Ser	Asp	Ser	Glu	Arg				
65					70					75					

<210> 1067

<211> 418

<212> DNA

<213> Homo sapiens

<400> 1067

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 120
 ggactagaca tctggaaagc ccgagtctcc gctgacatcg aaggcgactg gactatgcac
 180
 gttgaaggct ggtcagacac ctgggggcacg tggcatcaca atgccaatgc caagctcgcc
 240

gctgccatcg acgtcgaact ggtgtgcgcc gaaggccatg ccctcataaa cgaggcggtc
 300
 cggcacgccg agcaatccgg ggatactgac gcgatcacgg ctctgcgcga gaccgatgcc
 360
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 418

<210> 1068
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 1068
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 Gly Ala Ser Val Val Leu Thr Asp Pro Glu Gly Asn Arg His Leu Thr
 20 25 30
 Asp Met His Gln Val Glu Pro Trp Gly Leu Asp Ile Trp Lys Ala Arg
 35 40 45
 Val Ser Ala Asp Ile Glu Gly Asp Trp Thr Met His Val Glu Gly Trp
 50 55 60
 Ser Asp Thr Trp Gly Thr Trp His His Asn Ala Asn Ala Lys Leu Ala
 65 70 75 80
 Ala Ala Ile Asp Val Glu Leu Val Cys Ala Glu Gly His Ala Leu Ile
 85 90 95
 Asn Glu Ala Val Arg His Ala Glu Gln Ser Gly Asp Thr Asp Ala Ile
 100 105 110
 Thr Ala Leu Arg Glu Thr Asp Ala Asn Leu Thr Leu Asp Arg Ala Pro
 115 120 125
 Asp Ser Leu Gln Gln Val Ile Asn Thr Tyr Ala
 130 135

<210> 1069
 <211> 371
 <212> DNA
 <213> Homo sapiens

<400> 1069
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 120
 ttttctggag ctgaacatct caggtgccat gtaaggcttg gtgccagcca tggaggagac
 180
 ctgcgttatc acctgcaaca gaacgtccac ttcaaggaag aaacagtga gctcttcac
 240
 tgtgagctgg tcatggccct ggactacctg cagaaccagc gcatcattca cagggatatg
 300
 aagcctgaca atattttact tgacgaacat gggcacgtgc acatcacaga tttcaacatt
 360
 gctgcgatgc t
 371

<210> 1070

<211> 123
 <212> PRT
 <213> Homo sapiens

<400> 1070
 Xaa Tyr Asn Phe Leu Ala Gly Ser Thr Gly Ala Asn Met Ile Arg Ser
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 Pro Ala Ser Gln Gln Phe Ile Cys Arg His Ser Gln Gly Pro Pro Val
 20 25 30
 Asn Ser Lys Gly Ile Ala Cys Ser Phe Ser Gly Ala Glu His Leu Arg
 35 40 45
 Cys His Val Arg Leu Gly Ala Ser His Gly Gly Asp Leu Arg Tyr His
 50 55 60
 Leu Gln Gln Asn Val His Phe Lys Glu Glu Thr Val Lys Leu Phe Ile
 65 70 75 80
 Cys Glu Leu Val Met Ala Leu Asp Tyr Leu Gln Asn Gln Arg Ile Ile
 85 90 95
 His Arg Asp Met Lys Pro Asp Asn Ile Leu Leu Asp Glu His Gly His
 100 105 110
 Val His Ile Thr Asp Phe Asn Ile Ala Ala Met
 115 120

<210> 1071
 <211> 998
 <212> DNA
 <213> Homo sapiens

<400> 1071
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 120
 cccacccgaa gtacgtggcc ttggagtgcc attcgcactc cacttggcca ccgtttgcat
 180
 tcgacctaac cagcaattgc atctcgtttg acctgctcgc gttgtcaaca tcatagcaac
 240
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 360
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 420
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 480
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 540
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 660
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 720
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 780

gcgtaccctt tgggttgtgg cgcttacggt ggtgatgatg gttggcgaaa tcgtcgccgg
840
ctatctcact ggctcaatgg ctttacttgc cgacggggtt tcacaaggca accccatgca
900
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998

<210> 1072
<211> 72
<212> PRT
<213> Homo sapiens

<400> 1072
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Arg Ile Ala Gly Gln Ile Gln Ala Val Glu Arg Ala Leu Glu Ser Asp
20 25 30
Ala Asp Cys Ala Lys Thr Leu His Leu Val Ala Ala Thr Arg Gly Ala
35 40 45
Ile Asn Gly Leu Met Asp Glu Ile Ile Glu Asp His Ala Arg Lys His
50 55 60
Val Ala Ser Pro Thr Leu Ser Asp
65 70

<210> 1073
<211> 468
<212> DNA
<213> Homo sapiens

<400> 1073
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ttccccact gataaaatct tgcttctctt caaactccta ggcaaatttc tctacttca
180
gaaagtcttg tttctccata tccttcgtaa ccaccacctg gtgcacatgc tgaaggcaga
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300
catcctctgt ataataattg gttttcacct ctttatgaac tcttttgat tctcattact
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468

<210> 1074
<211> 134
<212> PRT
<213> Homo sapiens

<400> 1074

Met Asp Asn Phe Leu Phe Phe Lys Tyr Thr Leu Pro Met Ser Gln Leu
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 Gly Cys Phe Ser Pro Thr Asp Lys Ile Leu Leu Leu Phe Lys Leu Leu
 20 25 30
 Gly Lys Phe Leu Leu Leu Gln Lys Val Leu Phe Leu His Ile Leu Arg
 35 40 45
 Asn His His Leu Val His Met Leu Lys Ala Glu Phe Ile Val Ser Ser
 50 55 60
 Pro Ser Leu Ser Asn Ser Phe Ala Gln Thr Leu Arg Tyr Ser Phe Ile
 65 70 75 80
 Leu Cys Ile Ile Phe Gly Phe His Leu Phe Met Asn Ser Phe Val Phe
 85 90 95
 Ser Leu Leu Ala Leu Glu Pro Arg Thr Tyr His Gly Phe Lys Val Cys
 100 105 110
 Phe Asn Glu Leu Asn Gly Ile Asn Phe Val Val Leu Met Gln Ile Gln
 115 120 125
 Met Pro Leu Asn Thr Asp
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<210> 1075

<211> 1633

<212> DNA

<213> Homo sapiens

<400> 1075

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 180
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 240
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 300
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 480
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 600
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 660
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 720
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 780
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cgtcagggtgc catgtgctgg agaagatcgt ggagccccgc ggctgcttcg gcctcaccgc
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 1080
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 1200
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 1620
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 1633

<210> 1076
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 1076
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 Cys Ser Pro Thr Glu Glu Gln Gly Gln Pro Thr Leu Gln Thr Ser Pro
 20 25 30
 Pro Gly Ala Pro Pro Ala Val Trp Pro Thr Ser Ala Pro Pro Ile Ala
 35 40 45
 Thr Ser Thr Ser Trp Lys Cys Pro Thr Pro Arg Pro Pro Pro Gln Trp
 50 55 60
 Ala Gly Pro Ser Ala Ser Ala Leu Asp Ala Asn Pro Pro Ser Ser Ala
 65 70 75 80
 Leu Thr Arg Ser Lys Ala Thr
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<210> 1077
 <211> 419
 <212> DNA
 <213> Homo sapiens

<400> 1077

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 180
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 240
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 300
 gtgctcccgc cagatgtcgt tactcctgca gaacttgatg ctatcgttgc acgcgacgcc
 360
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 419

<210> 1078
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 1078
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 Trp Thr Cys Asn Ala Asn Glu Ala Thr Cys Leu Arg Leu Ala Gly Ala
 20 25 30
 Pro Ser Pro Ser Asp Ala Leu Phe His Pro Glu Phe Thr Tyr Pro Ile
 35 40 45
 Phe Gly Glu Ala Glu Ala Ile Tyr Gly Tyr Asn Gly Leu His Met Asn
 50 55 60
 Leu Ala Phe Ala Ser Gly Ser Leu Val Pro Ser Leu Glu Ile Thr Tyr
 65 70 75 80
 Arg Ala Lys Asn Thr Thr Thr Ser Ala Lys Val Asp Asp Val Glu Gln
 85 90 95
 Ala Leu Arg Gly Val Leu Pro Pro Asp Val Val Thr Pro Ala Glu Leu
 100 105 110
 Asp Ala Ile Val Ala Arg Asp Ala Arg Ala Val Arg Ala His Leu Arg
 115 120 125
 Arg Arg Ala Pro Arg Leu Arg Arg Thr Leu Ala
 130 135

<210> 1079
 <211> 584
 <212> DNA
 <213> Homo sapiens

<400> 1079
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 120
 gctcaaactg ctcccaagc cagcagggag gggaaccatg ctgcctgctg acctgggtag
 180
 ttctatttag gtcttgtgac acaacagtgg gcaaggtgat gccctctgtg accaaaagta
 240

ttaccacca gttccccag gccctccctt tcgtctgcaa agacacacat ctgtttcact
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 gtgtcttctg caaagacaca catctgtttc actgggggtt tctgcaaaga caccatttg
 360
 tttcccttt taagggtttt ccctccatc ttgtctattt ttaaaaaaat aaaccgggtt
 420
 cccaggatag ccttcccccc cagatcaaga gcccatgtga aatgaggggg cgcacttgac
 480
 cacagcacct tgttcccttc tgtaatctag acacttctgc acaatagagg gccaccct
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 584

<210> 1080
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 1080
 Met Leu His Val Val Ser Ala Ser Gln Pro Trp Glu Met Tyr Pro His
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 Ala Val Ala Ser Thr Ile Gly Leu Leu Phe Leu Leu Cys Ser Asn Cys
 20 25 30
 Phe Pro Ser Gln Gln Gly Gly Glu Pro Cys Cys Leu Leu Thr Trp Val
 35 40 45
 Val Leu Phe Arg Ser Cys Asp Thr Thr Val Gly Lys Val Met Pro Ser
 50 55 60
 Val Thr Lys Ser Ile Tyr Pro Lys Phe Pro Gln Ala Leu Pro Phe Val
 65 70 75 80
 Cys Lys Asp Thr His Leu Phe His Cys Val Phe Cys Lys Asp Thr His
 85 90 95
 Leu Phe His Trp Gly Phe Leu Gln Arg His Pro Phe Val Ser Pro Phe
 100 105 110
 Lys Gly Phe Pro Leu His Leu Val Tyr Phe
 115 120

<210> 1081
 <211> 3077
 <212> DNA
 <213> Homo sapiens

<400> 1081
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 120
 tatatccaca atgggaagaa atccagggcc ttaagcccc tatctcctgt ggccatagag
 180
 cagacatctc ttaagatgat gcaggcagta ggaggtgcac ctgcacgtcc cactggagaa
 240
 tatatctgta atcaatgtgg tgctaagtac acatccctag acagctttca gactcaccta
 300
 aaaactcatc tcgacactgt gcttccaaaa ttgacctgtc ctgagtgcac caaggaattc
 360

cccaaccaag aatccttgct gaagcatgtt accattcact ttatgatcac ttcaacgtat
420
tacatctgtg agagttgtga caagcaattc acatcagtgg atgaccttca gaaacacctg
480
ctggacatgc acacctttgt cttctttegc tgcaccctct gccaggaagt ttttgactca
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660
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720
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780
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840
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1020
gcctacacta tggaaacttt gctgcagaat caccagctcc gagaccacaa catcagacct
1080
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<211> 757

<212> PRT

<213> Homo sapiens

<400> 1082

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Lys	Asn	Ile	Pro	Leu	Ala	Leu	Asn	Tyr	Ile	His	Asn	Gly	Lys	Lys	Ser
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Arg	Ala	Leu	Ser	Pro	Leu	Ser	Pro	Val	Ala	Ile	Glu	Gln	Thr	Ser	Leu
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Lys	Met	Met	Gln	Ala	Val	Gly	Gly	Ala	Pro	Ala	Arg	Pro	Thr	Gly	Glu
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Tyr	Ile	Cys	Asn	Gln	Cys	Gly	Ala	Lys	Tyr	Thr	Ser	Leu	Asp	Ser	Phe

1017

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 Arg Gln Gly Gly Gly Thr Glu Thr Arg Cys Ser Ser Cys Asn Val Lys
 580 585 590
 Phe Glu Ser Glu Ser Glu Leu Gln Asn His Ile Gln Thr Ile His Arg
 595 600 605
 Glu Leu Val Pro Asp Ser Asn Ser Thr Gln Leu Lys Thr Pro Gln Val
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 Ser Pro Met Pro Arg Ile Ser Pro Ser Gln Ser Asp Glu Lys Lys Thr
 625 630 635 640
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 645 650 655
 Gln Val His Val Ala Asn His Met Ile Asp Glu Gly Leu Asn His Glu
 660 665 670
 Cys Lys Leu Cys Ser Gln Thr Phe Asp Ser Pro Ala Lys Leu Gln Cys
 675 680 685
 His Leu Ile Glu His Ser Phe Glu Gly Met Gly Gly Thr Phe Lys Cys
 690 695 700
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 Ile Phe Ser Ala His Gly Gln Glu Asp Lys Ile Tyr Asp Cys Thr Gln
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 <212> DNA
 <213> Homo sapiens

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 420
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<210> 1084
<211> 142
<212> PRT
<213> Homo sapiens

<400> 1084
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35 40 45
Asp Asp Val Val Ser Leu Val Lys Asp Ala Asn Leu Arg Gly Arg Gly
50 55 60
Gly Ala Gly Phe Pro Thr Gly Met Lys Trp Ser Phe Val Pro Lys Asp
65 70 75 80
Asn Pro Asn Pro Thr Tyr Leu Val Val Asn Gly Asp Glu Ser Glu Pro
85 90 95
Gly Thr Cys Lys Asp Met Pro Leu Met Met Ala Ser Pro His Thr Leu
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Val Glu Gly Val Ile Ile Ala Ser Tyr Ala Ile Lys Ala Lys Met Ala
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Phe Ile Tyr Ile Arg Gly Glu Val Leu His Val Val Arg Arg
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<210> 1085
<211> 374
<212> DNA
<213> Homo sapiens

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<400> 1086

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Phe Phe Tyr Arg Asp Ile Tyr Lys Ser Asp Tyr Ser Phe Asp Leu His
           35           40           45
Gln Asp Tyr Glu Arg Ser Lys Glu Asn Phe Leu Lys Met Ile Gly Asp
           50           55           60
Ser Leu Leu Ala Glu Leu Asn Leu Val Asp Ile Asp Thr Val Arg Lys
65           70           75           80
Ile Ala Asn Ser Pro Leu Gly Ser Ser Glu Thr Leu Tyr Asp Phe Glu
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Arg Met Thr His Met Glu Val Trp Leu Arg Glu Asn Tyr Val
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<210> 1087

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<212> DNA

<213> Homo sapiens

<400> 1087

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<210> 1088

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<212> PRT

<213> Homo sapiens

<400> 1088

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Asp His Gly Val Ser Ile Arg Val Xaa His His Cys Ala Trp Pro Ile
           35           40           45
His Arg Ser Leu Gly Val Gln Ser Thr Ala Arg Ala Ser Phe Tyr Phe
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Tyr Asn Thr Phe Pro Glu Val Asp Ala Leu Ala Ser Ala Val Arg Ala

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<210> 1089
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<210> 1090
 <211> 103
 <212> PRT
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 35 40 45
 Phe Asn Leu Ala Lys Gly Leu Leu Gly Gln Gly His Pro Ser Leu Leu
 50 55 60
 Leu Gly Ala Ser Ile Phe Leu His Ser Val Lys Asn Gly Gly Val Ile
 65 70 75 80
 Gln Lys Tyr Pro Pro Tyr Cys Gln Gly Phe Gly Glu Gly Ser Lys Lys

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 <212> PRT
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 35 40 45
 Gly Arg Lys Gln Pro Pro Val Ser Glu Ser His Trp Arg Thr Leu Leu
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 Gln Asp Met Leu Thr Met Gln Gln Asn Val Tyr Thr Cys Leu Asp Ser
 65 70 75 80
 Asp Ala Cys Tyr Glu Ile Phe Thr Glu Ser Leu Leu Cys Ser Ser Arg
 85 90 95
 Leu Glu Asn Ile His Leu Ala Gly Gln Met Met His Cys Ser Ala Cys
 100 105 110
 Ser Glu Asn Pro Pro Ala Gly Ile Ala His Lys Gly Lys Pro His Tyr
 115 120 125
 Arg Val Ser Tyr Glu Lys Ser Ile Asp Leu Val Leu Ala Ala Ser Arg
 130 135 140
 Glu Tyr Phe Asn Ser Ser Thr Asn Leu Thr Asp Ser Cys Met Asp Leu
 145 150 155 160
 Ala Arg Cys Cys Leu Gln Leu Ile Thr Asp Arg Pro Pro Ala Ile Gln
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 Glu Glu Leu Asp Leu Ile Gln Ala Val Gly Cys Leu Glu Glu Phe Gly
 180 185 190
 Val Lys Ile Leu Pro Leu Gln Val Arg Leu Cys Pro Asp Arg Ile Ser
 195 200 205
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 Thr Lys Leu Leu Gly Leu Ala Glu Leu Leu Arg Val Ala Gly Glu Asn
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 Pro Glu Glu Arg Arg Gly Gln Val Leu Ile Leu Leu Val Glu Gln Ala
 245 250 255
 Leu Arg Phe His Asp Tyr Lys Ala Ala Ser Met His Cys Gln Glu Leu
 260 265 270
 Met Ala Thr Gly Tyr Pro Lys Ser Trp Asp Val Cys Ser Gln Leu Gly

1029

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Thr	Asp	Glu	Asn	Met	Ser	Pro	Leu	Glu	Ala	Leu	Glu	Pro	Val	Leu	Ser
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Ser	Gln	Asn	Ile	Leu	Ser	Ile	Ser	Lys	Leu	Val	Pro	Lys	Ile	Pro	Glu
785				790					795					800	
Lys	Asp	Gly	Gln	Met	Leu	Ser	Pro	Ser	Ser	Leu	Tyr	Thr	Ile	Trp	Leu
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Gly	Ser	Ser	Pro	Glu	Trp	Leu	His	Ala	Tyr	Asp	Val	Cys	Met	Lys	Tyr
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Phe	Asp	Arg	Leu	His	Pro	Gly	Asp	Leu	Ile	Thr	Val	Val	Asp	Ala	Val
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	995						1000						1005		
Ile	Ile	Ser	Ala	Leu	Ser	Gly	Gly	Ser	Ala	Asp	Leu	Gly	Gly	Pro	Arg
	1010					1015					1020				
Asp	Pro	Leu	Lys	Val	Leu	Glu	Gly	Val	Val	Ala	Ala	Val	His	Thr	Ser
1025				1030						1035				1040	
Val	Asp	Lys	Gly	Glu	Glu	Leu	Val	Ser	Pro	Glu	Asp	Leu	Leu	Glu	Trp
			1045						1050					1055	
Leu	Arg	Pro	Phe	Cys	Ala	Asp	Asp	Ala	Trp	Pro	Val	Arg	Pro	Arg	Ile
		1060						1065					1070		
His	Val	Leu	Gln	Ile	Leu	Gly	Gln	Ser	Phe	His	Leu	Thr	Glu	Glu	Asp
	1075					1080					1085				
Ser	Lys	Leu	Leu	Val	Phe	Phe	Arg	Thr	Glu	Ala	Ile	Leu	Lys	Ala	Ser
	1090					1095					1100				
Trp	Pro	Gln	Arg	Gln	Val	Asp	Ile	Ala	Asp	Ile	Glu	Asn	Glu	Glu	Asn
1105				1110					1115					1120	
Arg	Tyr	Cys	Leu	Phe	Met	Glu	Leu	Leu	Glu	Ser	Ser	His	His	Glu	Ala
			1125						1130					1135	
Glu	Phe	Gln	His	Leu	Val	Leu	Leu	Leu	Gln	Ala	Trp	Pro	Pro	Met	Lys

1140	1145	1150
Ser Glu Tyr Val Ile Thr Asn Asn Pro Trp Val Arg Leu Ala Thr Val		
1155	1160	1165
Met Leu Thr Arg Cys Thr Met Glu Asn Lys Glu Gly Leu Gly Asn Glu		
1170	1175	1180
Val Leu Lys Met Cys Arg Ser Leu Tyr Asn Thr Lys Gln Met Leu Pro		
1185	1190	1195
Ala Glu Gly Val Lys Glu Leu Cys Leu Leu Leu Leu Asn Gln Ser Leu		1200
1205	1210	1215
Leu Leu Pro Ser Leu Lys Leu Leu Leu Glu Ser Arg Asp Glu His Leu		
1220	1225	1230
His Glu Met Ala Leu Glu Gln Ile Thr Ala Val Thr Thr Val Asn Asp		
1235	1240	1245
Ser Asn Cys Asp Gln Glu Leu Leu Ser Leu Leu Leu Asp Ala Lys Leu		
1250	1255	1260
Leu Val Lys Cys Val Ser Thr Pro Phe Tyr Pro Arg Ile Val Asp His		
1265	1270	1275
Leu Leu Ala Ser Leu Gln Gln Gly Arg Trp Asp Ala Glu Glu Leu Gly		1280
1285	1290	1295
Arg His Leu Arg Glu Ala Gly His Glu Ala Glu Ala Gly Ser Leu Leu		
1300	1305	1310
Leu Ala Val Arg Gly Thr His Gln Ala Phe Arg Thr Phe Ser Thr Ala		
1315	1320	1325
Leu Arg Ala Ala Gln His Trp Val		
1330	1335	

<210> 1099

<211> 309

<212> DNA

<213> Homo sapiens

<400> 1099

acgcgtgctc tctcccgctt ggcaatcagc atggcctttt cgagctcggc ggtgcgcaat
60tgaaccattt cttccagttg cgattttttca gaaagcagcg tcgattgacc ttcggtcagc
120ttgcgcacat agcgcttggt gcggctggca aggatatagg cgagtatcaa tgcacctgcg
180agggcgagga tcgaggcaat ggtcagccag aagcgcaact tgtccatggc tatgttgcg
240gcgattagcc gacgatcttc ttcacccagg aaactgttga tggttttcct gacgtcatcc
300

atctggcca

309

<210> 1100

<211> 100

<212> PRT

<213> Homo sapiens

<400> 1100

Met Asp Asp Val Arg Lys Thr Ile Asn Ser Phe Leu Gly Glu Glu Asp

1

5

10

15

Arg Arg Leu Ile Ala Arg Asn Ile Ala Met Asp Lys Leu Arg Phe Trp

	20		25		30										
Leu	Thr	Ile	Ala	Ser	Ile	Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ile	Leu	Ala
	35		40		45										
Tyr	Ile	Leu	Ala	Ser	Arg	Thr	Lys	Arg	Tyr	Val	Arg	Lys	Leu	Thr	Glu
	50		55		60										
Gly	Gln	Ser	Thr	Leu	Leu	Ser	Glu	Lys	Ser	Gln	Leu	Glu	Glu	Met	Val
65			70		75									80	
Gln	Leu	Arg	Thr	Ala	Glu	Leu	Glu	Lys	Ala	Met	Leu	Ile	Ala	Lys	Arg
		85			90									95	
Glu	Arg	Ala	Arg												
		100													

<210> 1101
 <211> 540
 <212> DNA
 <213> Homo sapiens

<400> 1101
 gtcgacgtta ccaactacgt catgttggag tctggtcagc cgcttcatgc ctatgatgcc
 60
 gacaacgtca gcgggacgat tgtggtccgt aaggccacg agggtagagca tctattgacc
 120
 ctcgacgaca ccgatcgac cctcgatcct gacgatctag tcatcgccga cgactcggga
 180
 gccattggcc tggctggcgt catgggtggt gcggccaccg aagtgactgc tgagacgacg
 240
 tcaatcatcc tcgagggcgc tcaactcgac ccgatgacgg gcgctcgtgc ttaccgacgc
 300
 cacaagctcg gttcggaggc ctcccgcgc tttgagcggg gcgttgatcc gatttgcgcc
 360
 cataccgcag ccgttcgcgc agcggaattg ctcgcccagt acggcggtgc caccgtcggg
 420
 gagcccaccg tcgttggtga ggtccccgag atgccacgtc aaacgatcaa cgctgattta
 480
 cctaaccgga ttctcggcac gaaggtgcc aactgaagagg tcatcgagat cttgacgcgt
 540

<210> 1102
 <211> 180
 <212> PRT
 <213> Homo sapiens

Val	Asp	Val	Thr	Asn	Tyr	Val	Met	Leu	Glu	Ser	Gly	Gln	Pro	Leu	His
1				5					10					15	
Ala	Tyr	Asp	Ala	Asp	Asn	Val	Ser	Gly	Thr	Ile	Val	Val	Arg	Lys	Ala
		20						25					30		
His	Glu	Gly	Glu	His	Leu	Leu	Thr	Leu	Asp	Asp	Thr	Asp	Arg	Thr	Leu
	35						40					45			
Asp	Pro	Asp	Asp	Leu	Val	Ile	Ala	Asp	Asp	Ser	Gly	Ala	Ile	Gly	Leu
	50					55					60				
Ala	Gly	Val	Met	Gly	Gly	Ala	Ala	Thr	Glu	Val	Thr	Ala	Glu	Thr	Thr
65				70					75					80	
Ser	Ile	Ile	Leu	Glu	Gly	Ala	His	Phe	Asp	Pro	Met	Thr	Gly	Ala	Arg

				85					90					95					
Ala	Tyr	Arg	Arg	His	Lys	Leu	Gly	Ser	Glu	Ala	Ser	Arg	Arg	Phe	Glu				
				100					105					110					
Arg	Gly	Val	Asp	Pro	Ile	Cys	Ala	His	Thr	Ala	Ala	Val	Arg	Ala	Ala				
			115				120						125						
Glu	Leu	Leu	Ala	Gln	Tyr	Gly	Gly	Ala	Thr	Val	Gly	Glu	Pro	Thr	Val				
	130					135					140								
Val	Gly	Glu	Val	Pro	Glu	Met	Pro	Arg	Gln	Thr	Ile	Asn	Ala	Asp	Leu				
145					150				155					160					
Pro	Asn	Arg	Ile	Leu	Gly	Thr	Lys	Val	Pro	Thr	Glu	Glu	Val	Ile	Glu				
				165					170					175					
Ile	Leu	Thr	Arg																
			180																

<210> 1103
 <211> 537
 <212> DNA
 <213> Homo sapiens

<400> 1103
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 60
 cgtcaggttt accatcgctg tactcaacca aatggtagcc gtatccacct tccccaccga
 120
 tcgcgaccca ggtgatcttt ccctcggcat agattgacgt ggcattctcg tcggagtga
 180
 tcaagcagcg cttaggcagc tgctgggccc gcggttcgc ctagctcgcc ggagcacacg
 240
 aacccttccc gaagataacc gccaaaggcct ggcacacctt ctgctgcacc cattccggct
 300
 tgacgccgac cgccaccgca ctggtgaaca tagccgcaat aaggagaatt gcgatgtatt
 360
 ccggcgcggc ggcaccccga tcgtcccttg tccgcatggg tctccccctcc actacctacc
 420
 caatacaggg gagagcataa aaagaaaccc atagccgcac ctgagcccat ggccccaaac
 480
 cggggcccaa gccgggccc aaccatggga tcaaccggat gtccgtacat cacgcgt
 537

<210> 1104
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 1104
 Met Tyr Gly His Pro Val Asp Pro Met Val Trp Ala Arg Leu Gly Pro
 1 5 10 15
 Arg Phe Gly Ala Met Gly Ser Gly Ala Ala Met Gly Phe Phe Leu Cys
 20 25 30
 Ser Pro Leu Tyr Trp Val Gly Ser Gly Gly Glu Thr His Ala Asp Lys
 35 40 45
 Gly Arg Ser Gly Cys Arg Arg Ala Gly Ile His Arg Asn Ser Pro Tyr
 50 55 60
 Cys Gly Tyr Val His Gln Cys Gly Gly Gly Arg Arg Gln Ala Gly Met

145

<210> 1107

<211> 618

<212> DNA

<213> Homo sapiens

<400> 1107

acgcgttgat gaagtacctg ccacgcttca gcaatgacgg ctcggtgaac ggcttctata
 60
 tctttgttat cgatgagacc gaacgcaaac tcaccgaaga ggccctgcgc cacctcaacg
 120
 agaacctcga agagcgcgct gccacgcgca cacaggcgct ggctgaagcc aaccaacgcc
 180
 tggcaaaaaca aaatgttcaa acgcaagcgc gccgaagacg cgctgcgtca cgcgcagaaa
 240
 atggaagccg ggggccagct caccggcggc atcgcccatg atttcaacaa catgctgacc
 300
 gggattatcg gcagcctgga cttgatgcag cgctacatcn aggcggggcg cagcgacgaa
 360
 atcgggcgcnc ttactgacgc cgccgtatcg tccgcccacg gcgcggccgc cctcacccat
 420
 cggctgctgg cgttctcgcg ccgccagtcg ctggcccccc gcccgctgga cccaaccag
 480
 ctggtagcgt ccctggagga tctgttccag cgaaccaaag gcgcgcatat cagctcaaa
 540
 gtgcaactgg gccgcgatat ctggcccgtg aataccgatg ccagccagtt ggaaaacgcc
 600
 ctgctcaacc tggcgatc
 618

<210> 1108

<211> 182

<212> PRT

<213> Homo sapiens

<400> 1108

Met	Arg	Pro	Asn	Ala	Asn	Ser	Pro	Lys	Arg	Pro	Cys	Ala	Thr	Ser	Thr
1				5					10					15	
Arg	Thr	Ser	Lys	Ser	Ala	Ser	Pro	Ser	Ala	His	Arg	Arg	Trp	Leu	Lys
			20					25					30		
Pro	Thr	Asn	Ala	Trp	Gln	Asn	Lys	Met	Phe	Lys	Arg	Lys	Arg	Ala	Glu
		35					40				45				
Asp	Ala	Leu	Arg	His	Ala	Gln	Lys	Met	Glu	Ala	Gly	Gly	Gln	Leu	Thr
	50					55					60				
Gly	Gly	Ile	Ala	His	Asp	Phe	Asn	Asn	Met	Leu	Thr	Gly	Ile	Ile	Gly
65				70					75					80	
Ser	Leu	Asp	Leu	Met	Gln	Arg	Tyr	Ile	Xaa	Ala	Gly	Arg	Ser	Asp	Glu
			85					90					95		
Ile	Gly	Arg	Leu	Thr	Asp	Ala	Ala	Val	Ser	Ser	Ala	His	Arg	Ala	Ala
			100				105					110			
Ala	Leu	Thr	His	Arg	Leu	Leu	Ala	Phe	Ser	Arg	Arg	Gln	Ser	Leu	Ala
	115						120					125			
Pro	Arg	Pro	Leu	Asp	Pro	Asn	Gln	Leu	Val	Ala	Ser	Leu	Glu	Asp	Leu

130 135 140
 Phe Gln Arg Thr Lys Gly Ala His Ile Thr Leu Lys Val Gln Leu Gly
 145 150 155 160
 Arg Asp Ile Trp Pro Val Asn Thr Asp Ala Ser Gln Leu Glu Asn Ala
 165 170 175
 Leu Leu Asn Leu Ala Ile
 180

<210> 1109
 <211> 325
 <212> DNA
 <213> Homo sapiens

<400> 1109
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 60
 agcctcaaga tcgtcgcacc gctgggggggc atcctcgtgc ccctggatca ggtgcccgat
 120
 cccgttttcg cccagaagat ggtgggagac gggatctccc tggaccccat ctcaaacgaa
 180
 ttgctggcgc cggtcgccgg caccgtgacc cagctccaca acgcccacca cgcgctcacg
 240
 atcacgaccc cggaaggcat cgaggttctg gtccatatcg gactggatac cgtgatgctg
 300
 cgcgggcgaca gctatccccc ccccn
 325

<210> 1110
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 1110
 Thr Gly Glu His Gln Gly Gly Thr Met Gln Thr Thr Leu Pro Ser Ser
 1 5 10 15
 Leu Lys Pro Ser Ser Leu Lys Ile Val Ala Pro Leu Gly Gly Ile Leu
 20 25 30
 Val Pro Leu Asp Gln Val Pro Asp Pro Val Phe Ala Gln Lys Met Val
 35 40 45
 Gly Asp Gly Ile Ser Leu Asp Pro Ile Ser Asn Glu Leu Leu Ala Pro
 50 55 60
 Val Ala Gly Thr Val Thr Gln Leu His Asn Ala His His Ala Leu Thr
 65 70 75 80
 Ile Thr Thr Pro Glu Gly Ile Glu Val Leu Val His Ile Gly Leu Asp
 85 90 95
 Thr Val Met Leu Arg Gly Asp Ser Tyr Pro Pro Pro
 100 105

<210> 1111
 <211> 385
 <212> DNA
 <213> Homo sapiens

<400> 1111

nnacgcgtcg ccccggtgcg cctggcagtg ggagaagagc atgaccttac cgagctcgcg
 60
 actgaactcg tcaacgccgc ctatagccgg gttgacatgg tggaaacgccg tggcgaattc
 120
 gcagtacgtg gcggcatcgt cgacgtcttc ccaccggtgc tagaacaccc ggtccgtatc
 180
 gatttttttg gtgacgagat cgaggaaatg acctccttcg cggtagccga ccagcgatcc
 240
 accgacgaga ctcaccaaga actgatctgc gtccttgcc gtgagctcat cctcaccgac
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 360
 gagcggatcg gcaacggtca agctt
 385

<210> 1112
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 1112
 Xaa Arg Val Ala Pro Val Arg Leu Ala Val Gly Glu Glu His Asp Leu
 1 5 10 15
 Thr Glu Leu Ala Thr Glu Leu Val Asn Ala Ala Tyr Ser Arg Val Asp
 20 25 30
 Met Val Glu Arg Arg Gly Glu Phe Ala Val Arg Gly Gly Ile Val Asp
 35 40 45
 Val Phe Pro Pro Val Leu Glu His Pro Val Arg Ile Asp Phe Phe Gly
 50 55 60
 Asp Glu Ile Glu Glu Met Thr Ser Phe Ala Val Ala Asp Gln Arg Ser
 65 70 75 80
 Thr Asp Glu Thr His Gln Glu Leu Ile Cys Ala Pro Cys Arg Glu Leu
 85 90 95
 Ile Leu Thr Asp Glu Val Arg Ser Arg Ala Lys Ala Leu Leu Thr Asp
 100 105 110
 His Pro Glu Leu Ala Asp Met Leu Glu Arg Ile Gly Asn Gly Gln Ala
 115 120 125

<210> 1113
 <211> 400
 <212> DNA
 <213> Homo sapiens

<400> 1113
 nnnccgaccga tgagcgatcg cgaacccgtc aacctgggat acccctacgt cgagtctttc
 60
 cactcggact tctcggggac cggcggagtc gatcagaccg accgttctac caatatcgac
 120
 gagcacacca tcgaggagat gcatcagatc gcctcgcgtt accccgactc ccgttcggcg
 180
 ttgctgccga tcctgcacct ggttcagtcg gtggacggac gcatctcgcc ggtcgggtatt
 240
 gagactgcgg ctgaagtgct cggcattacc accgcccagg tatccgggggt ggcgaccttc
 300

tacaccatgt ataagaagca ccctgcgggc cagcatcaca tcggtgtctg caccacggcg
 360
 ctgtgcgccg tcatgggtgg cgaggaggtg cttgcccgtn
 400

<210> 1114
 <211> 133
 <212> PRT
 <213> Homo sapiens

<400> 1114
 Xaa Arg Pro Met Ser Asp Arg Glu Pro Val Asn Leu Gly Tyr Pro Tyr
 1 5 10 15
 Val Glu Ser Phe His Ser Asp Phe Ser Gly Thr Gly Gly Val Asp Gln
 20 25 30
 Thr Asp Arg Ser Thr Asn Ile Asp Glu His Thr Ile Glu Glu Met His
 35 40 45
 Gln Ile Ala Ser Arg Tyr Pro Asp Ser Arg Ser Ala Leu Leu Pro Ile
 50 55 60
 Leu His Leu Val Gln Ser Val Asp Gly Arg Ile Ser Pro Val Gly Ile
 65 70 75 80
 Glu Thr Ala Ala Glu Val Leu Gly Ile Thr Thr Ala Gln Val Ser Gly
 85 90 95
 Val Ala Thr Phe Tyr Thr Met Tyr Lys Lys His Pro Ala Gly Gln His
 100 105 110
 His Ile Gly Val Cys Thr Thr Ala Leu Cys Ala Val Met Gly Gly Glu
 115 120 125
 Glu Val Leu Ala Arg
 130

<210> 1115
 <211> 402
 <212> DNA
 <213> Homo sapiens

<400> 1115
 tctccgactg cacagattag agaaaggact gcgatgacca ttcgcaccac tcatgttggt
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 tccctgcccc gcacccccga gctgatcgag gcgaatcgtg cgcgccgtga gggttcgctc
 120
 ggcgaggctg acttcacgtc gctgctgcag gatcagggtg acggcggtgt gaagcgtcag
 180
 gctgagattg gcctggatat cgtcaatgac ggcgagtag gtcacgcgat gcttgacacg
 240
 gttgattacg gcgcgtggtg gacgtattcc atctctcggt tcggcgggct gtcctttgag
 300
 gacgtgcagc gttttgatgt gcgtcccccg gctggccgtg acggtcgcct gtctttctcg
 360
 tcgttcgctg agcgcgcgca ctggcagcgt ttccggacgc gt
 402

<210> 1116
 <211> 134
 <212> PRT

<213> Homo sapiens

<400> 1116

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Ser Pro Thr Ala Gln Ile Arg Glu Arg Thr Ala Met Thr Ile Arg Thr
 1           5           10           15
Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Ile Glu Ala Asn
           20           25           30
Arg Ala Arg Arg Glu Gly Ser Leu Gly Glu Ala Asp Phe Thr Ser Leu
           35           40           45
Leu Gln Asp Gln Val Asp Gly Val Val Lys Arg Gln Ala Glu Ile Gly
           50           55           60
Leu Asp Ile Val Asn Asp Gly Glu Tyr Gly His Ala Met Leu Asp Thr
65           70           75           80
Val Asp Tyr Gly Ala Trp Trp Thr Tyr Ser Ile Ser Arg Phe Gly Gly
           85           90           95
Leu Ser Phe Glu Asp Val Gln Arg Phe Asp Val Arg Pro Pro Ala Gly
           100          105          110
Arg Asp Gly Arg Leu Ser Phe Ser Ser Phe Ala Glu Arg Arg Asp Trp
           115          120          125
Gln Arg Phe Arg Thr Arg
           130

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<210> 1117

<211> 307

<212> DNA

<213> Homo sapiens

<400> 1117

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ggcgccggtc ttgccctggc tggaagtggc atgcagacct tgggtgcggaa cccgctggct
60
gaccctacc tgctaggtgt atcggctggc gcaagtgtgg gagcaaccgc agtcatcgct
120
ttggggatgt tcacttcgtg gggaaactcac cgactcactc ttggtgccct ttagggggcc
180
ttggcggcag ctgcattggt ctatctcatt tccatggcgc aaggaggcat gacgccgctt
240
cggttggtgc tgtcgggcgt ggtgttgtec tcggcgttct cgcgttggcg agtttcctcg
300
tctttcg
307

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<210> 1118

<211> 102

<212> PRT

<213> Homo sapiens

<400> 1118

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Gly Ala Gly Leu Ala Leu Ala Gly Ser Gly Met Gln Thr Leu Val Arg
 1           5           10           15
Asn Pro Leu Ala Asp Pro Tyr Leu Leu Gly Val Ser Ala Gly Ala Ser
           20           25           30
Val Gly Ala Thr Ala Val Ile Ala Leu Gly Met Phe Thr Ser Trp Gly
           35           40           45
Thr His Arg Leu Thr Leu Gly Ala Leu Val Gly Ala Leu Ala Ala Ala

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50 55 60
 Ala Leu Val Tyr Leu Ile Ser Met Ala Gln Gly Gly Met Thr Pro Leu
 65 70 75 80
 Arg Leu Val Leu Ser Gly Val Val Leu Ser Ser Ala Phe Ser Arg Trp
 85 90 95
 Arg Val Ser Ser Ser Phe
 100

<210> 1119
 <211> 353
 <212> DNA
 <213> Homo sapiens

<400> 1119
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 tatccgcac aactgtccgg tggccagcgt caacgggttc tgcttgccat ggcgttggtg
 120
 aactcgccgg atctgctcat ttgtgacgag ccgacgaccg ccttgacgt cacggtgcag
 180
 tctcaggtac tggcgactat cgatgaggtg cttgactcgg ttggtgccgc atgcctattt
 240
 attacccacg atttggcggg tgtctcgac atctgccggg agcttatcgt gatgacgtcg
 300
 ggcaaggctg ttgaagccgg atcagcgcgt gatgtgttat ctcaccctga tca
 353

<210> 1120
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 1120
 Arg Val Leu Glu Met Leu Glu Gln Val Gly Ile Glu Asp Pro Ala Arg
 1 5 10 15
 Val Met Asp Ser Tyr Pro His Gln Leu Ser Gly Gly Gln Arg Gln Arg
 20 25 30
 Val Leu Leu Ala Met Ala Leu Val Asn Ser Pro Asp Leu Leu Ile Cys
 35 40 45
 Asp Glu Pro Thr Thr Ala Leu Asp Val Thr Val Gln Ser Gln Val Leu
 50 55 60
 Ala Thr Ile Asp Glu Val Leu Asp Ser Val Gly Ala Ala Cys Leu Phe
 65 70 75 80
 Ile Thr His Asp Leu Ala Val Val Ser His Ile Cys Arg Glu Leu Ile
 85 90 95
 Val Met Thr Ser Gly Lys Val Val Glu Ala Gly Ser Ala Arg Asp Val
 100 105 110
 Leu Ser His Pro Asp
 115

<210> 1121
 <211> 406
 <212> DNA
 <213> Homo sapiens

<400> 1121

tgatcaccca tgctccactc gaccgcgcgc tcgacgatgc gacggctgag acgatgctcg
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 cccagggcac ggtgttcac cgcaccttga cgatgatgaa aggcgtcgcc gcgaatctca
 120
 ccgcagcggg cgttcccggg gtgagctatg cacacgcccc cgagagcacg cgcgcgatgc
 180
 atgccgcggg cgttccgggc ctggccggca ccgacgccta catcgggtcc ttcacacggg
 240
 catcgccgcc atacggcgag agcatgcacg acgaagacgc ctacatcggg ctctcgaac
 300
 gggcaatgcc gccatacggc gagagcatgc acgacgaact cgctctgctc gtggacgccg
 360
 gcctgtcaac agccgaagcg ctgcgcgctg ccacctcgac gggcgc
 406

<210> 1122

<211> 117

<212> PRT

<213> Homo sapiens

<400> 1122

Met	Leu	Ala	Gln	Gly	Thr	Val	Phe	Ile	Pro	Thr	Leu	Thr	Met	Met	Lys
1				5					10					15	
Gly	Val	Ala	Ala	Asn	Leu	Thr	Ala	Ala	Gly	Val	Pro	Gly	Val	Ser	Tyr
			20					25					30		
Ala	His	Ala	His	Glu	Ser	Thr	Arg	Ala	Met	His	Ala	Ala	Gly	Val	Pro
		35					40					45			
Val	Leu	Ala	Gly	Thr	Asp	Ala	Tyr	Ile	Gly	Ser	Phe	Thr	Arg	Ala	Ser
	50				55						60				
Pro	Pro	Tyr	Gly	Glu	Ser	Met	His	Asp	Glu	Asp	Ala	Tyr	Ile	Gly	Leu
65					70				75					80	
Leu	Glu	Arg	Ala	Met	Pro	Pro	Tyr	Gly	Glu	Ser	Met	His	Asp	Glu	Leu
			85					90					95		
Ala	Leu	Leu	Val	Asp	Ala	Gly	Leu	Ser	Thr	Ala	Glu	Ala	Leu	Arg	Ala
			100				105						110		
Ala	Thr	Ser	Thr	Gly											
			115												

<210> 1123

<211> 337

<212> DNA

<213> Homo sapiens

<400> 1123

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 cgctccacc gcccttgccg cagcggggat ggtgggggtgc tcgtccgagg gggcatcgcc
 120
 aagcgaatgc tcccctgttg atattgccgc agtgccgcgag gccctgccgc attcgctcgc
 180
 taaggcgaag ctcgaccgcg actccaccaa cgaggatgaa cactcctttt ccatgctcta
 240

ccgcgcgcaa gataaggagc aggtcagctt gctggggacg aagtatgagg ccgacggtgc
300

accggtctgc cccgatgacc ccaatgaggc agcgcgc
337

<210> 1124

<211> 110

<212> PRT

<213> Homo sapiens

<400> 1124

Met	Arg	Ser	Leu	Arg	Pro	Lys	Met	Arg	Arg	Arg	Leu	Pro	Ala	Phe	Leu
1				5				10						15	
Ala	Leu	Ala	Ser	Thr	Ala	Leu	Ala	Ala	Ala	Gly	Met	Val	Gly	Cys	Ser
			20					25					30		
Ser	Glu	Gly	Ala	Ser	Pro	Ser	Glu	Cys	Ser	Pro	Val	Asp	Ile	Ala	Ala
		35					40					45			
Val	Arg	Glu	Ala	Leu	Pro	His	Ser	Leu	Ala	Lys	Ala	Lys	Leu	Asp	Pro
	50					55				60					
His	Ser	Thr	Asn	Glu	Asp	Glu	His	Ser	Phe	Ser	Met	Leu	Tyr	Arg	Ala
65				70					75					80	
Gln	Asp	Lys	Glu	Gln	Val	Ser	Leu	Leu	Gly	Thr	Lys	Tyr	Glu	Ala	Asp
			85						90					95	
Gly	Ala	Pro	Val	Cys	Pro	Asp	Asp	Pro	Asn	Glu	Ala	Ala	Arg		
			100					105					110		

<210> 1125

<211> 555

<212> DNA

<213> Homo sapiens

<400> 1125

nncttgaatc gaatcggcat tgcgtctaaa catgacgttg agacactctc tgctaagctc
60
gaagagctga cggcattgct agaacgtgtc gcgcgtaaac actaaggaga catcgggatg
120
gctgttaaaa agactactca gaaagaaggc agctcgtgga tcggggaagt tgaaaaatat
180
tcccgtaaaa tctggcttgc tggtttaggc gtgtactcga aggttagcag tgacggcggc
240
aaatacttcg agacgttggt caaggacggc gagaaggccg agaagttgac caagagccca
300
gtcggtaaaa aagtagaggc ggcaaaagcg agcgccggtt ctgcgaaatc gagcatttcg
360
gatacctggg gcaagttgga agagactttc gacaagcgtc tcaacagtgc tatttcgcga
420
ttgggcgtgc ccagcaaagc ggaactgaag acgctgcaca gcaaggtcga taccctgacc
480
aagcaaatcg aaaaactcac cggtgccaaa gtggccccgg ctaaaacggc agccgctaaa
540
cctgctgcca agctt
555

<210> 1126

<211> 146
 <212> PRT
 <213> Homo sapiens

<400> 1126
 Met Ala Val Lys Lys Thr Thr Gln Lys Glu Gly Ser Ser Trp Ile Gly
 1 5 10 15
 Glu Val Glu Lys Tyr Ser Arg Lys Ile Trp Leu Ala Gly Leu Gly Val
 20 25 30
 Tyr Ser Lys Val Ser Ser Asp Gly Gly Lys Tyr Phe Glu Thr Leu Val
 35 40 45
 Lys Asp Gly Glu Lys Ala Glu Lys Leu Thr Lys Ser Pro Val Gly Lys
 50 55 60
 Lys Val Glu Ala Ala Lys Ala Ser Ala Gly Ser Ala Lys Ser Ser Ile
 65 70 75 80
 Ser Asp Thr Trp Gly Lys Leu Glu Glu Thr Phe Asp Lys Arg Leu Asn
 85 90 95
 Ser Ala Ile Ser Arg Leu Gly Val Pro Ser Lys Ala Glu Leu Lys Thr
 100 105 110
 Leu His Ser Lys Val Asp Thr Leu Thr Lys Gln Ile Glu Lys Leu Thr
 115 120 125
 Gly Ala Lys Val Ala Pro Ala Lys Thr Ala Ala Ala Lys Pro Ala Ala
 130 135 140
 Lys Leu
 145

<210> 1127
 <211> 352
 <212> DNA
 <213> Homo sapiens

<400> 1127
 cccgaccgcg tactcgtggt cgggtgccgga gtgatgggtg cagcacacgc acacgcgctc
 60
 cgcggtccc tccaggcagt cgtgtgcggc gtggtcgacc tgcaggagcg agcagcgcaa
 120
 tcactcgctt cggaagtggg cgtaccggg ttcaccgacc tggatgaaggc gatcgagtcg
 180
 accgctccgg acgccgcggt catcgccacg ccggactcgg ctcaccgcca accggctgag
 240
 accgccatcg acgccggcct tgccgtcctg gtcgagaaac cgctcgccac gaccgtcgat
 300
 gacgccgaag cgatcgtgct ccgcgctgaa cgggccggcg tccgtctcat ga
 352

<210> 1128
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 1128
 Pro Asp Arg Val Leu Val Val Gly Ala Gly Val Met Gly Ala Ala His
 1 5 10 15
 Ala His Ala Leu Arg Gly Ser Leu Gln Ala Val Val Cys Gly Val Val

```

      20      25      30
Asp Leu Gln Glu Arg Ala Ala Gln Ser Leu Ala Ser Glu Val Gly Val
      35      40      45
Pro Gly Phe Thr Asp Leu Val Lys Ala Ile Glu Ser Thr Ala Pro Asp
      50      55      60
Ala Ala Val Ile Ala Thr Pro Asp Ser Ala His Arg Gln Pro Ala Glu
65      70      75      80
Thr Ala Ile Asp Ala Gly Leu Ala Val Leu Val Glu Lys Pro Leu Ala
      85      90      95
Thr Thr Val Asp Asp Ala Glu Ala Ile Val Leu Arg Ala Glu Arg Ala
      100      105      110
Gly Val Arg Leu Met
      115

```

<210> 1129
 <211> 336
 <212> DNA
 <213> Homo sapiens

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<400> 1129
ntggcagccc tggaggagcc gatggtggac ctggacggcg agctgccttt cgtgcggccc
60
ctgccccaca ttgccgtgct ccaggacgag ctgccgcaac tcttccagga tgacgacgtc
120
ggggccgatg aggaagaggc agagttgcgg ggcgaacaca cgctcacaga gaagtttgtc
180
tgcctggatg actcctttgg ccatgactgc agcttgacct gtgatgactg caggaacgga
240
gggacctgcc tcttgggcct ggatggctgg gattgccccg agggctggac tgggctcatc
300
tgcaatgaga cttggtcctc gggctgcatg gatatt
336

```

<210> 1130
 <211> 112
 <212> PRT
 <213> Homo sapiens

```

<400> 1130
Xaa Ala Ala Leu Glu Glu Pro Met Val Asp Leu Asp Gly Glu Leu Pro
1      5      10      15
Phe Val Arg Pro Leu Pro His Ile Ala Val Leu Gln Asp Glu Leu Pro
      20      25      30
Gln Leu Phe Gln Asp Asp Asp Val Gly Ala Asp Glu Glu Glu Ala Glu
      35      40      45
Leu Arg Gly Glu His Thr Leu Thr Glu Lys Phe Val Cys Leu Asp Asp
50      55      60
Ser Phe Gly His Asp Cys Ser Leu Thr Cys Asp Asp Cys Arg Asn Gly
65      70      75      80
Gly Thr Cys Leu Leu Gly Leu Asp Gly Trp Asp Cys Pro Glu Gly Trp
      85      90      95
Thr Gly Leu Ile Cys Asn Glu Thr Trp Ser Ser Gly Cys Met Asp Ile
      100      105      110

```


<210> 1131
<211> 672
<212> DNA
<213> Homo sapiens

<400> 1131
gcgttggtgg tgctcatggc ccgggaaaat ccgctggatc aatacctctt tgagcacccc
60
gaattattgt tctcgtcctc ggtggaatcg actgtgttgc acccggataa cccgtatgtg
120
ctcgcccgcc acgtggccgc ggccgcccag gaggcatacc tctcccctgc ggacgaagag
180
ttttacgggt cggcctttgc cgggatatgc aaaacgctga caggccagaa cgtactgcga
240
cgtcgcggaa atcggctgtt ctggactcgt ccggaacggg ctgtcgacgc catcgacctg
300
cgatcggcgg caggcaaagg gattgacatt atcgacgtgt ccaccgggag ggtcatcggg
360
gtagtcgacg aagccgcccgc agaccgtacc gtgcatccag gcgcggtgta cctgcatcag
420
ggggatcagt ggctggtcga cgaatacaac ccggtcgagc accacgcctt ggtgcaccag
480
gacctgccgg gatattggac tcaaccgcag tcagcgtcga cggtgagaat ccttcgggag
540
gagagacgtc gcgcttgtgg tcccggatat gtggcgtgcg ggcaggtgga actgacagag
600
caagttgttg ggtatctgcg tcgcgacgaa ttcaccaatg atgtgtggta ctcgctggcc
660
ctcgagatgc cc
672

<210> 1132
<211> 224
<212> PRT
<213> Homo sapiens

<400> 1132
Ala Leu Val Val Leu Met Ala Arg Glu Asn Pro Leu Asp Gln Tyr Leu
1 5 10 15
Phe Glu His Pro Glu Leu Leu Phe Ser Ser Ser Val Glu Ser Thr Val
20 25 30
Leu His Pro Asp Asn Pro Tyr Val Leu Gly Pro His Val Ala Ala Ala
35 40 45
Ala Gln Glu Ala Tyr Leu Ser Pro Ala Asp Glu Glu Phe Tyr Gly Ser
50 55 60
Ala Phe Ala Gly Ile Cys Lys Thr Leu Thr Gly Gln Asn Val Leu Arg
65 70 75 80
Arg Arg Gly Asn Arg Leu Phe Trp Thr Arg Pro Glu Arg Ala Val Asp
85 90 95
Ala Ile Asp Leu Arg Ser Ala Ala Gly Lys Gly Ile Asp Ile Ile Asp
100 105 110
Val Ser Thr Gly Arg Val Ile Gly Val Val Asp Glu Ala Ala Ala Asp
115 120 125
Arg Thr Val His Pro Gly Ala Val Tyr Leu His Gln Gly Asp Gln Trp

130		135		140
Leu Val Asp Glu Tyr Asn Pro Val Glu His His Ala Leu Val His Gln				
145		150		155
Asp Leu Pro Gly Tyr Trp Thr Gln Pro Gln Ser Ala Ser Thr Val Arg				
	165		170	175
Ile Leu Arg Glu Glu Arg Arg Arg Ala Cys Gly Pro Gly Tyr Val Ala				
	180		185	190
Cys Gly Gln Val Glu Leu Thr Glu Gln Val Val Gly Tyr Leu Arg Arg				
	195		200	205
Asp Glu Phe Thr Asn Asp Val Trp Tyr Ser Leu Ala Leu Glu Met Pro				
210		215		220

<210> 1133
 <211> 796
 <212> DNA
 <213> Homo sapiens

<400> 1133
 acgcgtgaag gggggtccag cgggtgtggc actcgatgac aagacagttt gagagcggct
 60
 tgtctccggg gacctggcgt aggtctcttc tgccttaacc cttggctttt gcacttcttc
 120
 tgtctgtcct ccatacaagc ttcttgcccc tagggaggac gggcttctta acagggggag
 180
 ccggttcctg tcctaaccac actggcatct tacactctgg gagatagctt cccctgaga
 240
 ggcgagtgag ccacgtaagg ggaggtgggc gatggcttcc cttctgtctt ggggtggggg
 300
 agtcaggtag agtatttttt cttttaaaagc atcattgatc acataataag gtttgtcata
 360
 gtccttaatc acagacctgt gaaatttgga gaattcacgg cacctaggat gggagtgagc
 420
 ttctgattgt gagctgattt gggagctaac ctcaaggaaa ctctcttgc aagccccctg
 480
 ctgggtgtcg gggccttcgc caggacctc ccggggactc tggacgctct ttgtctgccc
 540
 ttccttttcc ctacctcgc tccccgtga gaaagtgggg ctcatgcagc tcagctcagt
 600
 gacagagggt ttattagggg tagctctggg accatcttt tggtgatttc ttctctctct
 660
 ttctctaattg gaataattgt ttctgtctac acttctttat tttctctct ctacagctgc
 720
 cttctaaaaa tgtgcttttc tgttcctgca gaactgaagc ttgcatggcc tttgttgatga
 780
 ctttcccttc acgcgt
 796

<210> 1134
 <211> 147
 <212> PRT
 <213> Homo sapiens

<400> 1134
 Met Gly Pro Arg Ala Thr Pro Asn Lys Pro Ser Val Thr Glu Leu Ser

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      1             5             10             15
Cys Met Ser Pro Thr Phe Ser Arg Gly Ser Glu Val Arg Glu Lys Glu
      20             25             30
Gly Gln Thr Lys Ser Val Gln Ser Pro Arg Glu Val Pro Gly Glu Gly
      35             40             45
Pro Asp Thr Gln Gln Gly Ala Cys Lys Arg Ser Phe Leu Glu Val Ser
      50             55             60
Ser Gln Ile Ser Ser Gln Ser Glu Ala His Ser His Pro Arg Cys Arg
      65             70             75             80
Glu Phe Ser Lys Phe His Arg Ser Val Ile Lys Asp Tyr Asp Lys Pro
      85             90             95
Tyr Tyr Val Ile Asn Asp Ala Leu Lys Glu Lys Ile Leu Tyr Leu Thr
      100            105            110
Pro Pro Thr Gln Asp Arg Arg Glu Ala Ile Ala His Leu Pro Leu Arg
      115            120            125
Gly Ser Leu Ala Ser Gln Gly Glu Ala Ile Ser Gln Ser Val Arg Cys
      130            135            140
Gln Trp Gly
145

```

<210> 1135
 <211> 376
 <212> DNA
 <213> Homo sapiens

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<400> 1135
gatcaggcca cacaggacaa cttcgagaag ggctccatct tcccaccctt caccagcatc
60
agaaagatct ctgcgcacat cgctgcagcc gtggctgcaa aagcctacga gctcgggtctg
120
gcgaccgctc tgcctccccc cagcgacctg gtgaaatatg cagagaactg catgtacact
180
cccgtctacc gcaactaccg gtagtgctgc ggggatcaat tttgcagtaa taaaaaatct
240
actatcaacg cggatggtac tctgttgttt atagtccctg ctgctaacca cccttgttgc
300
tggtgctgct ggagaggcat tgtacctgct catgcatata tgatatatat atgttgtaac
360
gttgtgaaag caaact
376

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<210> 1136
 <211> 67
 <212> PRT
 <213> Homo sapiens

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<400> 1136
Asp Gln Ala Thr Gln Asp Asn Phe Glu Lys Gly Ser Ile Phe Pro Pro
      1             5             10             15
Phe Thr Ser Ile Arg Lys Ile Ser Ala His Ile Ala Ala Val Ala
      20             25             30
Ala Lys Ala Tyr Glu Leu Gly Leu Ala Thr Arg Leu Pro Pro Pro Ser
      35             40             45
Asp Leu Val Lys Tyr Ala Glu Asn Cys Met Tyr Thr Pro Val Tyr Arg

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60

<400> 1139
gtgcacaggt cgtctgaggc catgccgcgg acgategatc cgagtatggc ggcaccttca
60

ccaatcccgt aggaccgctc tcgtccagca tcgaccaagg cgctgttgag gcgttcggct
 120
 tcggtaatga actcgatgcg ctcaatatcc acgggggtag cgaaatcgta gatcttgccc
 180
 agactgaggc cttggaggag cgcggccgctc ggggggacgt ggctgcggc cgggcgttcc
 240
 ttgctctcaa ggacttcgctc gtcgcggctg acaaggaata cgtttggtg gtcgcctgca
 300
 atgcatgctc gagcgtggtg accatcgagg tgaaggacgg ttccggcata gaggtcatcg
 360
 tccacatcgg ccacagttag ttcgacgact cctgagtcga ctagatgacg cgccttctct
 420
 gccgcgtctt cgctgacgctc ggccaggacc gctagc
 456

<210> 1140
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 1140
 Met Trp Thr Met Thr Ser Met Pro Lys Pro Ser Phe Thr Ser Met Val
 1 5 10 15
 Thr Thr Leu Glu His Ala Leu Gln Ala Thr Thr Gln Thr Tyr Ser Leu
 20 25 30
 Ser Ala Ala Thr Thr Lys Ser Leu Arg Ala Arg Asn Ala Arg Pro Gln
 35 40 45
 Ala Thr Ser Pro Arg Arg Pro Arg Ser Ser Lys Ala Ser Val Trp Pro
 50 55 60
 Arg Ser Thr Ile Ser Leu Pro Pro Trp Ile Leu Ser Ala Ser Ser Ser
 65 70 75 80
 Leu Pro Lys Pro Asn Ala Ser Thr Ala Pro Trp Ser Met Leu Asp Glu
 85 90 95
 Thr Gly Pro Thr Gly Leu Val Lys Val Pro Pro Tyr Ser Asp Arg Ser
 100 105 110
 Ser Ala Ala Trp Pro Gln Thr Thr Cys Ala
 115 120

<210> 1141
 <211> 354
 <212> DNA
 <213> Homo sapiens

<400> 1141
 ggccgcatgc tcggcgggct ggtgctgggt gtggccgaag cctttggcgc cgatatcttc
 60
 ggcgaccagt acaaggacgt ggtggcggtt ggctgttggt ttctggtgct gttgttccgt
 120
 ccgaccggca ttctgggccc tccggagggt gagaaagtat gagcagatat cttaaatcgg
 180
 cgtttttcag cgccctgttg gtgtgggccc tggcctttcc ggtactcggc ctcaagctga
 240
 gcattgtcgg gatcaaccac gaagtgcatt gcaccgggtcc cgtgaccttg accatcatcg
 300

ccctgtgctc ggtgccgatg ttcttgccgcg tgctgtttac ccagcaagtc ggtg
354

<210> 1142
<211> 53
<212> PRT
<213> Homo sapiens

<400> 1142
Gly Ala Met Leu Gly Gly Leu Val Leu Gly Val Ala Glu Ala Phe Gly
1 5 10 15
Ala Asp Ile Phe Gly Asp Gln Tyr Lys Asp Val Val Ala Phe Gly Leu
20 25 30
Leu Val Leu Val Leu Leu Phe Arg Pro Thr Gly Ile Leu Gly Arg Pro
35 40 45
Glu Val Glu Lys Val
50

<210> 1143
<211> 353
<212> DNA
<213> Homo sapiens

<400> 1143
acgcgttgca catccccag gaccatcaac cgcggcattg ccgcatagac ctggagatcc
60
catgcaacgt gaaatgaagt tcgaatcgat caaggcaaag gccaaggcga tgctcatcgg
120
cgcagccgac gacacagcaa gcgcaggcgc gaccaaccga gggtaggctca acagcgccgc
180
attcgaaatc ctggcccacg tggccgtcaa tgcccaacac tacgcgctct ccgagagacc
240
ggcgctggag gagttcgcca agagcttcca gccgcgcaac aaccaggact acgtggccgc
300
gatcgccaag aaggccgcga accacaccat gcatcccggc aggcagtcga ttt
353

<210> 1144
<211> 102
<212> PRT
<213> Homo sapiens

<400> 1144
Met His Gly Val Val Arg Gly Leu Leu Gly Asp Arg Gly His Val Val
1 5 10 15
Leu Val Val Ala Arg Leu Glu Ala Leu Gly Glu Leu Leu Gln Arg Arg
20 25 30
Ser Leu Gly Glu Arg Val Val Leu Gly Ile Asp Gly His Val Gly Gln
35 40 45
Asp Phe Glu Cys Gly Ala Val Glu Pro Pro Ser Val Gly Arg Ala Cys
50 55 60
Ala Cys Cys Val Val Gly Cys Ala Asp Glu His Arg Leu Gly Leu Cys
65 70 75 80
Leu Asp Arg Phe Glu Leu His Phe Thr Leu His Gly Ile Ser Arg Ser

85 90 95
Met Arg Gln Cys Arg Gly
100

<210> 1145
<211> 360
<212> DNA
<213> Homo sapiens

<400> 1145
gtcttcggcg ggctcggcct gttctattgc gtcacgaccc cgggtgtactg gttctcggcc
60
catgaagtgg ccggcacctg ggtactcggg ctgtcggcgg cgatggctct gatgggtgtt
120
ttctacgtcc aggtcatcgc caagaagatc aatcctcgac cctccgacga gaaggacgcc
180
gaggtgatcg acggggctgg tccggtcggg ttcttcccgc cacagagtat ctggccgttc
240
tggtgcgcgc tcgttgtcgc catcatgtgc ctcgcccca tcttcggctg gtggatctct
300
ctgctcgggc tgggcattgt tatctgggcc gcctcggggtt gggcttttga gtactaccgc
360

<210> 1146
<211> 120
<212> PRT
<213> Homo sapiens

<400> 1146
Val Phe Gly Gly Leu Gly Leu Phe Tyr Cys Val Met Thr Pro Val Tyr
1 5 10 15
Trp Phe Ser Ala His Glu Val Ala Gly Thr Trp Val Leu Gly Leu Ser
20 25 30
Ala Ala Met Ala Leu Met Val Phe Phe Tyr Val Gln Val Ile Ala Lys
35 40 45
Lys Ile Asn Pro Arg Pro Ser Asp Glu Lys Asp Ala Glu Val Ile Asp
50 55 60
Gly Ala Gly Pro Val Gly Phe Phe Pro Pro Gln Ser Ile Trp Pro Phe
65 70 75 80
Trp Cys Ala Leu Val Val Ala Ile Met Cys Leu Gly Pro Ile Phe Gly
85 90 95
Trp Trp Ile Ser Leu Leu Gly Leu Gly Ile Val Ile Trp Ala Ala Ser
100 105 110
Gly Trp Ala Phe Glu Tyr Tyr Arg
115 120

<210> 1147
<211> 409
<212> DNA
<213> Homo sapiens

<400> 1147
tgtacattgg ctatgcagtc tggcctcctg aagggttatga tagtagccaa aaatatagaa
60

gccaataaagg catccacctt cttcatcaat ccagaattga tcatgctcat gcctgtgggt
 120
 ggatcactat gtgctctcca aattgggagg ggaagtctac tctcctctct cctctctctc
 180
 ccaccttccc ctctctcttc tctcctttct attcccaggg cagtgggaaca tgatgaggtt
 240
 cttttccctt catggatata ctctttctgc cctccacata aaggggcatt gatggatctt
 300
 caagaatggg atgcctttcc ctagaaaggc taaatattca tgaggctgaa tgtgaggatc
 360
 cagagtacac tgaaatataa ctgggtcatca gtacacatag aatctgatn
 409

<210> 1148
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 1148
 Met Gln Ser Gly Leu Leu Lys Val Met Ile Val Ala Lys Asn Ile Glu
 1 5 10 15
 Ala Lys Lys Ala Ser Thr Phe Phe Ile Asn Pro Glu Leu Ile Met Leu
 20 25 30
 Met Pro Val Gly Gly Ser Leu Cys Ala Leu Gln Ile Gly Arg Gly Ser
 35 40 45
 Leu Leu Ser Ser Leu Leu Ser Leu Pro Pro Ser Pro Leu Ser Ser Leu
 50 55 60
 Leu Ser Ile Pro Arg Ala Val Glu His Asp Glu Val Leu Phe Pro Ser
 65 70 75 80
 Trp Ile Ser Ser Phe Cys Pro Pro His Lys Gly Ala Leu Met Asp Leu
 85 90 95
 Gln Glu Trp Asp Ala Phe Pro
 100

<210> 1149
 <211> 309
 <212> DNA
 <213> Homo sapiens

<400> 1149
 gtcgacttct gcatggaaaa acgcgatctg gtgattgagc acgttgcgga gatgtacggc
 60
 cgtgaggcgg tatcgcatat cattaccttc ggtaccatgg cggcgaaagc gggtattcgt
 120
 gacgtgggccc gtgtactggg tcacccgtat ggcttcgctc atcgcatctc caagctgggtg
 180
 ccgccccgatc cgggcatgac gctggaaaaa gcctttgccg ccgaaccgca gttgccggaa
 240
 atctacgagg ccgatgagga agtcaaagcg ctgatcgaca tggcgcgcaa gctgggaagg
 300
 gtgacgcgg
 309

<210> 1150

<211> 103
 <212> PRT
 <213> Homo sapiens

<400> 1150
 Val Asp Phe Cys Met Glu Lys Arg Asp Leu Val Ile Glu His Val Ala
 1 5 10 15
 Glu Met Tyr Gly Arg Glu Ala Val Ser Gln Ile Ile Thr Phe Gly Thr
 20 25 30
 Met Ala Ala Lys Ala Val Ile Arg Asp Val Gly Arg Val Leu Gly His
 35 40 45
 Pro Tyr Gly Phe Val Asp Arg Ile Ser Lys Leu Val Pro Pro Asp Pro
 50 55 60
 Gly Met Thr Leu Glu Lys Ala Phe Ala Ala Glu Pro Gln Leu Pro Glu
 65 70 75 80
 Ile Tyr Glu Ala Asp Glu Glu Val Lys Ala Leu Ile Asp Met Ala Arg
 85 90 95
 Lys Leu Gly Arg Val Thr Arg
 100

<210> 1151
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 1151
 gcgcgcattt tttgcaaccc aagcgacgtc attatggccg agtcgccggc ttatgtcggg
 60
 gcgctcaata ccttcgcctc gtaccaaact gaggtcattc acgtcgacat ggacgacagc
 120
 gggttgggtc cggaatccct gcgtgagaaa gtgactgcag cgcgtcaaga cggcaagtcg
 180
 gtgaagttcc ttacacgggt tcctaactac tcgaaccctg cggaatctc gcaatccacc
 240
 gagcgtcgcc gggagatcct agcgggtggct gacgagctgg atctgttggt ggttgaggac
 300
 aaccggtacg ggttactcaa cctcgatggg gatccactgc cgacgttgaa gtcgatggat
 360

<210> 1152
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 1152
 Ala Arg Ile Phe Cys Asn Pro Ser Asp Val Ile Met Ala Glu Ser Pro
 1 5 10 15
 Ala Tyr Val Gly Ala Leu Asn Thr Phe Ala Ser Tyr Gln Thr Glu Val
 20 25 30
 Ile His Val Asp Met Asp Asp Ser Gly Leu Val Pro Glu Ser Leu Arg
 35 40 45
 Glu Lys Val Thr Ala Ala Arg Gln Asp Gly Lys Ser Val Lys Phe Leu
 50 55 60
 Tyr Thr Val Pro Asn Tyr Ser Asn Pro Ser Gly Ile Ser Gln Ser Thr

65 70 75 80
 Glu Arg Arg Arg Glu Ile Leu Ala Val Ala Asp Glu Leu Asp Leu Leu
 85 90 95
 Val Val Glu Asp Asn Pro Tyr Gly Leu Leu Asn Leu Asp Gly Asp Pro
 100 105 110
 Leu Pro Thr Leu Lys Ser Met Asp
 115 120

<210> 1153
 <211> 416
 <212> DNA
 <213> Homo sapiens

<400> 1153
 gcgtggattc gtcctggcgg cgctcgctacc gacctgccc agaccgggct cgaccagttg
 60
 cgtgacctca tcaagcggat ggaaaagtac ctccccgaga tcggtcagtt ctgcaatgag
 120
 aatccgatct ttaaggcccg cactcagggc attggttacg ctgatctgtc tacctgtatg
 180
 gccctgggag ttactgggtcc tgctctgcgc gctaccggcc tgccgtggga cctgcgcaag
 240
 acccagccct attgcgatta cgacacgtat gacttcgacg tcgccacctg ggatacctgt
 300
 gactgttacg ggcgtttccg catccgcctg gaagagatgg accagtcggt gcgcattctc
 360
 aagcaatgcc tcaaacgcct cgaggacacc cagggtgacc gtaatatggt cgagga
 416

<210> 1154
 <211> 138
 <212> PRT
 <213> Homo sapiens

<400> 1154
 Ala Trp Ile Arg Pro Gly Gly Val Ala Thr Asp Leu Pro Glu Thr Gly
 1 5 10 15
 Leu Asp Gln Leu Arg Asp Leu Ile Lys Arg Met Glu Lys Tyr Leu Pro
 20 25 30
 Glu Ile Gly Gln Phe Cys Asn Glu Asn Pro Ile Phe Lys Ala Arg Thr
 35 40 45
 Gln Gly Ile Gly Tyr Ala Asp Leu Ser Thr Cys Met Ala Leu Gly Val
 50 55 60
 Thr Gly Pro Ala Leu Arg Ala Thr Gly Leu Pro Trp Asp Leu Arg Lys
 65 70 75 80
 Thr Gln Pro Tyr Cys Asp Tyr Asp Thr Tyr Asp Phe Asp Val Ala Thr
 85 90 95
 Trp Asp Thr Cys Asp Cys Tyr Gly Arg Phe Arg Ile Arg Leu Glu Glu
 100 105 110
 Met Asp Gln Ser Val Arg Ile Leu Lys Gln Cys Leu Lys Arg Leu Glu
 115 120 125
 Asp Thr Gln Gly Asp Arg Asn Met Val Glu
 130 135

<210> 1155
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 1155
 ctttaagttat tttggtcttt gcctctctcc tcaggttgtg aagattacag aaatctggga
 60
 tggttatgg gacgcttctc agccctaagt aggaaaacag cagtgaaaat ggcaaccaaa
 120
 acatcacgca ggactggggg ttttggggaa acagctcact ttagagcagt gcagtgtaga
 180
 gctttccgtc ttctaccagg gtccaccttt aacactgttt atctgaaaat tttccccctg
 240
 gcttactcgc ttgcagctgc ccactttgca gaaagatggc gctctgatct ctacgctccc
 300
 tgttccttca gggactccat agtatttttt ttcacgcgt
 339

<210> 1156
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 1156
 Met Gly Arg Phe Ser Ala Leu Ser Arg Lys Thr Ala Val Lys Met Ala
 1 5 10 15
 Thr Lys Thr Ser Arg Arg Thr Gly Gly Phe Gly Glu Thr Ala His Phe
 20 25 30
 Arg Ala Val Gln Cys Arg Ala Phe Arg Leu Leu Pro Gly Ser Thr Phe
 35 40 45
 Asn Thr Val Tyr Leu Lys Ile Phe Pro Leu Ala Tyr Ser Leu Ala Ala
 50 55 60
 Ala His Phe Ala Glu Arg Trp Arg Ser Asp Leu Tyr Ala Pro Cys Ser
 65 70 75 80
 Phe Arg Asp Ser Ile Val Phe Phe Phe Thr Arg
 85 90

<210> 1157
 <211> 426
 <212> DNA
 <213> Homo sapiens

<400> 1157
 nnacagctc tctccgaccc ggcggcggtt gcacacgtcc ccgtctgagg agtattcgtg
 60
 ctggcaaaac tcgtgaccgc acacctgagg gcctatcggt tgcacgttgc cgtcatcatc
 120
 gttatgcagg tttgcgccca aatcgcggcc ctgaccttgc caaccatcaa cgcagacatc
 180
 atcaacaagg gcgtcgtgac agcggatacc ggatatgtca ccaccactc cctcttcatg
 240
 ctggcggtcg ctttagggca ggccatctgc caggtcattg cggtttatct cgccgctcag
 300

gtggcgatgg gaatgggccc tgacgttcgc gacgccatct tcacccgcac ccttgacttc
 360
 tcggccccggg agatcaacaa attcggagca ccatcactca ttacccggac taccaacgac
 420
 gtccag
 426

<210> 1158
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 1158
 Val Leu Ala Lys Leu Val Thr Arg His Leu Arg Ala Tyr Arg Leu His
 1 5 10 15
 Val Ala Val Ile Ile Val Met Gln Val Cys Ala Gln Ile Ala Ala Leu
 20 25 30
 Thr Leu Pro Thr Ile Asn Ala Asp Ile Ile Asn Lys Gly Val Val Thr
 35 40 45
 Ala Asp Thr Gly Tyr Val Thr Thr His Ser Leu Phe Met Leu Ala Val
 50 55 60
 Ala Leu Gly Gln Ala Ile Cys Gln Val Ile Ala Val Tyr Leu Ala Ala
 65 70 75 80
 Gln Val Ala Met Gly Met Gly Arg Asp Val Arg Asp Ala Ile Phe Thr
 85 90 95
 Arg Thr Leu Asp Phe Ser Ala Arg Glu Ile Asn Lys Phe Gly Ala Pro
 100 105 110
 Ser Leu Ile Thr Arg Thr Thr Asn Asp Val Gln
 115 120

<210> 1159
 <211> 434
 <212> DNA
 <213> Homo sapiens

<400> 1159
 tctctccgac cgcgcctggg gcccggtggg gtccctgcggg gacgcgggag aggacggcgc
 60
 ggacgaggca ggagcaggcc gggctctcgc catgggtcac tgcgcctct gccacgggaa
 120
 gttttcctcg agaagcctgc gcagcatctc cgagagggcg cctggagcga gcatggagag
 180
 gccatccgca gaggagcgcg tgctcgtacg ggacttccag cgctgcttg gtgtggctgt
 240
 ccgccaggac cccaccttgt ctccgtttgt ctgcaagagc tgccacgecc agttctacca
 300
 gtgccacagc cttctcaagt ccttcctgca gaggggtcaac gcctccccgg ctggtcgccg
 360
 gaagccttgt gcaaaggctg gtgcccagcc cccaacaggg gcagaggagg gagcgtgtct
 420
 ggtggatctg atca
 434

<210> 1160

<211> 114
 <212> PRT
 <213> Homo sapiens

<400> 1160
 Met Gly His Cys Arg Leu Cys His Gly Lys Phe Ser Ser Arg Ser Leu
 1 5 10 15
 Arg Ser Ile Ser Glu Arg Ala Pro Gly Ala Ser Met Glu Arg Pro Ser
 20 25 30
 Ala Glu Glu Arg Val Leu Val Arg Asp Phe Gln Arg Leu Leu Gly Val
 35 40 45
 Ala Val Arg Gln Asp Pro Thr Leu Ser Pro Phe Val Cys Lys Ser Cys
 50 55 60
 His Ala Gln Phe Tyr Gln Cys His Ser Leu Leu Lys Ser Phe Leu Gln
 65 70 75 80
 Arg Val Asn Ala Ser Pro Ala Gly Arg Arg Lys Pro Cys Ala Lys Val
 85 90 95
 Gly Ala Gln Pro Pro Thr Gly Ala Glu Glu Gly Ala Cys Leu Val Asp
 100 105 110
 Leu Ile

<210> 1161
 <211> 355
 <212> DNA
 <213> Homo sapiens

<400> 1161
 ctgcacacac accaggccac gccacgagg acggccagtc agcatgcagc caatacaccc
 60
 acagagggat ggggagcagc cctcagtgcc agctccaaca ggcccactgc aggtcctgtc
 120
 actgcaccca aggagctgcc ttccatttca cctgacattt ccactaaggc cccagcgttt
 180
 atcattccag aagagcagca ggcagaacct tcacctccca agagctgcaa gtgcgctgtg
 240
 gcaggaaaag aagatctggc gtctgaagtc agctcctgct ctccaggaaa agagggacga
 300
 tgacatagga cttgagcaaa atgagagccc cgtgatggga gagaacacct gatca
 355

<210> 1162
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 1162
 Met Gln Pro Ile His Pro Gln Arg Asp Gly Glu Gln Pro Ser Val Pro
 1 5 10 15
 Ala Pro Thr Gly Pro Leu Gln Val Leu Ser Leu His Pro Arg Ser Cys
 20 25 30
 Leu Pro Phe His Leu Thr Phe Pro Leu Arg Ala Gln Arg Leu Ser Phe
 35 40 45
 Gln Lys Ser Ser Arg Gln Asn Leu His Leu Pro Arg Ala Ala Ser Ala

50 55 60
 Leu Trp Gln Glu Lys Lys Ile Trp Arg Leu Lys Ser Ala Pro Ala Leu
 65 70 75 80
 Gln Glu Lys Arg Asp Asp Asp Ile Gly Leu Glu Gln Asn Glu Ser Pro
 85 90 95
 Val Met Gly Glu Asn Thr
 100

<210> 1163
 <211> 466
 <212> DNA
 <213> Homo sapiens

<400> 1163
 ngcgcgccag gaagcgggag gtcagctgta caccaggggt aatagaactt ctaccctcag
 60
 aggagtcaaa gagaaggcag aactatggca ggaaagctcc ggaagtccca catccctgga
 120
 gtgagcatct ggcagctggg ggaggagatc cctgaaggct gcagcacgcc ggactttgag
 180
 cagaagcccg tcacctcggc tctgccagag gggaaaaatg ctgtctttcg ggctgtggtc
 240
 tgtggggagc ccaggcccga ggtgcgttgg cagaactcca aaggtgacct cagtgattcc
 300
 agcaagtaca agatctcttc cagccctggc agcaaggagc acgtgctgca gatcaacaag
 360
 ctgacaggcg aggacacgga tctgtaccac tgcacagcag taaatgcgta cggagaggcc
 420
 gcttgctcag tgagactcac cgtcatcgaa gttggctttc ggaaga
 466

<210> 1164
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 1164
 Met Ala Gly Lys Leu Arg Lys Ser His Ile Pro Gly Val Ser Ile Trp
 1 5 10 15
 Gln Leu Val Glu Glu Ile Pro Glu Gly Cys Ser Thr Pro Asp Phe Glu
 20 25 30
 Gln Lys Pro Val Thr Ser Ala Leu Pro Glu Gly Lys Asn Ala Val Phe
 35 40 45
 Arg Ala Val Val Cys Gly Glu Pro Arg Pro Glu Val Arg Trp Gln Asn
 50 55 60
 Ser Lys Gly Asp Leu Ser Asp Ser Ser Lys Tyr Lys Ile Ser Ser Ser
 65 70 75 80
 Pro Gly Ser Lys Glu His Val Leu Gln Ile Asn Lys Leu Thr Gly Glu
 85 90 95
 Asp Thr Asp Leu Tyr His Cys Thr Ala Val Asn Ala Tyr Gly Glu Ala
 100 105 110
 Ala Cys Ser Val Arg Leu Thr Val Ile Glu Val Gly Phe Arg Lys
 115 120 125

<210> 1165
 <211> 414
 <212> DNA
 <213> Homo sapiens

<400> 1165
 tgggtggttc cggacacana aaatcacgtg ttgaaccgaa tttcaggcat ggtgaaaggc
 60
 tgcttttagta aagtccttgt tgagccgcgt ctgctcaagc tcaacttgac nattatgtgt
 120
 ctgcacattc tgctgatgtc cacgttcgtg gccctgcccg gtcagttggc tgcagcagga
 180
 ttccccgccg ctgaacactg gaaagtgtat ctggtgacga tgctcatctc ctctgtctcc
 240
 gttgtccctt tcattatcta tgcagaagtg aaacgccgca tgaagcgcgt attcctgacg
 300
 tgtgttgcg c tgctgttgat tgccgaaatc gtactatggg gctccggtcc acacttctgg
 360
 gaactggtca tcggcgtaca gcttttcttc ctgccttta atctcatgga agcc
 414

<210> 1166
 <211> 138
 <212> PRT
 <213> Homo sapiens

<400> 1166
 Trp Val Val Pro Asp Thr Xaa Asn His Val Leu Asn Arg Ile Ser Gly
 1 5 10 15
 Met Val Lys Gly Cys Phe Ser Lys Val Leu Val Glu Pro Arg Leu Leu
 20 25 30
 Lys Leu Asn Leu Thr Ile Met Cys Leu His Ile Leu Leu Met Ser Thr
 35 40 45
 Phe Val Ala Leu Pro Gly Gln Leu Ala Ala Ala Gly Phe Pro Ala Ala
 50 55 60
 Glu His Trp Lys Val Tyr Leu Val Thr Met Leu Ile Ser Phe Val Ser
 65 70 75 80
 Val Val Pro Phe Ile Ile Tyr Ala Glu Val Lys Arg Arg Met Lys Arg
 85 90 95
 Val Phe Leu Thr Cys Val Ala Leu Leu Leu Ile Ala Glu Ile Val Leu
 100 105 110
 Trp Gly Ser Gly Pro His Phe Trp Glu Leu Val Ile Gly Val Gln Leu
 115 120 125
 Phe Phe Leu Ala Phe Asn Leu Met Glu Ala
 130 135

<210> 1167
 <211> 464
 <212> DNA
 <213> Homo sapiens

<400> 1167
 gtcgaccccc tgggcaagag tcgcggcccc tgacgataac ttcacccccg cggccttgag
 60

ctggttgggac cggttggtta aggcctgggc accggtagcg gcctggtgga taccctcatg
 120
 tagccgggtg acctgcctga ccattctcgg caaaccagtg cgcagttgtg tggatgaactc
 180
 attgacccct cgagacagtc gtgaggaacc gtcagcaagt tcgtcgatgc cgtcgtcgat
 240
 gctcttgcca gagttcggat ccttgatcgc catcgccctg acggccaccc ccgaccacgc
 300
 ccgcacgccc agggcgatcc catcggtcat cgcgtcgcgg acgatgggta ccaggtcgtg
 360
 gcattcctgc gcggtgtggc ttgcacgca tcgacgcagg aagtcagcct cgccccggga
 420
 cagggttcc ttactaagtt ccgcggtttt ctttcccgac gcgt
 464

<210> 1168
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 1168
 Met Thr Asp Gly Tyr Ala Leu Gly Val Arg Ala Gly Ser Gly Val Ala
 1 5 10 15
 Val Lys Ala Met Ala Ile Lys Asp Pro Asn Ser Gly Lys Ser Ile Asp
 20 25 30
 Asp Gly Ile Asp Glu Leu Ala Asp Gly Ser Ser Arg Leu Ser Arg Gly
 35 40 45
 Val Asn Glu Phe Thr Thr Gln Leu Arg Thr Gly Leu Pro Lys Met Val
 50 55 60
 Arg Gln Val Thr Arg Leu His Glu Gly Ile His Gln Ala Ala Thr Gly
 65 70 75 80
 Ala Gln Ala Leu Ala Ser Arg Ser Gln Gln Leu Lys Ala Gly Gly Val
 85 90 95
 Lys Leu Ser Ser Gly Ala Ala Thr Leu Ala His Gly Val Asp
 100 105 110

<210> 1169
 <211> 486
 <212> DNA
 <213> Homo sapiens

<400> 1169
 nacgcgtgaa gggagcagaa cggacaccag ttactagtgg ctctggtcgg ggacagcctc
 60
 ctagagcctt tctggccaat gggaacagga atagcccggg gctttctagc tgctatggac
 120
 tctgcctgga tgggccgaag ttggtctcta ggaacgagcc ctttggaagt gctggcagag
 180
 agggaaagta ttacagggtt gctgcctcag accaccctg agaatgtgag taagaacttc
 240
 agccagtaca gtatcgaccc tgtcactcgg tatcccaata tcaacgtcaa cttcctccgg
 300
 ccaagccagg tgcgccattt atatgatact ggcgaaacaa aagatattca cctggaaatg
 360

gagagcctgg tgaattcccg aaccaccccc aaattgactc gcaatgagtc tgtagctcgt
 420
 tcaagcaaac tgctgggttg gtgccagagg cagacagatg gctatgcagg ggtaaactg
 480
 acagat
 486

<210> 1170
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 1170
 Arg Glu Gln Asn Gly His Gln Leu Leu Val Ala Leu Val Gly Asp Ser
 1 5 10 15
 Leu Leu Glu Pro Phe Trp Pro Met Gly Thr Gly Ile Ala Arg Gly Phe
 20 25 30
 Leu Ala Ala Met Asp Ser Ala Trp Met Val Arg Ser Trp Ser Leu Gly
 35 40 45
 Thr Ser Pro Leu Glu Val Leu Ala Glu Arg Glu Ser Ile Tyr Arg Leu
 50 55 60
 Leu Pro Gln Thr Thr Pro Glu Asn Val Ser Lys Asn Phe Ser Gln Tyr
 65 70 75 80
 Ser Ile Asp Pro Val Thr Arg Tyr Pro Asn Ile Asn Val Asn Phe Leu
 85 90 95
 Arg Pro Ser Gln Val Arg His Leu Tyr Asp Thr Gly Glu Thr Lys Asp
 100 105 110
 Ile His Leu Glu Met Glu Ser Leu Val Asn Ser Arg Thr Thr Pro Lys
 115 120 125
 Leu Thr Arg Asn Glu Ser Val Ala Arg Ser Ser Lys Leu Leu Gly Trp
 130 135 140
 Cys Gln Arg Gln Thr Asp Gly Tyr Ala Gly Val Asn Val Thr Asp
 145 150 155

<210> 1171
 <211> 429
 <212> DNA
 <213> Homo sapiens

<400> 1171
 acgcgttcaa caaagcacag aaccggagat gcagtgggag ccgagagcag gaagcgcgga
 60
 ggcagcgcca ggtgctggcg ctgcccagagg ccccgtagca agtggggccc atagcagccg
 120
 actcgctaga ccctcccaaa acgcacacca cgcgcgacca ggaccgagag gcccgcacgg
 180
 ccctgctagg ccacaaacac tccactgtct ccagggtaaa agacaaacac agcctcgctt
 240
 gtccctccaa gagtacaacc tctgtctgat gaaaaacaaa cgaccagag aggaggcagc
 300
 tgccgggaca ctgcaggctg ggcccgcgc gcccttgag ggcagggtcaa aatcccggaa
 360
 caggcacagt gttcaggctg attgactgtc ccaggccagg gcggcctcaa ctgccagagc
 420

acctcctac
429

<210> 1172
<211> 118
<212> PRT
<213> Homo sapiens

<400> 1172
Met Gln Trp Glu Pro Arg Ala Gly Ser Ala Glu Ala Ala Pro Gly Ala
1 5 10 15
Gly Ala Ala Arg Gly Pro Val Pro Ser Gly Ala His Ser Ser Arg Leu
20 25 30
Ala Arg Pro Ser Gln Asn Ala His His Ala Arg Pro Gly Pro Arg Gly
35 40 45
Pro His Gly Pro Ala Arg Pro Gln Thr Leu His Cys Leu Gln Gly Lys
50 55 60
Arg Gln Thr Gln Pro Arg Leu Ser Leu Gln Glu Tyr Asn Leu Cys Leu
65 70 75 80
Met Lys Asn Lys Arg Pro Arg Glu Glu Ala Ala Ala Gly Thr Leu Gln
85 90 95
Ala Gly Pro Ala Ala Pro Leu Glu Gly Arg Ser Lys Ser Arg Asn Arg
100 105 110
His Ser Val Gln Ala Asp
115

<210> 1173
<211> 435
<212> DNA
<213> Homo sapiens

<400> 1173
cgcggtcaatg acgacggcga gcattctgcc gagcaggtga tgcgagccac ccgcggtgct
60
ggacttgggg ccgaggccaa gcgtcgcatc atcttgggta cctatgcctt gtcggctggg
120
tactatgacg cctactacgg ctcggtcag aaagtccgta ccctcatcca acgcgacttc
180
gagaaagcat ggcagatgtg cgatgtgctc gtgtcaccgg ccacgccaac gactgccttc
240
cggctgggtg agcgtactgc tgaccgatg gcgatgtacc gctccgatct atgcacggtc
300
ccggccaata tggccggaag tcccgcagga tctttcccga tcggtctatc agagaccgac
360
ggcatgcccc tcggcatgca ggtgatggcg ccaatcatgg cggacgatcg aatctaccga
420
gttggggccg ctcta
435

<210> 1174
<211> 145
<212> PRT
<213> Homo sapiens

<400> 1174

Arg Val Asn Asp Asp Gly Glu His Ser Ala Glu Gln Val Met Arg Ala
 1 5 10 15
 Thr Arg Gly Ala Gly Leu Gly Ala Glu Ala Lys Arg Arg Ile Ile Leu
 20 25 30
 Gly Thr Tyr Ala Leu Ser Ala Gly Tyr Tyr Asp Ala Tyr Tyr Gly Ser
 35 40 45
 Ala Gln Lys Val Arg Thr Leu Ile Gln Arg Asp Phe Glu Lys Ala Trp
 50 55 60
 Gln Met Cys Asp Val Leu Val Ser Pro Ala Thr Pro Thr Thr Ala Phe
 65 70 75 80
 Arg Leu Gly Glu Arg Thr Ala Asp Pro Met Ala Met Tyr Arg Ser Asp
 85 90 95
 Leu Cys Thr Val Pro Ala Asn Met Ala Gly Ser Pro Ala Gly Ser Phe
 100 105 110
 Pro Ile Gly Leu Ser Glu Thr Asp Gly Met Pro Val Gly Met Gln Val
 115 120 125
 Met Ala Pro Ile Met Ala Asp Asp Arg Ile Tyr Arg Val Gly Ala Ala
 130 135 140
 Leu
 145

<210> 1175

<211> 729

<212> DNA

<213> Homo sapiens

<400> 1175

gatcgactg caatccaccc acatctactt gatatgaaaa ttggtcaagg caaatatgag
 60
 caggggttct ttccaaagtt acagtcgat gtcttggaac caggaccaac cagtaacaat
 120
 cgctgggtaa gtcggagtgc cactgcacag cgcaggaaag gacgccttcg ccagcattct
 180
 gagcatgttg ggctggacaa cgacttgagg gagaaatata tgcaagaggc acgaagttaa
 240
 ggaaaaaacc tgaggcaacc caaactgtca gacctctctc ctgcagttat tgcacagacc
 300
 aactgtaaat tcgtagaagg cttattaaaa gaatgtagaa ataagacaaa gcgcatgttg
 360
 gtggagaaga tgggacatga agcgggtggaa cttggccatg gagaagcaaa catcaccggc
 420
 ctggaggaga acaccttgat cgccagcctt tgtgacctgc tggagaggat atggagccat
 480
 ggcttgagg tcaagcaggg gaagtcggtt ttgtggtcac atttaattcc ttttcaggac
 540
 agagaagaga accaagagcc ccttgcagaa tcaccagttg ccttcggacc agaaagaaaa
 600
 aaatctgact caggagttat gttgccaacg ctcagggtct ctcttattca ggacatgagg
 660
 catattcaaa acatgagtga gatcaagact gatgttggaac gagctcgggc gtggataaga
 720
 ctgtctcta
 729

<210> 1176
 <211> 243
 <212> PRT
 <213> Homo sapiens

<400> 1176
 Asp Arg Thr Ala Ile His Pro His Leu Leu Asp Met Lys Ile Gly Gln
 1 5 10 15
 Gly Lys Tyr Glu Gln Gly Phe Phe Pro Lys Leu Gln Ser Asp Val Leu
 20 25 30
 Ala Thr Gly Pro Thr Ser Asn Asn Arg Trp Val Ser Arg Ser Ala Thr
 35 40 45
 Ala Gln Arg Arg Lys Gly Arg Leu Arg Gln His Ser Glu His Val Gly
 50 55 60
 Leu Asp Asn Asp Leu Arg Glu Lys Tyr Met Gln Glu Ala Arg Ser Leu
 65 70 75 80
 Gly Lys Asn Leu Arg Gln Pro Lys Leu Ser Asp Leu Ser Pro Ala Val
 85 90 95
 Ile Ala Gln Thr Asn Cys Lys Phe Val Glu Gly Leu Leu Lys Glu Cys
 100 105 110
 Arg Asn Lys Thr Lys Arg Met Leu Val Glu Lys Met Gly His Glu Ala
 115 120 125
 Val Glu Leu Gly His Gly Glu Ala Asn Ile Thr Gly Leu Glu Glu Asn
 130 135 140
 Thr Leu Ile Ala Ser Leu Cys Asp Leu Leu Glu Arg Ile Trp Ser His
 145 150 155 160
 Gly Leu Gln Val Lys Gln Gly Lys Ser Val Leu Trp Ser His Leu Ile
 165 170 175
 Pro Phe Gln Asp Arg Glu Glu Asn Gln Glu Pro Leu Ala Glu Ser Pro
 180 185 190
 Val Ala Leu Gly Pro Glu Arg Lys Lys Ser Asp Ser Gly Val Met Leu
 195 200 205
 Pro Thr Leu Arg Val Ser Leu Ile Gln Asp Met Arg His Ile Gln Asn
 210 215 220
 Met Ser Glu Ile Lys Thr Asp Val Gly Arg Ala Arg Ala Trp Ile Arg
 225 230 235 240
 Leu Ser Leu

<210> 1177
 <211> 581
 <212> DNA
 <213> Homo sapiens

<400> 1177
 acgcgtgatg agttgcgcga gaccagcaac tgcagccgaa tacagttttc ttgtgtaccc
 60
 cgtcgcacag ctgcgagagg tgggcattgc cgagtgaggc aacgatgtct aaggcggaaa
 120
 gctcatcctc ggcagacggg aagactttgt cgtcggggat gttgtcaatg agagcgggga
 180
 cgtcgatctc ggtactgcc atggcgatcat gaaggatcgc gcgatacggg gcgacgaccc
 240

cgatgagggc gtcgtcgaat ccagcgatga tcgatacctc tctcggtagc acgtccgtgg
 300
 ccaacaggtg gtcgacttgg gcgggggcta gccatgtaat tgttccgagc acatggaggg
 360
 tggctgccag gaggcggatg gccgggttctg gggcatcttt ggagatcttc agccggacat
 420
 cagtgggcag tccggccggg acttggcaga gggcctgggc gggatgggag cgctgggcga
 480
 cgacgaaacg ccccgacgcc gtaacgccgt gggcttggag atcgcaggtc cacttctctg
 540
 ggctttcacc ggcagagatc atggtgtgga ccaccattgt g
 581

<210> 1178
 <211> 192
 <212> PRT
 <213> Homo sapiens

<400> 1178
 Met Val Val His Thr Met Ile Ser Ala Gly Glu Ser Pro Glu Lys Trp
 1 5 10 15
 Thr Cys Asp Leu Gln Ala His Gly Val Thr Ala Ser Gly Arg Phe Val
 20 25 30
 Val Ala Gln Arg Ser His Pro Ala Gln Ala Leu Cys Gln Val Pro Ala
 35 40 45
 Gly Leu Pro Thr Asp Val Arg Leu Lys Ile Ser Lys Asp Ala Pro Glu
 50 55 60
 Pro Ala Ile Arg Leu Leu Ala Ala Thr Leu His Val Leu Gly Thr Ile
 65 70 75 80
 Thr Trp Leu Ala Pro Ala Gln Val Asp His Leu Leu Ala Thr Asp Val
 85 90 95
 Leu Pro Arg Glu Val Ser Ile Ile Ala Gly Phe Asp Asp Ala Leu Ile
 100 105 110
 Gly Val Val Ala Pro Tyr Arg Ala Ile Leu His Asp Ala Met Gly Ser
 115 120 125
 Thr Glu Ile Asp Val Pro Ala Leu Ile Asp Asn Ile Pro Asp Asp Lys
 130 135 140
 Val Phe Pro Ser Ala Glu Asp Glu Leu Ser Ala Leu Asp Ile Val Ala
 145 150 155 160
 Ser Leu Gly Asn Ala His Leu Ser Gln Leu Cys Asp Gly Val His Lys
 165 170 175
 Lys Thr Val Phe Gly Cys Ser Cys Trp Ser Arg Ala Thr His His Ala
 180 185 190

<210> 1179
 <211> 597
 <212> DNA
 <213> Homo sapiens

<400> 1179
 gtgcactttc tggcttctaa ctgtggcccc agccctgact ccttgaggtg ctctgtgct
 60
 gattggggct tctggacatg ctgccacaag atgtctggaa actccagggg gcacctgccg
 120

agaccctgcc ctgggaacgg ccggaagaat cccaaaacat gagattccgg tgcagctgag
 180
 ccccgccaat tcattgtctc tttcagtcctc ttctgaaggc tgcatttggc aatgtgaccc
 240
 tcgggggtggg gaaggcatca gaggaatata ggctatggga cgccagaggc agcgtcctgg
 300
 ggacaaagcc cacttcttcc catgcccagg gcttcctcat ggaccagca tggaggacgt
 360
 ggccctcaga cgtccatggg tggtagggga ggcacgtgct gtttggecct gtctctgctc
 420
 agagtctcat aggaagatgc atgggccaca caacagttag tcggcagggg gtccaggctt
 480
 cccctcccaa ccagtgggtg tgagacgctt ggtttataac ccaagatccc ttgtcccatt
 540
 ggtgcctcct gaatctccca cctcccggcg cacctgcatg gcctctacct gacgcgt
 597

<210> 1180
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 1180
 Met Gly Arg Gln Arg Gln Arg Pro Gly Asp Lys Ala His Phe Phe Pro
 1 5 10 15
 Cys Pro Gly Leu Pro His Gly Pro Ser Met Val Asp Val Ala Leu Arg
 20 25 30
 Arg Pro Trp Val Val Gly Glu Ala Arg Ala Val Trp Pro Cys Leu Cys
 35 40 45
 Ser Glu Ser His Arg Lys Met His Gly Pro His Asn Ser Glu Ser Ala
 50 55 60
 Gly Ser Pro Gly Phe Pro Ser Gln Pro Val Val Leu Arg Arg Leu Val
 65 70 75 80
 Tyr Asn Pro Arg Ser Leu Val Pro Leu Val Pro Pro Glu Ser Pro Thr
 85 90 95
 Ser Arg Gly Thr Cys Met Ala Ser Thr
 100 105

<210> 1181
 <211> 352
 <212> DNA
 <213> Homo sapiens

<400> 1181
 gtcgactacc tcgatgtttc cccgcgtcag atggctctccg tggctactgc catgattccg
 60
 ttctctgagc acgacgacgc taaccgtgcc ctgatgggtg cgaacatgca gcgtcaggct
 120
 gtgccgctgc tgcgttcgga ggctccgttc gtcggtaccg gtagggagca gcgtgctgct
 180
 tacgacgccg gcgatgtcat tgctcgcttcg gccacagggtg tggctcgagac cgtgtcggca
 240
 ggcttcatca ccatcatgga cgatgagggc cagcgccaca cctacctgct gcgcaagttc
 300

gagcgcacca accagggcac ctgctacaac cagaagccac tggtgacgag gg
352

<210> 1182
<211> 117
<212> PRT
<213> Homo sapiens

<400> 1182
Val Asp Tyr Leu Asp Val Ser Pro Arg Gln Met Val Ser Val Ala Thr
1 5 10 15
Ala Met Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala Leu Met
20 25 30
Gly Ala Asn Met Gln Arg Gln Ala Val Pro Leu Leu Arg Ser Glu Ala
35 40 45
Pro Phe Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr Asp Ala Gly
50 55 60
Asp Val Ile Val Ala Ser Ala Thr Gly Val Val Glu Thr Val Ser Ala
65 70 75 80
Gly Phe Ile Thr Ile Met Asp Asp Glu Gly Gln Arg His Thr Tyr Leu
85 90 95
Leu Arg Lys Phe Glu Arg Thr Asn Gln Gly Thr Cys Tyr Asn Gln Lys
100 105 110
Pro Leu Leu Thr Arg
115

<210> 1183
<211> 432
<212> DNA
<213> Homo sapiens

<400> 1183
gacccctctg ggcgctgggc caagcgctg gtgaggccgt cctctcctgc agaaccgccg
60
cctcttcgcc cctgcccgt cactgttct gtctgctca cctcctccag gaagcctgcc
120
tggccttctc catgctgatg ggcgtggccc ttgtccctgc agccatgcat tgacctccgt
180
ggctcctgga ggccaggcca cgtcctcatc cctctgggt gagtgagagg cacagcctgg
240
gtgcgtgggg ccgtggcggc tccgaggggc caccgctgtg tcctctcatg agtgggtgcc
300
gtccaggtct gtccctgggt ggctgcgagg aggaggttg cctcgcgcgg ccatgtgcgt
360
gacagtggag acatcgccag cctcctgctt gcacagctga cggcagcccc tctctctcca
420
gcatgtccc ca
432

<210> 1184
<211> 141
<212> PRT
<213> Homo sapiens

<400> 1184

Met Ala Gly Glu Arg Gly Ala Ala Val Ser Cys Ala Ser Arg Arg Leu
 1 5 10 15
 Ala Met Ser Pro Leu Ser Arg Thr Trp Pro Arg Glu Ala Asn Leu Leu
 20 25 30
 Leu Ala Ala Ser Pro Gly Gln Thr Trp Thr Ala Pro Thr His Glu Arg
 35 40 45
 Thr Gln Arg Trp Arg Leu Gly Ala Ala Thr Ala Pro Arg Thr Gln Ala
 50 55 60
 Val Pro Leu Thr His Pro Glu Gly Met Arg Thr Trp Pro Gly Leu Gln
 65 70 75 80
 Glu Pro Arg Arg Ser Met His Gly Cys Arg Asp Lys Gly His Ala His
 85 90 95
 Gln His Gly Glu Gly Gln Ala Gly Phe Leu Glu Glu Val Ser Arg Thr
 100 105 110
 Glu Gln Val Ser Gly Gln Gly Arg Arg Gly Arg Gly Ser Ala Gly Glu
 115 120 125
 Asp Gly Leu Thr Thr Arg Leu Asp Gln Arg Pro Glu Gly
 130 135 140

<210> 1185

<211> 423

<212> DNA

<213> Homo sapiens

<400> 1185

accggtgaat ttggccttaa cagcgatgga actcctggcc catcttatga acctggcatg
 60
 gaattacgcg gcaaataatgt attgttgggt gaaggtgtac ggggctctct atctaaacaa
 120
 gtcataata aataccaatt atccgagggt catgaaccac aaaagttcgg ccttggtta
 180
 aaagaaattt gggaaataga cccagaaaaa cacaagaag gcagagtcag tcataccatg
 240
 ggctggccat taaatggcaa tgctggcggc gggttcttta tttatcatgc agaaaacaat
 300
 caagtcttta tcggctttgt ggtgcatctt aattacgcca acccttacct atccccttac
 360
 caagaatttc aacgctttaa acaccatccg attatcgcg agctattaac tggcggtaaa
 420
 cgc
 423

<210> 1186

<211> 141

<212> PRT

<213> Homo sapiens

<400> 1186

Thr Gly Glu Phe Gly Leu Asn Ser Asp Gly Thr Pro Gly Pro Ser Tyr
 1 5 10 15
 Glu Pro Gly Met Glu Leu Arg Gly Lys Tyr Val Leu Leu Gly Glu Gly
 20 25 30
 Val Arg Gly Ser Leu Ser Lys Gln Val Ile Asn Lys Tyr Gln Leu Ser


```

      35              40              45
Glu Gly His Glu Pro Gln Lys Phe Gly Leu Gly Leu Lys Glu Ile Trp
  50              55              60
Glu Ile Asp Pro Glu Lys His Lys Glu Gly Arg Val Ser His Thr Met
  65              70              75              80
Gly Trp Pro Leu Asn Gly Asn Ala Gly Gly Gly Ser Phe Ile Tyr His
      85              90              95
Ala Glu Asn Asn Gln Val Phe Ile Gly Phe Val Val His Leu Asn Tyr
      100             105             110
Ala Asn Pro Tyr Leu Ser Pro Tyr Gln Glu Phe Gln Arg Phe Lys His
      115             120             125
His Pro Ile Ile Ala Glu Leu Leu Thr Gly Gly Lys Arg
      130             135             140

```

<210> 1187
 <211> 387
 <212> DNA
 <213> Homo sapiens

```

<400> 1187
acgcgtgctg gtagatttaa attgaatgct gatggtaatt tggtagacgaa ttcaggggct
  60
aaggtccagg gctataatgc aatagatggc atagtcgggtg ggaacttaga agatatggta
 120
gtaccactg ctcgaatttc tctcaagca acatcaagtg ttgatttaaa agtgaatctt
 180
aattccgaag gtgaggatgt gccgccttat attcgagcgg actttgatcc agccaatcca
 240
gatacttatg actataactca gacccaaacg gttgcggatg ggagtggtaa taatcattta
 300
attagttatt actatgctaa aagtgatgta gcaaatacct atcaggttta tgccacggta
 360
gatgggaagt cgactgatga taccggt
 387

```

<210> 1188
 <211> 129
 <212> PRT
 <213> Homo sapiens

```

<400> 1188
Thr Arg Ala Gly Glu Phe Lys Leu Asn Ala Asp Gly Asn Leu Val Thr
  1              5              10              15
Asn Ser Gly Ala Lys Val Gln Gly Tyr Asn Ala Ile Asp Gly Ile Val
      20              25              30
Gly Gly Asn Leu Glu Asp Met Val Val Pro Thr Ala Arg Ile Ser Pro
      35              40              45
Gln Ala Thr Ser Ser Val Asp Leu Lys Val Asn Leu Asn Ser Glu Gly
      50              55              60
Glu Asp Val Pro Pro Tyr Ile Arg Ala Asp Phe Asp Pro Ala Asn Pro
  65              70              75              80
Asp Thr Tyr Asp Tyr Thr Gln Thr Gln Thr Val Ala Asp Gly Ser Gly
      85              90              95
Asn Asn His Leu Ile Ser Tyr Tyr Tyr Ala Lys Ser Asp Val Ala Asn

```

	100		105		110										
Thr	Tyr	Gln	Val	Tyr	Ala	Thr	Val	Asp	Gly	Lys	Ser	Thr	Asp	Asp	Thr
	115		120									125			
Gly															

<210> 1189
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 1189
 tcgacgccc accgcccggg ccttgccccc ggcacgatcg gtggcctggt ggccagcacc
 60
 ctgggtgctg gtttcattgg cggcatcggt gcaggttttc tggccgggta cagcgccaag
 120
 gccattgccc gctgggcacg gctgcccagc agcctggatg cgctcaaacc gattctgac
 180
 atttcgctgc tggccagcct gttcactggg ttggtgatga tctacgtggt cggccagccg
 240
 gtggcggcca tgctcggagg cctgacacac tttctcgaca gcatgggtac caccaacgcc
 300
 attctcctgg gcntgttgct cggcggctag
 330

<210> 1190
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 1190
 Ser Ile Ala Asp Arg Pro Gly Leu Ala Pro Gly Met Ile Gly Gly Leu
 1 5 10 15
 Leu Ala Ser Thr Leu Gly Ala Gly Phe Ile Gly Gly Ile Val Ala Gly
 20 25 30
 Phe Leu Ala Gly Tyr Ser Ala Lys Ala Ile Ala Arg Trp Ala Arg Leu
 35 40 45
 Pro Ser Ser Leu Asp Ala Leu Lys Pro Ile Leu Ile Ile Ser Leu Leu
 50 55 60
 Ala Ser Leu Phe Thr Gly Leu Val Met Ile Tyr Val Val Gly Gln Pro
 65 70 75 80
 Val Ala Ala Met Leu Gly Gly Leu Thr His Phe Leu Asp Ser Met Gly
 85 90 95
 Thr Thr Asn Ala Ile Leu Leu Gly Xaa Leu Leu Gly Gly
 100 105

<210> 1191
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 1191
 cggccgacga tgtgcggtga gcaagagatt tggagagcca tgatgacgtc agcagacaaa
 60

gcagggacta acggacagac catgcagaca ccgccggtgg tgtcgccgca ggactgggag
 120
 gcagcccgtc agcaactgct cgtgaaggaa aaggcgcata cccgtgcccg cgacgcactc
 180
 gccgccgaac ggaggcgcat gccgtggatg gaagtgacaa aaacctacgc attcgaggcg
 240
 ccctcgggca aggccagtct gctcgatctg ttccagggcc ggaagcagct gatcctgtac
 300
 cgggccttct tcgagccggg cgtgttcggc tggcccagacc atgcctgccg c
 351

<210> 1192
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 1192
 Met Cys Gly Glu Gln Glu Ile Trp Arg Ala Met Met Thr Ser Ala Asp
 1 5 10 15
 Lys Ala Gly Thr Asn Gly Gln Thr Met Gln Thr Pro Pro Val Val Ser
 20 25 30
 Pro Gln Asp Trp Glu Ala Ala Arg Gln Gln Leu Leu Val Lys Glu Lys
 35 40 45
 Ala His Thr Arg Ala Arg Asp Ala Leu Ala Ala Glu Arg Arg Arg Met
 50 55 60
 Pro Trp Met Glu Val Thr Lys Thr Tyr Ala Phe Glu Ala Pro Ser Gly
 65 70 75 80
 Lys Ala Ser Leu Leu Asp Leu Phe Gln Gly Arg Lys Gln Leu Ile Leu
 85 90 95
 Tyr Arg Ala Phe Phe Glu Pro Gly Val Phe Gly Trp Pro Asp His Ala
 100 105 110
 Cys Arg

<210> 1193
 <211> 722
 <212> DNA
 <213> Homo sapiens

<400> 1193
 ggatcccagc ctccagatcc catctttag tag ctcttctttc tctacactna ggttgctccc
 60
 cgacttagga cgcccagttt gtactcagtg tttgctcttt tatggcagag cctctgcact
 120
 cccagcctcc tggccccttc tgtacatgat tttcctttag gccactccat gcatttttct
 180
 tggctcagga cttagtgggc ctccatggga cttggtacct ctacttggtc ccttctggaa
 240
 tctgtaactt tgtgttcccc accattcttt cctttatgaa ccgatggtgc aacagcatga
 300
 ctacctgaaa ttcttagtca ctcccagctg ctttagtgga gggaaaatgc ccacagcaca
 360
 ggaaatagtc ctgcccttcg agagaggcca ggggatggga gcgtgtccag agaagggcga
 420

tgggttgatg aaggggtggcc acagcgcccc ggaggaaggg gccagaacgc tctctgttct
 480
 gttccatgag gaggattatg ttggtgtgtg tagtccccctg gttcagagtt gtccagaaat
 540
 agctcagtgt aaggaacaat tttccaaaga tcaaaagagc tgtctcaaga tagcagtgcg
 600
 ttcccagccc ctacaggtgt atacagcaca aagggagggg cccctagtgt tggctgtcac
 660
 agaggggaagt ggacgtcctg tggtttgacc ccaccagatg gcttttagaga tctgggcccc
 720
 ag
 722

<210> 1194
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 1194
 Met Val Gln Gln His Asp Tyr Leu Lys Phe Leu Val Thr Pro Ser Cys
 1 5 10 15
 Phe Ser Gly Gly Lys Met Pro Thr Ala Gln Glu Ile Val Leu Pro Phe
 20 25 30
 Glu Arg Gly Gln Gly Met Gly Ala Cys Pro Glu Lys Gly Asp Gly Leu
 35 40 45
 Met Lys Gly Gly His Ser Ala Arg Glu Glu Gly Ala Arg Thr Leu Ser
 50 55 60
 Val Leu Phe His Glu Glu Asp Tyr Val Gly Val Cys Ser Pro Leu Val
 65 70 75 80
 Gln Ser Cys Pro Glu Ile Ala Gln Cys Lys Glu Gln Phe Ser Lys Asp
 85 90 95
 Gln Lys Ser Cys Leu Lys Ile Ala Val Arg Ser Gln Pro Leu Gln Val
 100 105 110
 Tyr Thr Ala Gln Arg Glu Gly Pro Pro Ser Val Ala Val Thr Glu Gly
 115 120 125
 Ser Gly Arg Pro Val Val
 130

<210> 1195
 <211> 391
 <212> DNA
 <213> Homo sapiens

<400> 1195
 tctagagcat gatattccgc gggcgcggcc ggggtggactt tggttcgaga gtggaactaa
 60
 gtgagtaatg ggggcggcgc ggccagacgc gctcccagcc tcctggcgag agtgctgccc
 120
 ggtttcccgg gggcacggga gtgtgtctag gaggggaggc caggatcctt cctcgagtcc
 180
 tgtcctgaac aaaagaaaac gaggtgggtg gtgcttgaac ggccctgttt actctgcaga
 240
 tagccgaact ggtaggactc cggcgcgccc tatttatctt gattggctct gcctgaaggc
 300

aagcgттаат cccgtccaac ctgtatcact gcgaagagct cgttcgggag cgctttttgg
 360
 aaatgcagat tcttagcccc caccagatc t
 391

<210> 1196
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 1196
 Met Gly Ala Ala Arg Pro Asp Ala Leu Pro Ala Ser Trp Arg Glu Cys
 1 5 10 15
 Cys Pro Val Ser Arg Gly His Gly Ser Val Ser Arg Arg Gly Gly Gln
 20 25 30
 Asp Pro Ser Ser Ser Pro Val Leu Asn Lys Arg Lys Arg Gly Gly Trp
 35 40 45
 Cys Leu Asn Gly Pro Val Tyr Ser Ala Asp Ser Arg Thr Gly Arg Thr
 50 55 60
 Pro Ala Arg Pro Ile Tyr Leu Asp Trp Leu Cys Leu Lys Ala Ser Val
 65 70 75 80
 Asn Pro Val Gln Pro Val Ser Leu Arg Arg Ala Arg Ser Gly Ala Leu
 85 90 95
 Phe Gly Asn Ala Asp Ser
 100

<210> 1197
 <211> 386
 <212> DNA
 <213> Homo sapiens

<400> 1197
 acgcgtagtg atcatgaaaa tggtagagag cgtctagcag aagtcgcctc tgtgatgggc
 60
 tggcagcaag atgaaatcat cgттаacgta caaggggatg aaccctttct gcctgttgca
 120
 cttattcatg ccacggttaa agcgtagcc gatgatgctg aatctgaaat ggccacgatt
 180
 gcctgtgcga ttgataacgt agcagagctg tttaacccaa atgtagttaa agtcgtttgt
 240
 gatgaaaaac agcgcgcctt gtatttcagt cgtgcgccta tgccatggga cegtaatggt
 300
 tttatggaaa aaacagacga tcaagcgтта ccagcggatt ttctgcggtt gcgtcatatt
 360
 ggtccgtatg tttaccgcac gacatn
 386

<210> 1198
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 1198
 Thr Arg Asp Asp His Glu Asn Gly Thr Glu Arg Leu Ala Glu Val Ala

```

      1           5           10           15
Ser Val Met Gly Trp Gln Gln Asp Glu Ile Ile Val Asn Val Gln Gly
      20           25           30
Asp Glu Pro Phe Leu Pro Val Ala Leu Ile His Ala Thr Val Lys Ala
      35           40           45
Leu Ala Asp Asp Ala Glu Ser Glu Met Ala Thr Ile Ala Cys Ala Ile
      50           55           60
Asp Asn Val Ala Glu Leu Phe Asn Pro Asn Val Val Lys Val Val Cys
      65           70           75           80
Asp Glu Lys Gln Arg Ala Leu Tyr Phe Ser Arg Ala Pro Met Pro Trp
      85           90           95
Asp Arg Asn Gly Phe Met Glu Lys Thr Asp Asp Gln Ala Leu Pro Ala
      100           105           110
Asp Phe Pro Ala Leu Arg His Ile Gly Pro Tyr Val Tyr Arg Thr Thr
      115           120           125

```

<210> 1199
 <211> 318
 <212> DNA
 <213> Homo sapiens

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<400> 1199
acgcgttcag cgatcatgtac agccccgggc cgggtcaattt gatgggcctc aatgccgggc
60
ttacgggcaa attgcgtcgc tccagcgggt tctacatcgg cgtgggggtgc gcgatgctgc
120
tgatgggtcgg gctgggttggg ctcaccggcg aagcgatcat ctcccaggcg gcgctgccgt
180
atatttcttt gattggcggg gtgtacacgc tgtacctcgc ctaccagggtg ttcaccgcac
240
gtaccgaagt ggatgacgcc ccaagcgcgc ctgccaaagac cttgaccttc tggaatggcc
300
tggtgatcca gttgctcc
318

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<210> 1200
 <211> 101
 <212> PRT
 <213> Homo sapiens

```

<400> 1200
Met Tyr Ser Pro Gly Pro Val Asn Leu Met Gly Leu Asn Ala Gly Leu
1           5           10           15
Thr Gly Lys Leu Arg Arg Ser Ser Gly Phe Tyr Ile Gly Val Gly Cys
20           25           30
Ala Met Leu Leu Met Val Gly Leu Val Gly Leu Thr Gly Glu Ala Ile
35           40           45
Ile Ser Gln Ala Ala Leu Pro Tyr Ile Ser Leu Ile Gly Gly Val Tyr
50           55           60
Thr Leu Tyr Leu Ala Tyr Gln Val Phe Thr Ala Arg Thr Glu Val Asp
65           70           75           80
Asp Ala Pro Ser Ala Pro Ala Lys Thr Leu Thr Phe Trp Asn Gly Leu
85           90           95
Val Ile Gln Leu Leu

```


100

<210> 1201
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 1201
 gtcgacgcac aactccagct ggctcgctccc aacagcccga acatccccct ttatcgcgat
 60
 atgatacctca ccgtgctgcg catggccaag gatgaccgca accgttgga tgcacaaaatc
 120
 acgctgcagg cgatccgcga gctggataac gccttccgcg tgctggaaca gttcaagggc
 180
 cgccgcaagg tcacgggtgtt tggtcggcg cgacgcccgg tcgaaagccc gctgtacgcc
 240
 ttggcaaggg aagtcggcac gctgctggcg caatccgacc tgatggtgat caccggcggt
 300
 ggcggcggca tcattggcgc tgcccacgag ggcgcaaggt ctggaacaca gcctgggggt
 360

<210> 1202
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 1202
 Val Asp Ala Gln Leu Gln Leu Val Ala Pro Asn Ser Pro Asn Ile Pro
 1 5 10 15
 Leu Tyr Arg Asp Met Ile Leu Thr Val Leu Arg Met Ala Lys Asp Asp
 20 25 30
 Arg Asn Arg Trp Asn Ala Lys Ile Thr Leu Gln Ala Ile Arg Glu Leu
 35 40 45
 Asp Asn Ala Phe Arg Val Leu Glu Gln Phe Lys Gly Arg Arg Lys Val
 50 55 60
 Thr Val Phe Gly Ser Ala Arg Thr Pro Val Glu Ser Pro Leu Tyr Ala
 65 70 75 80
 Leu Ala Arg Glu Val Gly Thr Leu Leu Ala Gln Ser Asp Leu Met Val
 85 90 95
 Ile Thr Gly Gly Gly Gly Gly Ile Met Ala Ala Ala His Glu Gly Ala
 100 105 110
 Arg Ser Gly Thr Gln Pro Gly Gly
 115 120

<210> 1203
 <211> 477
 <212> DNA
 <213> Homo sapiens

<400> 1203
 ccggatatgg cagctcgact tcattcgacc agagttcttg gaacatttg ctatcatgca
 60
 cctgagtatg caatgactgg acaacttagc tctaagagt acgtttacag ttttgaggt
 120

ggtcttctgg agctcctgac tggaagaaag cctgtggatc ttccattacc aagaggacag
 180
 caaagtcttg tgacatgggc aactccacgg ctttgtgaag ataaagttag gcaatgcggt
 240
 gattcaagac ttggagtaga atatcctcct aaatccggtg caaagtttgc agctgttgct
 300
 gcactgtgtg tgcaatatga agctgacttt cgacccaaca tgagcatcgt ggtgaaggcg
 360
 cttcagcccc tgctgaatgc acgtgcatcc aacaaccctg gatgaatgaa tgaatgactg
 420
 ccgttgcttt tccctgacga gagtatctga atcagacaat catgtagcat tgaattc
 477

<210> 1204

<211> 134

<212> PRT

<213> Homo sapiens

<400> 1204

Pro	Asp	Met	Ala	Ala	Arg	Leu	His	Ser	Thr	Arg	Val	Leu	Gly	Thr	Phe
1				5					10					15	
Gly	Tyr	His	Ala	Pro	Glu	Tyr	Ala	Met	Thr	Gly	Gln	Leu	Ser	Ser	Lys
			20					25					30		
Ser	Asp	Val	Tyr	Ser	Phe	Gly	Val	Gly	Leu	Leu	Glu	Leu	Leu	Thr	Gly
		35					40					45			
Arg	Lys	Pro	Val	Asp	Leu	Pro	Leu	Pro	Arg	Gly	Gln	Gln	Ser	Leu	Val
	50					55				60					
Thr	Trp	Ala	Thr	Pro	Arg	Leu	Cys	Glu	Asp	Lys	Val	Arg	Gln	Cys	Val
65					70					75				80	
Asp	Ser	Arg	Leu	Gly	Val	Glu	Tyr	Pro	Pro	Lys	Ser	Val	Ala	Lys	Phe
			85						90					95	
Ala	Ala	Val	Ala	Ala	Leu	Cys	Val	Gln	Tyr	Glu	Ala	Asp	Phe	Arg	Pro
			100					105					110		
Asn	Met	Ser	Ile	Val	Val	Lys	Ala	Leu	Gln	Pro	Leu	Leu	Asn	Ala	Arg
		115					120					125			
Ala	Ser	Asn	Asn	Pro	Gly										

<210> 1205

<211> 407

<212> DNA

<213> Homo sapiens

<400> 1205

acgcgttgcc attgaagact ggcaattaca cgatttacac atcattgatg ctgcagttga
 60
 tgtgcacagg gaaacactag ctaccgtgca gcaggaaatg atgggagaaa tcagccatgg
 120
 taacaagaac caagccatcc tggacacaga cggccgggggt tgtgcgaacg gaacgttagt
 180
 ctatcaatgt gttgcggaac gattcaaggg atgctggccc ccccatcac ttgccaatc
 240
 aagatgtgga gggaatctgt ctgcgcagaa cctggatctc gtggttgtag gacgttgctc
 300

ccttctcgct cggacgccgc tcatgctccg ccacgtcgct gagcgagtga caaggtatcc
360

tgggaccatg cgtatgggtt caactgaagc gctggcgaat cgtaaan
407

<210> 1206

<211> 103

<212> PRT

<213> Homo sapiens

<400> 1206

Met	Met	Gly	Glu	Ile	Ser	His	Gly	Asn	Lys	Asn	Gln	Ala	Ile	Leu	Asp
1				5					10					15	
Thr	Asp	Gly	Arg	Gly	Cys	Ala	Asn	Gly	Thr	Leu	Val	Tyr	Gln	Cys	Val
			20					25					30		
Ala	Glu	Arg	Phe	Lys	Gly	Cys	Trp	Pro	Pro	Pro	Ser	Leu	Ala	Gln	Ser
		35					40					45			
Arg	Cys	Gly	Gly	Asn	Leu	Ser	Ala	Gln	Asn	Leu	Asp	Leu	Val	Val	Val
	50				55					60					
Arg	Arg	Cys	Pro	Leu	Leu	Ala	Arg	Thr	Pro	Leu	Met	Leu	Arg	His	Val
65				70						75				80	
Ala	Glu	Arg	Val	Thr	Arg	Tyr	Pro	Gly	Thr	Met	Arg	Met	Val	Ser	Thr
			85					90					95		
Glu	Ala	Leu	Ala	Asn	Arg	Lys									
							100								

<210> 1207

<211> 292

<212> DNA

<213> Homo sapiens

<400> 1207

gctagcatgt cacttttttc ttcagtagat ggcactggag agacattgca ggatgaagag
60
gcttgccctc attcctatgt gctttcccgt ccttgcttct ccagccatgt gtgggacaac
120
caggggtgct caccacctag tgagtttcag ggacactcca catgtcccag caagtcttat
180
cagcatctta gctggcttct caacaagact cagtggcacc cctgtggatg tctcccatca
240
agtttcatta gtgccccagg gggagactcc cagaaagttt cagcagcacc ac
292

<210> 1208

<211> 95

<212> PRT

<213> Homo sapiens

<400> 1208

Met	Ser	Leu	Phe	Ser	Ser	Val	Asp	Gly	Thr	Gly	Glu	Thr	Leu	Gln	Asp
1				5					10					15	
Glu	Glu	Ala	Cys	Leu	His	Ser	Tyr	Val	Leu	Ser	Arg	Pro	Cys	Phe	Ser
			20					25					30		
Ser	His	Val	Trp	Asp	Asn	Gln	Gly	Cys	Ser	Pro	Pro	Ser	Glu	Phe	Gln

```

<400> 1210
Leu Val Pro Ile Met Ala Val Ala Tyr Ile Phe Ala Gly Ile Ile Ile
  1             5             10             15
Leu Leu Met His Ala Ser Glu Val Ile Pro Ala Ile Ser Thr Ile Val
      20             25             30
Glu Tyr Ala Phe Thr Pro Ala Ser Ala Gln Gly Gly Phe Ala Gly Ala
      35             40             45
Thr Val Trp Met Ala Ile Arg Phe Gly Val Ala Arg Gly Val Phe Ser
      50             55             60
Asn Glu Ala Gly Leu Gly Ser Ala Pro Ile Ala His Ala Ser Ala Gln
65             70             75             80
Thr Asn Glu Pro Val Arg Gln Gly Leu Val Ala Met Leu Gly Thr Phe
      85             90             95
Leu Asp Thr Leu Ile Ile Cys Thr Gly Leu Val Ile Val Ile Ser Gly
      100            105            110
Ala Trp Thr Glu Gly Leu Ser Gly Ala Ala Leu Thr Ser Ala Ala Phe
      115            120            125
Asn Leu Ala Leu Pro Gly Trp Gly Gly Tyr Leu Val Ala Ile Ser

```

130

135

140

<210> 1211

<211> 480

<212> DNA

<213> Homo sapiens

<400> 1211

gaggaggac gagaggctgg tgagatggag tccagcacc tgcaggagag cccagggcc
60
agagccgaag ctgtgcttct ccatgagatg gatgaagatg atctggccaa tgccttgatc
120
tggcctgaga ttcaacagga gctgaaaatc attgaatctg aggaggagct ctcatcgctg
180
ccacctcctg ctctgaagac cagcccaatt cagcctatc tgcagtcgag tctggggccc
240
tttatccct cagagcctcc tgggagcttg ccttgtggct ccttcctgc tccagtctcc
300
accctctgg aggtgtggac tagggatcca gccaatcaga gcacacaggg ggcttccaca
360
gcagccagca gagagaagcc ggaacctgag cagggcctgc acccagacct cgccagcctg
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<210> 1212

<211> 160

<212> PRT

<213> Homo sapiens

<400> 1212

Glu	Glu	Gly	Arg	Glu	Ala	Gly	Glu	Met	Glu	Ser	Ser	Thr	Leu	Gln	Glu
1				5				10						15	
Ser	Pro	Arg	Ala	Arg	Ala	Glu	Ala	Val	Leu	Leu	His	Glu	Met	Asp	Glu
			20					25					30		
Asp	Asp	Leu	Ala	Asn	Ala	Leu	Ile	Trp	Pro	Glu	Ile	Gln	Gln	Glu	Leu
		35					40					45			
Lys	Ile	Ile	Glu	Ser	Glu	Glu	Glu	Leu	Ser	Ser	Leu	Pro	Pro	Pro	Ala
	50					55					60				
Leu	Lys	Thr	Ser	Pro	Ile	Gln	Pro	Ile	Leu	Glu	Ser	Ser	Leu	Gly	Pro
65					70					75				80	
Phe	Ile	Pro	Ser	Glu	Pro	Pro	Gly	Ser	Leu	Pro	Cys	Gly	Ser	Phe	Pro
			85						90					95	
Ala	Pro	Val	Ser	Thr	Pro	Leu	Glu	Val	Trp	Thr	Arg	Asp	Pro	Ala	Asn
			100					105					110		
Gln	Ser	Thr	Gln	Gly	Ala	Ser	Thr	Ala	Ala	Ser	Arg	Glu	Lys	Pro	Glu
		115					120					125			
Pro	Glu	Gln	Gly	Leu	His	Pro	Asp	Leu	Ala	Ser	Leu	Ala	Pro	Leu	Glu
	130					135				140					
Ile	Val	Pro	Phe	Glu	Lys	Ala	Ser	Pro	Glu	Ala	Gly	Val	Cys	Ser	Arg
145					150					155				160	

<210> 1213

<211> 1141

<212> DNA

<213> Homo sapiens

<400> 1213

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120
tacaacgagg ctgggtcact catcagcgcg acggggcccc gcacacaaca taactggact
180
cacgacgcct atggccggct caccagccac gccacatccg gaaccgacac caccttcgcc
240
tgggaccagg aaggccacct ggcgcagacg tgtacgcgtg cacacgggca tgccactgcc
300
accagtatc gctatgacgc agcgggacgg cgcgtcagtg cgaccagctc agacggccag
360
gaggagcggt actcctggga tggacgggggt tggctgtctg acatcaccac cgacgccacg
420
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480
caggtacgag tggactggga cctcgtgacc ggagccccca cctcgattga tggtcgtcct
540
gtgcttcccc tgcccggagg acgcatcctc ggcgccacac ccatcggcga taccaacct
600
tggcgtgagg tcatgcccac cgaccctgac aacccttacc agcccgccac ggccactatt
660
gagggtgtcc ccgagacgat caggatggcc gggaacacgc tagtggttga tggtcaccct
720
tggtgggggc gcgcctctac gacccaacta ccaccacctt cttgtctcct gaccggttaa
780
ccccgcccgc cggcgcgcta tgggccaaca acccctacga ctacgccaac aacaaccccc
840
tcaccctcac cgatcctctc gggaccacc ccgtcaccga cgaccaactg gcactcctca
900
cccaccccat cggcacactc gcacactacg tcgccaactc cgtcagcaca ctcgtgcac
960
acatcaccga tccgatcagc cactggtggg ccaccacaa agaccggatc ctctcccggg
1020
acttctgat cggtgccggc ctcgtcatcg gcggtatcgc gtagcggcca cgggcgtagg
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1140
c
1141

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<210> 1214

<211> 259

<212> PRT

<213> Homo sapiens

<400> 1214

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Xaa His Asp Gly Gly Leu Val Cys Gly Tyr Val His Asp Gly Arg Val
 1           5           10          15
Thr Arg Val Ala Arg Asp Ala Gln Gly Arg Val Thr Gly Ile Glu Gly

```



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<210> 1216
<211> 102
<212> PRT
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<213> Homo sapiens

<400> 1216

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Met Tyr Cys Gly Glu Pro Thr Leu Phe Ser Thr Met Asn Ala Ser Thr
 1           5           10           15
Arg Pro Arg Asp Ser Asp Gly Ser Ser Pro Pro Lys Val Val Pro Arg
      20           25           30
Tyr Phe Phe His Ala Pro Thr Pro Ala Thr Ala Arg Thr Pro Pro Pro
      35           40           45
Arg Ser Gly Val Leu Pro Val Met Ala Gly Leu Thr Pro Gly Ala Val
      50           55           60
Pro Ile Lys Gly Lys Gln Val Gly Ile Pro Pro Asp Ala Gly Cys Arg
65           70           75           80
His Ala His Val Val His Pro Gln Val Asp Arg Ala His Arg Arg Leu
      85           90           95
Asp Leu Gln Arg Thr Arg
      100

```

<210> 1217

<211> 548

<212> DNA

<213> Homo sapiens

<400> 1217

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cgttgtcggg tgaatgatgt ttctggtgat agtcagtgga tagagatgcg aggcagtgtg
120
acaggttggg acagccgtca tcgagctcag atggtgagag ggacattcga gcgtattaac
180
catcttattg acgctgaaaa tgaattaatt gcggcccgtg aagatgctca gcgacgagag
240
cttattttat cggctttgct aaataatatt ccagaccctg tttggtctaa agatgaaagc
300
ggtcggttatt tggactgtaa ccatgcgttt tgtctgttta atggtttaga gcagagtgat
360
gttcaggggc aaaaagacag tgaattaaac ttagataata atggccaata ttatcaagat
420
atgggcggtg aggtattagc gcgaggggag atttttcatg aacattggtg gggtagcct
480
gcagatggaa gtgacaaccg cttgtttgaa gtatatcgag tccctatcaa agagcctacc
540
gtgaattc
548

```

<210> 1218

<211> 182

<212> PRT

<213> Homo sapiens

<400> 1218

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Xaa Ala Trp Val Asp Ala Leu Leu Asn Asp Lys Ser Lys Lys Thr Phe
 1           5           10           15
Pro His Leu Leu Arg Cys Arg Val Asn Asp Val Ser Gly Asp Ser Gln

```

	20		25		30										
Trp	Ile	Glu	Met	Arg	Gly	Ser	Val	Thr	Gly	Trp	Asp	Ser	Arg	His	Arg
	35						40					45			
Ala	Gln	Met	Val	Arg	Gly	Thr	Phe	Glu	Arg	Ile	Asn	His	Leu	Ile	Asp
	50					55					60				
Ala	Glu	Asn	Glu	Leu	Ile	Ala	Ala	Arg	Glu	Asp	Ala	Gln	Arg	Arg	Glu
65					70					75					80
Leu	Ile	Leu	Ser	Ala	Leu	Leu	Asn	Asn	Ile	Pro	Asp	Pro	Val	Trp	Ser
			85					90					95		
Lys	Asp	Glu	Ser	Gly	Arg	Tyr	Leu	Asp	Cys	Asn	His	Ala	Phe	Cys	Leu
		100						105					110		
Phe	Asn	Gly	Leu	Glu	Gln	Ser	Asp	Val	Gln	Gly	Gln	Lys	Asp	Ser	Glu
	115						120					125			
Leu	Asn	Leu	Asp	Asn	Asn	Gly	Gln	Tyr	Tyr	Gln	Asp	Met	Gly	Gly	Glu
	130					135					140				
Val	Leu	Ala	Arg	Gly	Glu	Ile	Phe	His	Glu	His	Cys	Trp	Gly	Thr	Pro
145					150					155					160
Ala	Asp	Gly	Ser	Asp	Asn	Arg	Leu	Phe	Glu	Val	Tyr	Arg	Val	Pro	Ile
			165						170					175	
Lys	Glu	Pro	Thr	Val	Asn										
				180											

<210> 1219
 <211> 308
 <212> DNA
 <213> Homo sapiens

<400> 1219
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 120
 gttcccagac caccctccct cttttcaaac taaaacaggg atggctctta accaccaccc
 180
 aaaggcaagg ggggtcttaa aaccctaaacc aagtggggca ggggccagcc tcttcaggag
 240
 ggcccaaccc tgcagcctct gccattttgg gaaagaccgt gagttggaat tatgggtcgg
 300
 tgggggggc
 308

<210> 1220
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 1220
 Met Glu Lys Trp Val His Gln Lys Met Met Arg Val Pro Pro Glu Lys
 1 5 10 15
 Ile Thr Lys Thr Ile Leu Leu Val Phe Ser Ser Ser Thr Gly Leu Trp
 20 25 30
 Lys Phe Pro Asp His Pro Pro Ser Phe Gln Thr Lys Thr Gly Met Ala
 35 40 45
 Leu Asn His His Pro Lys Ala Arg Gly Val Leu Lys Pro Lys Pro Ser

50		55		60											
Gly	Ala	Gly	Ala	Ser	Leu	Phe	Arg	Arg	Ala	Gln	Pro	Cys	Ser	Leu	Cys
65			70						75					80	
Pro	Phe	Gly	Lys	Asp	Arg	Glu	Leu	Glu	Leu	Trp	Val	Gly	Gly	Gly	
			85					90					95		

<210> 1221
 <211> 569
 <212> DNA
 <213> Homo sapiens

<400> 1221
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 gcccgtccag gaaagctgca cctcagagaa gcagtttctt tccttacctg ggaagtttct
 120
 tctgtaacac gttaagcccc acaggtaagg cctgatcccc cctggacggc tccccctctcc
 180
 agtggtccca gtctggagggt antcttttct aagccatcct ctcagaatgt gatgggtacc
 240
 aggatgcaca cccggtggcc ctgtggtgtg aggcctcagc aaacacggtc agaagatgaa
 300
 cacacagaga cccgcccgtc ggaaggagag gagggagcgg atacggaggc ccacgtgccca
 360
 gaaggggtccc ttgcagtgggt gtggttatgt gcctgcaatc ccagagtgtc ctcgaaggac
 420
 ctcagatcta acgagctcag ccggcagctg cacgtgggac cagccctctg agcttcactt
 480
 gtttttctct gtgccatcag aaaccaatac gaagataaaa tgggaaaaaa aaaaatccca
 540
 ttcacggcac agcctgccga gaaacgcgt
 569

<210> 1222
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 1222
Met Asn Thr Gln Arg Pro Ala Arg Arg Lys Glu Arg Arg Glu Arg Ile
1 5 10 15
Arg Arg Pro Thr Cys Gln Lys Gly Pro Leu Gln Trp Cys Gly Tyr Val
20 25 30
Pro Ala Ile Pro Glu Cys Pro Arg Arg Thr Ser Asp Leu Thr Ser Ser
35 40 45
Ala Gly Ser Cys Thr Trp Asp Gln Pro Ser Glu Leu His Leu Phe Ser
50 55 60
Ser Val Pro Ser Glu Thr Asn Thr Lys Ile Lys Trp Glu Lys Lys Lys
65 70 75 80
Ser His Ser Arg His Ser Leu Pro Arg Asn Ala
85 90

<210> 1223
 <211> 450

<212> DNA

<213> Homo sapiens

<400> 1223

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 ttgtgcgctc accgagaggg gccatacggg gtagacgagt ggtctcagcg catggttact
 120
 gtactttcag atgtgttgcc tgggtgtggc caaggccggt gggttctcgg cgaaactgca
 180
 atagtaacgc ataacctcgc acaattggga gtcaataacg gtgattgcgg ggtcatcggt
 240
 gaaacaaggc ccgtccccac gatagctcta ccgggacccg gtggagtccc cagacgggtg
 300
 ccctgttccc tcatcccatc gctgcaaccc ttacaggcga tgacgattca caaagcgcag
 360
 ggcagccaat tcacggacgt aacggtggtc ctgccaccac ccgactcgcc cctcctctct
 420
 cgtgagttgc tctataccgc catcacgcgt
 450

<210> 1224

<211> 150

<212> PRT

<213> Homo sapiens

<400> 1224

Lys	Leu	Ala	Gln	Ala	Ser	Ala	Asp	Ala	Ala	Ala	Leu	Lys	Leu	Val	Asp
1			5					10						15	
Ala	His	Arg	Leu	Leu	Cys	Ala	His	Arg	Glu	Gly	Pro	Tyr	Gly	Val	Asp
		20						25					30		
Glu	Trp	Ser	Gln	Arg	Met	Val	Thr	Val	Leu	Ser	Asp	Val	Leu	Pro	Gly
	35					40					45				
Val	Gly	Gln	Gly	Arg	Trp	Val	Leu	Gly	Glu	Thr	Ala	Ile	Val	Thr	His
	50					55					60				
Asn	Leu	Ala	Gln	Leu	Gly	Val	Asn	Asn	Gly	Asp	Cys	Gly	Val	Ile	Val
65				70					75					80	
Glu	Thr	Arg	Pro	Val	Pro	Thr	Ile	Ala	Leu	Pro	Gly	Pro	Gly	Gly	Val
			85					90					95		
Pro	Arg	Arg	Leu	Pro	Cys	Ser	Leu	Ile	Pro	Ser	Leu	Gln	Pro	Leu	Gln
			100					105					110		
Ala	Met	Thr	Ile	His	Lys	Ala	Gln	Gly	Ser	Gln	Phe	Thr	Asp	Val	Thr
		115					120					125			
Val	Val	Leu	Pro	Pro	Pro	Asp	Ser	Pro	Leu	Leu	Ser	Arg	Glu	Leu	Leu
	130					135					140				
Tyr	Thr	Ala	Ile	Thr	Arg										
145					150										

<210> 1225

<211> 436

<212> DNA

<213> Homo sapiens

<400> 1225

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 120
 caaagcccc cgaaagtaag aagtagaaaa aaacccgacc ccgaccagat gaagggacct
 180
 gggaagtgtt tggaagagag actgctgaag tgtctccttg caggcatcac cgtgagctgg
 240
 ggctttgcac acagcatctt catggctttc cacaatgatc ccagaactga tccagagaaa
 300
 cccagggatc aggggttgac ccgaccctgt catcatccca ttctacaaat gaggacactg
 360
 aggcctgggtg aaaagggagg ggtggatgga accaggtggc ctggctctaa gaccagagg
 420
 ctggagtgtg ctcatg
 436

<210> 1226
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 1226
 Met Val Asn Thr Gly Met Ala Thr Trp Glu Leu Lys Val Leu Ser Val
 1 5 10 15
 Gly Gly Gln Gly Pro Gln Phe Leu Ala His Trp Pro Arg Glu Val Met
 20 25 30
 Lys Thr Gln Ser Pro Pro Lys Val Arg Ser Arg Lys Lys Pro Asp Pro
 35 40 45
 Asp Gln Met Lys Gly Pro Gly Lys Phe Leu Glu Lys Arg Leu Leu Lys
 50 55 60
 Cys Leu Leu Ala Gly Ile Thr Val Ser Trp Gly Phe Ala His Ser Ile
 65 70 75 80
 Phe Met Ala Phe His Asn Asp Pro Arg Thr Asp Pro Glu Lys Pro Arg
 85 90 95
 Asp Gln Gly Leu Thr Arg Pro Cys His His Pro Ile Leu Gln Met Arg
 100 105 110
 Thr Leu Arg Pro Gly Glu Lys Gly Val Asp Gly Thr Arg Trp Pro
 115 120 125
 Gly Ser Lys Thr Gln Arg Leu Glu Cys Ala His
 130 135

<210> 1227
 <211> 756
 <212> DNA
 <213> Homo sapiens

<400> 1227
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 aatggtattg gaataccgat taacaaggta gataaaatct ttgatagatt ctaccgtgtc
 120
 gacaaagcac gtacacgtaa gatgggcggt acaggactag gtctagctat ttccaaagag
 180

attgtcgaag cacataatgg ccgtatttgg gcaaatagtg tcgaaggaca aggtacatct
 240
 atcttcatta ccctaccatg tgaaattatt gaagatgggtg attgggatga atagtaaaga
 300
 atacatcaaa acgattatcc tgatactact tgtattaatg agtatcgtct taacctacat
 360
 ggtatggaac ttctcacctg atctatcaaa tgctgatagt acgtcatcag ataataagaa
 420
 agataattct aaacctattg gaaaaccaat gagtgcgaaa acggataaaa ccatcacacc
 480
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 540
 agtatctcaa attttaagcc cattaaaaga taaaaatggt gattcagtac aacatttaaa
 600
 acgaaatcat aacttaatta ttctgaatt aagtataac tttatcgttc ttgatttcac
 660
 atatgattta ccgttatcaa ttacttaag ccaagtatta aacatagatg ctaagacacc
 720
 taatcatttt aactttaatc gactactgat tgatca
 756

<210> 1228

<211> 97

<212> PRT

<213> Homo sapiens

<400> 1228

Val	Glu	Phe	His	Val	Lys	Gln	Asn	Ala	Leu	Tyr	Asn	Arg	Met	Thr	Ile
1				5					10					15	
Arg	Ile	Lys	Asp	Asn	Gly	Ile	Gly	Ile	Pro	Ile	Asn	Lys	Val	Asp	Lys
			20				25						30		
Ile	Phe	Asp	Arg	Phe	Tyr	Arg	Val	Asp	Lys	Ala	Arg	Thr	Arg	Lys	Met
		35				40					45				
Gly	Gly	Thr	Gly	Leu	Gly	Leu	Ala	Ile	Ser	Lys	Glu	Ile	Val	Glu	Ala
	50				55						60				
His	Asn	Gly	Arg	Ile	Trp	Ala	Asn	Ser	Val	Glu	Gly	Gln	Gly	Thr	Ser
65				70						75				80	
Ile	Phe	Ile	Thr	Leu	Pro	Cys	Glu	Ile	Ile	Glu	Asp	Gly	Asp	Trp	Asp
			85						90					95	

Glu

<210> 1229

<211> 377

<212> DNA

<213> Homo sapiens

<400> 1229

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 120
 ccgctggccg tgctatctaa ctgtccgcgg atgctctggg actatttcag tcagcttttc
 180

gctcaggtaa ccaatccgcc cttggacgct atccgcgagg agcttggtcac ctccctgacg
 240
 ggcaccatcg gcccgagggc gaacttgctt gagcctggcc cggaatcatg tcggcaagtg
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 gtcgtcaact acccgatcat cgattccgac cagcttgcca agatcattca catcgacgct
 360
 gacggggagc atccgga
 377

<210> 1230
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 1230
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 Leu Val Ala Pro Met Ala Asn Gln Gly Val Glu Ala Thr Gly Ala Met
 20 25 30
 Gly Thr Asp Thr Pro Leu Ala Val Leu Ser Asn Cys Pro Arg Met Leu
 35 40 45
 Trp Asp Tyr Phe Ser Gln Leu Phe Ala Gln Val Thr Asn Pro Pro Leu
 50 55 60
 Asp Ala Ile Arg Glu Glu Leu Val Thr Ser Leu Thr Gly Thr Ile Gly
 65 70 75 80
 Pro Glu Ala Asn Leu Glu Pro Gly Pro Glu Ser Cys Arg Gln Val
 85 90 95
 Val Val Asn Tyr Pro Ile Ile Asp Ser Asp Gln Leu Ala Lys Ile Ile
 100 105 110
 His Ile Asp Ala Asp Gly Glu His Pro
 115 120

<210> 1231
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 1231
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 120
 cacactgttc tggctttggt agaacatggc gaagatgttg tagtggttaga taatttatca
 180
 aactcttccg atgagtctct gcgtcgcgtt gagaaactcg cgggtagaag tgctcagttc
 240
 taccaaggcg atatcttgga tgctgagtgt ctgcatcgca tcttcgaggc tcacgacatc
 300
 tcggctgtga tccattttgc tgggctaaag ggtgtcggag agtcgacgcg t
 351

<210> 1232
 <211> 91
 <212> PRT

<213> Homo sapiens

<400> 1232

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Met Ala Val Leu Ile Thr Gly Asp Ala Gly Tyr Ile Gly Ser His Thr
 1           5           10           15
Val Leu Ala Leu Leu Glu His Gly Glu Asp Val Val Val Leu Asp Asn
          20           25           30
Leu Ser Asn Ser Ser Asp Glu Ser Leu Arg Arg Val Glu Lys Leu Ala
          35           40           45
Gly Arg Ser Ala Gln Phe Tyr Gln Gly Asp Ile Leu Asp Ala Glu Cys
          50           55           60
Leu His Arg Ile Phe Glu Ala His Asp Ile Ser Ala Val Ile His Phe
65           70           75           80
Ala Gly Leu Lys Gly Val Gly Glu Ser Thr Arg
          85           90

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<210> 1233

<211> 4982

<212> DNA

<213> Homo sapiens

<400> 1233

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120
cctgcctatc tcttttgcac tccaaagtcc agttttatta aatcccaggg tctaagattt
180
tttctttgag aatttatctc cagtgtttct atggaaatta aaaaagaaaa ttaggataat
240
tcaatgtcga aatgttgcac gcaccttttg agaaatttat attttgtagg ttgaaggact
300
tgcttttttg gcagcgtatt tttggagggt gaatgtagtt attttaataa ccatgtccta
360
attatttata gcttcctgcc tgacacagct cacttcaaga agtgcacaat gtcagaacgt
420
ggaattaagt gggcttgtga atattgtacg tatgaaaact ggccatctgc aatcaagtgt
480
accatgtgtc gtgccccaaag acctagtggg acaattatta cagaagatcc atttaaaagt
540
ggttcaagtg atgttggtag agattgggat ccttccagca ccgaaggagg aagtagtcct
600
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660
gcaaataagt ggtcatgcca catgtgtaca tatttgaact ggccaagagc aatcagatgt
720
accagtgtc tatcccaacg taggaccagg agtcctacag aatctcctca gtcctcagga
780
tctggctcaa gaccagttgc tttttctggt gatccttgtg aggaatacaa tgatagaaat
840
aaactgaaca ctaggacaca gcactggact tgctctgttt gcacatatga aaactgggcc
900
aaggctaaaa gatgtgttgt ttgtgatcat cccagacctt ataacattga agcaatagaa
960

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ttggcagaga ctgaagaggc ttcttcaata ataatgagc aagacagagc tcgatggagg
1020
ggaagtgtgca gtagtggttaa tagccaaagg agatcacctc ctgctacgaa gcgggactct
1080
gaagtgaaaa tggattttca gaggattgaa ttggctggtg ctgtgggaag caaggaggaa
1140
cttgaagtag actttaaaaa actaaagcaa attaaaaaca ggatgaaaaa gactgattgg
1200
ctcttctca atgcttgtgt gggggttgta gaaggtgatt tagctgccat agaagcatac
1260
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1320
cgctcttctg cctttgatgt tggctatact cttgtacact tggctatacg ttttcagagg
1380
caggatatgc tagcaatatt gcttacagag gtgtctcaac aagcagcaaa gtgtattcca
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1560
gcagatattg aagatttgcc cccaacagtc caagaaaaat tatttgatga ggtgcttgat
1620
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1680
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<210> 1234

<211> 708

<212> PRT

<213> Homo sapiens

<400> 1234

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			20					25					30		
Ser	Gly	Thr	Ile	Ile	Thr	Glu	Asp	Pro	Phe	Lys	Ser	Gly	Ser	Ser	Asp
		35					40					45			
Val	Gly	Arg	Asp	Trp	Asp	Pro	Ser	Ser	Thr	Glu	Gly	Gly	Ser	Ser	Pro
	50					55					60				
Leu	Ile	Cys	Pro	Asp	Ser	Ser	Ala	Arg	Pro	Arg	Val	Lys	Ser	Ser	Tyr
65					70					75					80
Ser	Met	Glu	Asn	Ala	Asn	Lys	Trp	Ser	Cys	His	Met	Cys	Thr	Tyr	Leu
			85						90					95	
Asn	Trp	Pro	Arg	Ala	Ile	Arg	Cys	Thr	Gln	Cys	Leu	Ser	Gln	Arg	Arg
			100					105					110		
Thr	Arg	Ser	Pro	Thr	Glu	Ser	Pro	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Arg
		115					120					125			
Pro	Val	Ala	Phe	Ser	Val	Asp	Pro	Cys	Glu	Glu	Tyr	Asn	Asp	Arg	Asn
	130					135					140				
Lys	Leu	Asn	Thr	Arg	Thr	Gln	His	Trp	Thr	Cys	Ser	Val	Cys	Thr	Tyr

145		150		155		160
Glu Asn Trp Ala Lys	Ala Lys Arg Cys Val	Val Cys Asp His Pro Arg				
	165	170		175		
Pro Asn Asn Ile Glu	Ala Ile Glu Leu Ala Glu Thr Glu Glu Ala Ser					
	180	185		190		
Ser Ile Ile Asn Glu Gln Asp	Arg Ala Arg Trp Arg Gly Ser Cys Ser					
	195	200		205		
Ser Gly Asn Ser Gln Arg Arg	Ser Pro Pro Ala Thr Lys Arg Asp Ser					
	210	215		220		
Glu Val Lys Met Asp Phe Gln Arg Ile Glu Leu Ala Gly Ala Val Gly						
225	230	235		240		
Ser Lys Glu Glu Leu Glu Val Asp Phe Lys Lys Leu Lys Gln Ile Lys						
	245	250		255		
Asn Arg Met Lys Lys Thr Asp Trp Leu Phe Leu Asn Ala Cys Val Gly						
	260	265		270		
Val Val Glu Gly Asp Leu Ala Ala Ile Glu Ala Tyr Lys Ser Ser Gly						
	275	280		285		
Gly Asp Ile Ala Arg Gln Leu Thr Ala Asp Glu Val Arg Leu Leu Asn						
	290	295		300		
Arg Pro Ser Ala Phe Asp Val Gly Tyr Thr Leu Val His Leu Ala Ile						
305	310	315		320		
Arg Phe Gln Arg Gln Asp Met Leu Ala Ile Leu Leu Thr Glu Val Ser						
	325	330		335		
Gln Gln Ala Ala Lys Cys Ile Pro Ala Met Val Cys Pro Glu Leu Thr						
	340	345		350		
Glu Gln Ile Arg Arg Glu Ile Ala Ala Ser Leu His Gln Arg Lys Gly						
	355	360		365		
Asp Phe Ala Cys Tyr Phe Leu Thr Asp Leu Val Thr Phe Thr Leu Pro						
	370	375		380		
Ala Asp Ile Glu Asp Leu Pro Pro Thr Val Gln Glu Lys Leu Phe Asp						
385	390	395		400		
Glu Val Leu Asp Arg Asp Val Gln Lys Glu Leu Glu Glu Glu Ser Pro						
	405	410		415		
Ile Ile Asn Trp Ser Leu Glu Leu Ala Thr Arg Leu Asp Ser Arg Leu						
	420	425		430		
Tyr Ala Leu Trp Asn Arg Thr Ala Gly Asp Cys Leu Leu Asp Ser Val						
	435	440		445		
Leu Gln Ala Thr Trp Gly Ile Tyr Asp Lys Asp Ser Val Leu Arg Lys						
	450	455		460		
Ala Leu His Asp Ser Leu His Asp Cys Ser His Trp Phe Tyr Thr Arg						
465	470	475		480		
Trp Lys Asp Trp Glu Ser Trp Tyr Ser Gln Ser Phe Gly Leu His Phe						
	485	490		495		
Ser Leu Arg Glu Glu Gln Trp Gln Glu Asp Trp Ala Phe Ile Leu Ser						
	500	505		510		
Leu Ala Ser Gln Pro Gly Ala Ser Leu Glu Gln Thr His Ile Phe Val						
	515	520		525		
Leu Ala His Ile Leu Arg Arg Pro Ile Ile Val Tyr Gly Val Lys Tyr						
	530	535		540		
Tyr Lys Ser Phe Arg Gly Glu Thr Leu Gly Tyr Thr Arg Phe Gln Gly						
545	550	555		560		
Val Tyr Leu Pro Leu Leu Trp Glu Gln Ser Phe Cys Trp Lys Ser Pro						
	565	570		575		
Ile Ala Leu Gly Tyr Thr Arg Gly His Phe Ser Ala Leu Val Ala Met						

580. 585 590
 Glu Asn Asp Gly Tyr Gly Asn Arg Gly Ala Gly Ala Asn Leu Asn Thr
 595 600 605
 Asp Asp Asp Val Thr Ile Thr Phe Leu Pro Leu Val Asp Ser Glu Arg
 610 615 620
 Lys Leu Leu His Val His Phe Leu Ser Ala Gln Glu Leu Gly Asn Glu
 625 630 635 640
 Glu Gln Gln Glu Lys Leu Leu Arg Glu Trp Leu Asp Cys Cys Val Thr
 645 650 655
 Glu Gly Gly Val Leu Val Ala Met Gln Lys Ser Ser Arg Arg Arg Asn
 660 665 670
 His Pro Leu Val Thr Gln Met Val Glu Lys Trp Leu Asp Arg Tyr Arg
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<210> 1235
 <211> 383
 <212> DNA
 <213> Homo sapiens

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 240
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 360
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 383

<210> 1236
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 1236
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 Ala Asp Leu Val Ala Phe Thr Gly His Lys Met Cys Gly Pro Thr Gly
 20 25 30
 Ile Gly Ile Leu Trp Gly Arg Tyr Asp Leu Leu Ala Glu Leu Pro Pro
 35 40 45
 Phe Leu Gly Gly Gly Glu Met Ile Glu Val Val Arg Met Glu Gly Ser
 50 55 60
 Thr Tyr Ala Glu Pro Pro His Arg Phe Glu Ala Gly Thr Pro Pro Ile

65		70		75		80									
Ala	Gln	Leu	Ala	Ala	Leu	Gly	Val	Ala	Ala	Asp	Tyr	Leu	Asp	Gly	Ile
			85						90					95	
Gly	Met	Gln	Ala	Ile	Ala	Glu	His	Glu	His	Glu	Leu	Ala	Ala	Arg	Met
			100					105					110		
Leu	Glu	Asp	Tyr	Gln	Thr	Val	Lys	Gly	Val	Gln	Pro	Glu	Arg	Gly	
		115					120					125			

<210> 1237

<211> 1608

<212> DNA

<213> Homo sapiens

<400> 1237

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120
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180
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240
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300
ggaaggatta tgtcaaata tagaagatt cccagaactg caacttccag tgagtccctc
360
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420
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1200

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<210> 1238

<211> 458

<212> PRT

<213> Homo sapiens

<400> 1238

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Gln	Gln	Pro	Leu	Cys	Arg	Lys	Glu	Gly	Leu	Cys	Gln	Ile	Val	Arg	Arg
			20					25					30		
Phe	Pro	Glu	Leu	Gln	Leu	Pro	Val	Ser	Pro	Ser	Val	Cys	Leu	Asp	Gln
		35					40					45			
Gly	Met	Gln	Leu	Lys	Pro	Ser	Thr	Ser	Ser	His	Leu	Leu	Lys	Thr	Val
	50					55					60				
Lys	Pro	Arg	Val	Trp	Lys	Pro	Gly	Asp	Trp	Ser	Arg	Glu	Gln	Leu	Asn
65					70					75				80	
Glu	Thr	Thr	Val	Leu	Ala	Pro	His	Glu	Thr	Ile	Phe	Arg	Ala	Lys	Asp
			85						90					95	
Leu	Ser	Val	Ile	Leu	Lys	Ala	Tyr	Val	Leu	Val	Thr	Ser	Leu	Thr	Pro
		100						105					110		
Leu	Arg	Ala	Phe	Ile	His	Ser	Thr	Gly	Thr	Val	Trp	Asn	Pro	Pro	Lys
	115						120					125			
Lys	Lys	Arg	Phe	Thr	Val	Lys	Leu	Gln	Thr	Phe	Phe	Glu	Thr	Phe	Leu
	130					135						140			
Arg	Ala	Ser	Ser	Pro	Gln	Gln	Ala	Phe	Asp	Ile	Met	Lys	Glu	Ala	Ile
145					150					155				160	
Gly	Lys	Leu	Leu	Leu	Ala	Ala	Glu	Val	Phe	Ser	Glu	Thr	Ser	Thr	Leu
			165						170					175	
Gly	Pro	Lys	Thr	Phe	His	Arg	Cys	Arg	Phe	Cys	Phe	Gln	Leu	Leu	Thr
		180						185					190		
Phe	Asp	Ile	Gly	Tyr	Gly	Ser	Phe	Met	Tyr	Pro	Val	Val	Leu	Gln	Val
	195					200						205			
His	Glu	His	Leu	Asn	Phe	Gln	Asp	Tyr	Asp	Asn	Met	Asp	Phe	Glu	Asp
	210					215					220				
Gln	Asn	Thr	Glu	Glu	Phe	Leu	Leu	Asn	Asp	Thr	Phe	Asn	Phe	Leu	Phe
225					230					235				240	
Pro	Asn	Glu	Ser	Ser	Leu	Ser	Ile	Phe	Ser	Glu	Ile	Phe	Gln	Arg	Leu
			245						250					255	
Tyr	Arg	Ser	Asp	Val	Phe	Lys	Gly	Glu	Asn	Tyr	Gln	Lys	Glu	Leu	Asn

	260		265		270
Gln Cys	Leu Ser Leu Glu Glu Ile	Asn Ser Ile Met Thr Phe Ile Lys			
	275		280		285
Glu Leu Gly Ser Leu Gly Gln Phe Gln Leu Leu Phe Pro Ser Thr Thr					
	290		295		300
Pro Gly Ile Gln Ser Leu Met His Glu Phe Tyr Asp Val Ala Asn Pro					
305		310		315	320
Val Gly Asn Pro Gly Ser Val Leu Thr Gln Tyr Trp Ser Leu Leu Asn					
	325		330		335
Val Phe Glu Gln Phe Gln Phe Met Asn Lys Lys Thr Gln Pro His Pro					
	340		345		350
Leu Glu Trp Asn Ser Phe Thr Glu Asp Lys Asn Ile Glu Lys Pro Gln					
	355		360		365
Val Pro Phe Asp Ala Ile Glu Asn Lys Lys Ala Ala Val Pro Gln Ile					
	370		375		380
Lys Asn Glu Asn Lys Glu Ile His Cys Ser Asp Asp Glu Asn Thr Pro					
385		390		395	400
Cys His Ile Lys Gln Ile Phe Thr His Pro His Leu Glu Leu Asn Pro					
	405		410		415
Asp Phe His Pro Lys Ile Lys Asp Tyr Tyr Cys Glu Val Pro Phe Asp					
	420		425		430
Val Val Thr Val Thr Ile Gly Val Glu Thr Pro Lys Cys Leu Cys Lys					
	435		440		445
Val His Leu Tyr Glu Gln Ala Gly Pro Ser					
	450		455		

<210> 1239

<211> 447

<212> DNA

<213> Homo sapiens

<400> 1239

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atgcagaagg atttggagaa tattacatcc aaagagataa gaacagagtt ggaaatgcaa

120

atggtgtgca acttgcggga attcaaggaa tttatagaca atgaaatgat agtgatcctt

180

gggtcaaattg atagccctac acagatattt gagcatgtgt tcctgggctc agaattggaat

240

gcctccaact tagaggactt acagaaccga ggggtacggt atatcttgaa tgtcactcga

300

gagatagata actttttccc aggagtcttt gagtatcata acattcgggt atatgatgaa

360

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420

aaacatggat ctaaattgcct tgtgcac

447

<210> 1240

<211> 149

<212> PRT

<213> Homo sapiens

<400> 1240

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 20 25 30
 Ile Arg Thr Glu Leu Glu Met Gln Met Val Cys Asn Leu Arg Glu Phe
 35 40 45
 Lys Glu Phe Ile Asp Asn Glu Met Ile Val Ile Leu Gly Gln Met Asp
 50 55 60
 Ser Pro Thr Gln Ile Phe Glu His Val Phe Leu Gly Ser Glu Trp Asn
 65 70 75 80
 Ala Ser Asn Leu Glu Asp Leu Gln Asn Arg Gly Val Arg Tyr Ile Leu
 85 90 95
 Asn Val Thr Arg Glu Ile Asp Asn Phe Phe Pro Gly Val Phe Glu Tyr
 100 105 110
 His Asn Ile Arg Val Tyr Asp Glu Glu Ala Thr Asp Leu Leu Ala Tyr
 115 120 125
 Trp Asn Asp Thr Tyr Lys Phe Ile Ser Lys Ala Lys Lys His Gly Ser
 130 135 140
 Lys Cys Leu Val His
 145

<210> 1241

<211> 489

<212> DNA

<213> Homo sapiens

<400> 1241

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 120
 taggaagatc aatgaggcgc gagtgtgtgt gtgtacgtgt gcgcgtgtgt gtgtgagaga
 180
 gagagaaaga aagaagaaag gtcccgattg caacgtgtca gatcttgcaa ccttcccccc
 240
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 300
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 360
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 489

<210> 1242

<211> 127

<212> PRT

<213> Homo sapiens

<400> 1242

Met Asn Asn Cys Glu Ala Ile Arg Leu His Ser Leu Arg Cys Ala Phe

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	20	25	30
Asn Ala Pro Pro Thr Ser Gln His Lys Ser Ser Phe Trp Pro Tyr Ser			
	35	40	45
Val Cys Thr Ile Ala Leu Pro Thr His Gly Ser Phe Asn Pro Glu Asp			
	50	55	60
Leu Gly Tyr Gln Ser Ala Met Val Phe Leu Cys Leu Arg Val Val Val			
65	70	75	80
Leu Gly Gly Gly Lys Val Ala Arg Ser Asp Thr Leu Gln Ser Gly Pro			
	85	90	95
Phe Phe Phe Leu Ser Leu Ser Leu Thr His Thr Arg Ala His Val His			
	100	105	110
Thr His Thr Arg Ala Ser Leu Ile Phe Leu Leu Val Arg Thr His			
	115	120	125

<210> 1243

<211> 390

<212> DNA

<213> Homo sapiens

<400> 1243

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120
gtcctagaga ggcgcgacga gggtttggtg cgtgccgtaa aagtcacgtt tggcgccgaa
180
ccgtctgaca cggaattgta cgggtggggt agccgtcatg gcaacgcact tatagagcga
240
ttggagtcta ccgtgctgt ccctaccacc cgcagtcctc gagccaagcg actgaacccc
300
aagagggcgt tacgagatgc agcgcgagct gcccaagcac accgtgccag cacgnccgca
360
caggccgcga ttaaggccga tcaggaagct
390

<210> 1244

<211> 130

<212> PRT

<213> Homo sapiens

<400> 1244

Xaa Asp Ser Val Asp Pro Leu Met Glu Asn Pro Val Cys Gln Val Pro			
1	5	10	15
Ser Ala Tyr Trp Glu Met Ile Tyr Leu Pro Gly Met Phe Thr Val Tyr			
	20	25	30
Phe Asp Gly Gln Phe Trp Val Gly Val Leu Glu Arg Arg Asp Glu Gly			
	35	40	45
Leu Val Arg Ala Val Lys Val Thr Phe Gly Ala Glu Pro Ser Asp Thr			
	50	55	60
Glu Leu Tyr Gly Trp Val Ser Arg His Gly Asn Ala Leu Ile Glu Arg			
65	70	75	80
Leu Glu Ser Thr Ala Ala Val Pro Thr Thr Arg Ser Pro Arg Ala Lys			

				85					90					95					
Arg	Leu	Asn	Pro	Lys	Arg	Ala	Leu	Arg	Asp	Ala	Ala	Arg	Ala	Ala	Gln				
			100						105					110					
Ala	His	Arg	Ala	Ser	Thr	Xaa	Ala	Gln	Ala	Ala	Ile	Lys	Ala	Asp	Gln				
		115					120					125							
Glu	Ala																		
	130																		

<210> 1245
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 1245
 gccaaagcagc aaaaaccaca gatcattgct atgggaaatg tgtcattttc ttgttcacaa
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 ccacaatcta tgcccgtgac ttttctgagc tccaggagtt ttttagcact gccagacttc
 120
 tctggagagg aggaggtttc tgccactttt caatttcgaa cttggaataa ggcagggctt
 180
 ctgctgttca gtgaacttca gctgatttca gggggtatcc tcctctttct gagtgatgga
 240
 aaacttaagt cgaatctcta ccagccaaga aaattacca gtgacatcac agcaggtgtc
 300
 gaattaaatg atgggcagtg gcattctgtc tctttatct
 339

<210> 1246
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 1246
 Ala Lys Gln Gln Lys Pro Gln Ile Ile Ala Met Gly Asn Val Ser Phe
 1 5 10 15
 Ser Cys Ser Gln Pro Gln Ser Met Pro Val Thr Phe Leu Ser Ser Arg
 20 25 30
 Ser Phe Leu Ala Leu Pro Asp Phe Ser Gly Glu Glu Glu Val Ser Ala
 35 40 45
 Thr Phe Gln Phe Arg Thr Trp Asn Lys Ala Gly Leu Leu Leu Phe Ser
 50 55 60
 Glu Leu Gln Leu Ile Ser Gly Gly Ile Leu Leu Phe Leu Ser Asp Gly
 65 70 75 80
 Lys Leu Lys Ser Asn Leu Tyr Gln Pro Arg Lys Leu Pro Ser Asp Ile
 85 90 95
 Thr Ala Gly Val Glu Leu Asn Asp Gly Gln Trp His Ser Val Ser Leu
 100 105 110
 Ser

<210> 1247
 <211> 366
 <212> DNA
 <213> Homo sapiens

<400> 1247

ttgacctcca acccgggcac gcgcacccctg cccagatcc cgatggatgg gcatgacctc
 60
 aaccgggtgt ggcgggacgt cggcctgac gtgcacccgc cgatgctcta catgggctac
 120
 gtcggtttct ccgtggcctt tgcgtttgcc atcgccgcct tgcctggcgg gcgcctcgat
 180
 gcggcctggg cgcgctggtc gcggccatgg accattgtgg cctgggcgtt cctcggtatc
 240
 ggtatcacc cgggttcgtg gtgggcctac tacgaactcg gctggnngcgg ctggtgggtc
 300
 tgggaccccg gggaaaaccc cttcttcacg ccctggctgg ggggcacccc gctgattcac
 360
 tgcgtg
 366

<210> 1248

<211> 122

<212> PRT

<213> Homo sapiens

<400> 1248

Leu	Thr	Ser	Asn	Pro	Gly	Thr	Arg	Ile	Leu	Pro	Gln	Ile	Pro	Met	Asp
1				5					10					15	
Gly	His	Asp	Leu	Asn	Pro	Val	Trp	Arg	Asp	Val	Gly	Leu	Ile	Val	His
			20					25					30		
Pro	Pro	Met	Leu	Tyr	Met	Gly	Tyr	Val	Gly	Phe	Ser	Val	Ala	Phe	Ala
		35				40					45				
Phe	Ala	Ile	Ala	Ala	Leu	Leu	Gly	Gly	Arg	Leu	Asp	Ala	Ala	Trp	Ala
	50				55				60						
Arg	Trp	Ser	Arg	Pro	Trp	Thr	Ile	Val	Ala	Trp	Ala	Phe	Leu	Gly	Ile
65				70					75					80	
Gly	Ile	Thr	Leu	Gly	Ser	Trp	Trp	Ala	Tyr	Tyr	Glu	Leu	Gly	Trp	Xaa
			85					90					95		
Gly	Trp	Trp	Phe	Trp	Asp	Pro	Gly	Glu	Asn	Pro	Phe	Phe	Met	Pro	Trp
			100				105						110		
Leu	Gly	Gly	Thr	Pro	Leu	Ile	His	Ser	Leu						
		115				120									

<210> 1249

<211> 374

<212> DNA

<213> Homo sapiens

<400> 1249

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 60
 ggcgcgcagt tgagcaagct gctgccggat gtgcacctgg tcaatggcac tgccgaggcc
 120
 attccactgg aaagcgccgt ggcggatgcg gtggtgtgcg cacaagcctt ccattggttt
 180
 tccagcgagg cggccctggc ggaaatccat cgggtactca aaccggatgg gcgcctgggg
 240

ctggtgtgga atgtgcgcga cgagtcggtg gattgggtcg ccgccattac tcaaatac
 300
 acgccttatg aaggcgacac gccgcgcttt cataccggcc gttggcgcca agccttcact
 360
 ggcgagtatt ttg
 374

<210> 1250
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 1250
 Thr Arg Val Leu Asn Thr Leu Ala Pro Thr Leu Ile Ala Val Glu Pro
 1 5 10 15
 Val Pro Ala Met Gly Ala Gln Leu Ser Lys Leu Leu Pro Asp Val His
 20 25 30
 Leu Val Asn Gly Thr Ala Glu Ala Ile Pro Leu Glu Ser Ala Val Ala
 35 40 45
 Asp Ala Val Val Cys Ala Gln Ala Phe His Trp Phe Ser Ser Glu Ala
 50 55 60
 Ala Leu Ala Glu Ile His Arg Val Leu Lys Pro Asp Gly Arg Leu Gly
 65 70 75 80
 Leu Val Trp Asn Val Arg Asp Glu Ser Val Asp Trp Val Ala Ala Ile
 85 90 95
 Thr Gln Ile Ile Thr Pro Tyr Glu Gly Asp Thr Pro Arg Phe His Thr
 100 105 110
 Gly Arg Trp Arg Glu Ala Phe Thr Gly Glu Tyr Phe
 115 120

<210> 1251
 <211> 742
 <212> DNA
 <213> Homo sapiens

<400> 1251
 accggtctct tcctcgaaa ggcagggccg aggggcttgc ggggcagcca tggaggcgac
 60
 gcggaggcgg cagcacgtgg gagcgacggg cggcccaggc gcgcagttgg gcgcctcctt
 120
 ccctgcaggc caggcatggc tctgtgagcg ctgatgaggc tgcccgcacg gctcccttcc
 180
 acctcgacct ctggttctac ttcacactgc agaactgggt tctggacttt gggcgtecca
 240
 ttgccatgct ggtattccct ctcgagtggg ttccactcaa caagcccagt gttggggact
 300
 acttccacat ggcctacaac gtcacacgc cctttctctt gctcaagctc atcgagcggg
 360
 cccccgcac cctgctacgc tccatcacgt acgtgagcat catcatcttc atcatgggtg
 420
 ccagcatcca cctggtgggt gactctgtca accaccgcct gctcttcagt ggctaccagc
 480
 accacctgtc tgtccgtgag aaccccatca tcaagaatct caagccggag acgctgatcg
 540

actcctttga gctgctctac tattatgatg agtacctggg tcaactgcatg tggtagatcc
 600
 ccttcttcct catcctcttc atgtacttca gcggtgctn ttactgcctc taaagctgag
 660
 agcttgattc cagggcctgc cctgctcctg gtggcaccca gtggcctgta ctactggtac
 720
 ctggtcaccg agggccagat ct
 742

<210> 1252
 <211> 80
 <212> PRT
 <213> Homo sapiens

<400> 1252
 Met Arg Leu Pro Ala Arg Leu Pro Ser Thr Ser Thr Ser Gly Ser Thr
 1 5 10 15
 Ser His Cys Arg Thr Gly Phe Trp Thr Leu Gly Val Pro Leu Pro Cys
 20 25 30
 Trp Tyr Ser Leu Ser Ser Gly Phe His Ser Thr Ser Pro Val Leu Gly
 35 40 45
 Thr Thr Ser Thr Trp Pro Thr Thr Ser Ser Arg Pro Phe Ser Cys Ser
 50 55 60
 Ser Ser Ser Ser Gly Pro Pro Ala Pro Cys Tyr Ala Pro Ser Arg Thr
 65 70 75 80

<210> 1253
 <211> 675
 <212> DNA
 <213> Homo sapiens

<400> 1253
 gggccccctc ccaggcgctt tctgggagct tttagaactg cgctctgaag tttccagaga
 60
 gcgaggagct tttgcggcag gcagagacaa tggaagaaaa tgaaagccag aaatgtgagc
 120
 cgtgccttcc ttactcagca gacagaagac agatgcagga acaaggcaaa ggcaatctgc
 180
 atgtaacatc accagaagat gcagaatgcc gcagaaccaa ggaacgcctt tctaattggaa
 240
 acagtcgtgg ttcagtttcc aagtcttccc gcaatatccc aaggagacac accctagggg
 300
 ggccccgaag ttccaaggaa atactgggaa tgcaaacatc tgagatggat cggaagagag
 360
 gaaaaagcgt tcctagaaca tctgaagcag aagtaccccc accacgcctc tgcaatcatg
 420
 ggtcaccaag agaggctgag agaccagaca aggatcccca aactgtctca cagtcctcaa
 480
 ccacccagtg tgggtgaccc ggtcgagcat ttatcagaga cgtccgctga ttctttggaa
 540
 gccatgtctg aggggggatgc tccaaccct tttccagag gcagccggac tcgtgcgagc
 600
 ctctctgtgg tgaggtcaac caaccagacg aaagaaagat ctctgggggt tctctatctc
 660

cagtatggag atgaa
675

<210> 1254
<211> 86
<212> PRT
<213> Homo sapiens

<400> 1254
Met Gly His Gln Glu Arg Leu Arg Asp Gln Thr Arg Ile Pro Lys Leu
1 5 10 15
Ser His Ser Pro Gln Pro Pro Ser Val Gly Asp Pro Val Glu His Leu
20 25 30
Ser Glu Thr Ser Ala Asp Ser Leu Glu Ala Met Ser Glu Gly Asp Ala
35 40 45
Pro Thr Pro Phe Ser Arg Gly Ser Arg Thr Arg Ala Ser Leu Pro Val
50 55 60
Val Arg Ser Thr Asn Gln Thr Lys Glu Arg Ser Leu Gly Val Leu Tyr
65 70 75 80
Leu Gln Tyr Gly Asp Glu
85

<210> 1255
<211> 401
<212> DNA
<213> Homo sapiens

<400> 1255
ncgccgatta ccaaggctat ggatgtgtgg gccttgggcg taacgctata ctgtctgctg
60
ttcggtcgag tgccatttga tgcagagacg gagtacttgc tgctggaaag taccctgcat
120
gacgattatg ccgtcccgac gcacatgggt agcgaccgcg tgttggtagg cccgcgacca
180
gcacgttggc cctcgtcgca agagacgccc aacgtgccgc tgtccggcga ggcgcatgca
240
gtacgccatc tgctcgatgc ccttctcgac aaggatccag cgacgcgcct cactctcgat
300
cgtgttataa cacacccatg gctcgtggca gagtcattgt aatagtagca attgtatata
360
ccctcatcac caagatggcc aaagcggtac aaggcccgcg g
401

<210> 1256
<211> 113
<212> PRT
<213> Homo sapiens

<400> 1256
Xaa Pro Ile Thr Lys Ala Met Asp Val Trp Ala Leu Gly Val Thr Leu
1 5 10 15
Tyr Cys Leu Leu Phe Gly Arg Val Pro Phe Asp Ala Glu Thr Glu Tyr
20 25 30
Leu Leu Leu Glu Ser Ile Leu His Asp Asp Tyr Ala Val Pro Thr His


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<210> 1259
<211> 417
<212> DNA
<213> Homo sapiens
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<400> 1259

nnacactcta gcctctgact caaggaagct gccagggctc ttgcccttcg gtttgggggg
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 atcccgtctc ccttcgtctg gagcagacat agtgagaacg tgagaagctg caggcgtggc
 120
 ctcaccgtgg tgtgttccaa gatgtccagg gccaaaggatg ccgtgtcctc cgggggtggc
 180
 agcgtgggtg acgtggctaa gggagtggc cagggaggcc tggacaccac tcggtctgca
 240
 cttacgggca ccaaggaggc ggtgtccagc ggggtcacag gggccatgga catggctaag
 300
 ggggccgtcc aaggggggtct ggacacctcg aaggctgtcc tcaccggcac caaggacacg
 360
 gtgtccactg ggctcacggg ggcagtgaat gtggccaaag ggcccgtaca ggccggc
 417

<210> 1260

<211> 133

<212> PRT

<213> Homo sapiens

<400> 1260

Leu	Lys	Glu	Ala	Ala	Gln	Gly	Leu	Ala	Leu	Arg	Phe	Gly	Gly	Ile	Pro
1				5					10					15	
Ser	Pro	Phe	Val	Trp	Ser	Arg	His	Ser	Glu	Asn	Val	Arg	Ser	Cys	Arg
			20					25					30		
Arg	Gly	Leu	Thr	Val	Val	Cys	Ser	Lys	Met	Ser	Arg	Ala	Lys	Asp	Ala
		35				40						45			
Val	Ser	Ser	Gly	Val	Ala	Ser	Val	Val	Asp	Val	Ala	Lys	Gly	Val	Val
	50					55				60					
Gln	Gly	Gly	Leu	Asp	Thr	Thr	Arg	Ser	Ala	Leu	Thr	Gly	Thr	Lys	Glu
65					70					75				80	
Ala	Val	Ser	Ser	Gly	Val	Thr	Gly	Ala	Met	Asp	Met	Ala	Lys	Gly	Ala
				85				90					95		
Val	Gln	Gly	Gly	Leu	Asp	Thr	Ser	Lys	Ala	Val	Leu	Thr	Gly	Thr	Lys
			100					105					110		
Asp	Thr	Val	Ser	Thr	Gly	Leu	Thr	Gly	Ala	Val	Asn	Val	Ala	Lys	Gly
		115					120					125			
Pro	Val	Gln	Ala	Gly											
				130											

<210> 1261

<211> 330

<212> DNA

<213> Homo sapiens

<400> 1261

ngtgcacgtg ccgttcggca tcaggagatg aacatggatt tgaacgctga agtcgatcag
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 ctggtccgcc aatcccagac ctggatcccc ttgatcatgg agtacggcag ccgcctgctg
 120tgaccctggc ggtcggctgg tggatcgaca acaaggtcag cgcccgcctg 180
 ggcaaactgg taggcctgcg caacgccgac ctggcactgc aaggctttat cagcaccttg
 240

tcgaacatcg ggctgaaagt gctgctgttc gtcagtgtgg cgtcgatgat cggcattgag
300

accacctcgt tcgtcgcgga catcggtgct
330

<210> 1262

<211> 110

<212> PRT

<213> Homo sapiens

<400> 1262

Xaa	Ala	Arg	Ala	Val	Arg	His	Gln	Glu	Met	Asn	Met	Asp	Leu	Asn	Ala
1				5				10					15		
Glu	Val	Asp	Gln	Leu	Val	Arg	Gln	Ser	Gln	Thr	Trp	Ile	Pro	Leu	Ile
			20					25					30		
Met	Glu	Tyr	Gly	Ser	Arg	Leu	Leu	Ala	Leu	Leu	Thr	Leu	Ala	Val	
		35					40				45				
Gly	Trp	Trp	Ile	Asp	Asn	Lys	Val	Ser	Ala	Arg	Leu	Gly	Lys	Leu	Val
	50					55					60				
Gly	Leu	Arg	Asn	Ala	Asp	Leu	Ala	Leu	Gln	Gly	Phe	Ile	Ser	Thr	Leu
65					70					75				80	
Ser	Asn	Ile	Gly	Leu	Lys	Val	Leu	Leu	Phe	Val	Ser	Val	Ala	Ser	Met
			85						90				95		
Ile	Gly	Ile	Glu	Thr	Thr	Ser	Phe	Val	Ala	Asp	Ile	Gly	Ala		
			100					105					110		

<210> 1263

<211> 351

<212> DNA

<213> Homo sapiens

<400> 1263

acgcgtggac gatggacttc gtcggtctgc ggtacgacga agggctcaac attgccggtg
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gcacgatga tgagtttgct cgcctgggca acacctagca gcaatggcat cgatagtcac
120
tgcccagcct gctccatttc gacgacgatg gtcgccgggt tcagtttctt ctcgctccac
180
gtcaacagac cgtcaccgtg gttgacgatc tcgccggtgg aggcgtcctt gacgacgatc
240
tggccacgcg ccagggaata catctcccca tccacccaaa agaacgcccc caagctgggc
300
atcttggcca gcccgatgat cgagagggtt tcaacaagcg actcgggatc c
351

<210> 1264

<211> 100

<212> PRT

<213> Homo sapiens

<400> 1264

Met	Pro	Ser	Leu	Gly	Ala	Phe	Phe	Trp	Val	Asp	Gly	Glu	Met	Tyr	Ser
1				5				10					15		
Leu	Ala	Arg	Gly	Gln	Ile	Val	Val	Lys	Asp	Ala	Ser	Thr	Gly	Glu	Ile

```

      20      25      30
Val Asn His Gly Asp Gly Leu Leu Thr Trp Ser Glu Lys Lys Leu Asn
      35      40      45
Pro Ala Thr Ile Val Val Glu Met Glu Gln Ala Gly Gln Gly Leu Ser
      50      55      60
Met Pro Leu Leu Leu Gly Val Ala Gln Ala Ser Lys Leu Ile Ile Asp
65      70      75      80
Ala Thr Gly Asn Val Glu Pro Phe Val Val Pro Gln Thr Asp Glu Val
      85      90      95
His Arg Pro Arg
      100

```

<210> 1265
 <211> 318
 <212> DNA
 <213> Homo sapiens

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<400> 1265
accggtgtat gcaactgaaa tgctgtccga tatgcctgcg ctccagctcg tgaatcgaaa
60
gttggataac gctcgcttgg tggaatcgtc gctacggaag cttatcaagg atacggatgc
120
tgctgcaccg ccaaaattat ggacgcccc cgacccact cgctctgacg ataccattgc
180
acagccgaaa gtgcaaccag cccaagcagt gggagatgac tcgatcatgt cggtcgatga
240
gcctgatgca accgtccatg acatgccact caccacgaca ctcgacaacg tgggtcgctc
300
agatccatcg cgacgcgt
318

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<210> 1266
 <211> 99
 <212> PRT
 <213> Homo sapiens

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<400> 1266
Met Leu Ser Asp Met Pro Ala Leu Gln Leu Val Asn Arg Lys Leu Asp
1      5      10      15
Asn Ala Arg Leu Val Glu Ser Ser Leu Arg Lys Leu Ile Lys Asp Thr
      20      25      30
Asp Ala Ala Ala Pro Pro Lys Leu Trp Thr Pro Pro Asp Pro Thr Arg
      35      40      45
Ser Asp Asp Thr Ile Ala Gln Pro Lys Val Gln Pro Ala Gln Ala Val
50      55      60
Gly Asp Asp Ser Ile Met Ser Val Asp Glu Pro Asp Ala Thr Val His
65      70      75      80
Asp Met Pro Leu Thr Thr Thr Leu Asp Asn Val Gly Arg Ser Asp Pro
      85      90      95
Ser Arg Arg

```

<210> 1267
 <211> 343

<212> DNA

<213> Homo sapiens

<400> 1267

nggacacttg tgggaaatgc cccacagcct gtgtttttat tccccttggtg aacacttggtg
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 ggaactgtcc cacggcccgt gtttctgtgc gcctgcagac actcgtggga aatgccccac
 120
 aacctgtgtt tttgttcccc ttgtgaacac tcgtgggaaa tgccccacaa cctgtgtttt
 180
 tattccccctt gtgaacactc gtgggaaatg tcccatggcc cgtgtttccg tgcacctgcy
 240
 gatactcatc aaacaccagg ctgtcattgg ggacaggggtg agctctgggt gttggtgcag
 300
 catggtagga agagcaccaa gtccctggact ctgttgattt ata
 343

<210> 1268

<211> 106

<212> PRT

<213> Homo sapiens

<400> 1268

Met	Pro	His	Ser	Leu	Cys	Phe	Tyr	Ser	Pro	Cys	Glu	His	Leu	Trp	Glu
1				5					10					15	
Leu	Ser	His	Gly	Pro	Cys	Phe	Cys	Ala	Pro	Ala	Asp	Thr	Arg	Gly	Lys
			20					25					30		
Cys	Pro	Thr	Thr	Cys	Val	Phe	Val	Pro	Leu	Val	Asn	Thr	Arg	Gly	Lys
		35					40					45			
Cys	Pro	Thr	Thr	Cys	Val	Phe	Ile	Pro	Leu	Val	Asn	Thr	Arg	Gly	Lys
	50					55					60				
Cys	Pro	Met	Ala	Arg	Val	Ser	Val	His	Leu	Arg	Ile	Leu	Ile	Lys	His
65					70					75				80	
Gln	Ala	Val	Ile	Gly	Asp	Arg	Val	Ser	Ser	Gly	Cys	Trp	Cys	Ser	Met
			85						90					95	
Val	Gly	Arg	Ala	Pro	Ser	Pro	Gly	Leu	Cys						
			100						105						

<210> 1269

<211> 391

<212> DNA

<213> Homo sapiens

<400> 1269

tcgcgatccg gagcgatcgg tgctgcagat ggctggcgac gccctgcggg gcgcattgcy
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 ggacgccgac ctggagccgg ccgcctaga cgggctgac gtccaggtgg ggtccccccg
 120
 cggcgccgac tacgacaccg tgtccgaaac ctttgggtctt tcgccacaat tctgcagcca
 180
 gacctggggc gcacggccgg ttcaccgcaa cgggtgacct ggcagcggcc atggcggtgt
 240
 ccagcggcct cgcgcggcgg gtggcttgcc tcatgggcat gaagaattcg gacctcgggc
 300

ggttgggtga ggcggacaat ccctttcatc atgagcaatt ccgggagaat ggcgggccgc
360

acggggaaga gggttggatc ggcattggcct c
391

<210> 1270

<211> 110

<212> PRT

<213> Homo sapiens

<400> 1270

Met	Met	Lys	Gly	Ile	Val	Arg	Leu	Thr	Gln	Pro	Pro	Glu	Val	Arg	Ile
1				5					10					15	
Leu	His	Ala	His	Glu	Ala	Ser	His	Pro	Pro	Arg	Glu	Ala	Ala	Gly	His
		20						25					30		
Arg	His	Gly	Arg	Cys	Gln	Asp	His	Arg	Cys	Gly	Glu	Pro	Ala	Val	Arg
		35					40					45			
Pro	Arg	Ser	Gly	Cys	Arg	Ile	Val	Ala	Lys	Asp	Gln	Arg	Phe	Arg	Thr
	50					55					60				
Arg	Cys	Arg	Ser	Pro	Arg	Arg	Gly	Gly	Thr	Pro	Pro	Gly	Arg	Ser	Ala
65					70					75				80	
Arg	Leu	Gly	Arg	Pro	Ala	Pro	Gly	Arg	Arg	Pro	Ala	Met	Arg	Pro	Ala
				85					90				95		
Gly	Arg	Arg	Gln	Pro	Ser	Ala	Ala	Pro	Ile	Ala	Pro	Asp	Arg		
			100					105					110		

<210> 1271

<211> 661

<212> DNA

<213> Homo sapiens

<400> 1271

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60
accagaaagc gtcattcgggg tgggtgaacga gaacgggcca tggtgtggtg ggacggataa
120
cccccggttg cgtcaccata tggcccacta aagagttcac cagggttgat ttaccagccc
180
cggtcgaccc tcctaccacc gccagaagcg gcgcatcaat agtctctaag cgcggcaaaa
240
tatagtcggtt aagctgggta gcgatgcgtc gtgccagccc ggcctgagta atagcctccg
300
gcaaatccaa ggggaactgg gcctgacgca gggtgtgccg cagatcggtc aacgacagca
360
gtatctgctc agtgttcatg gtgattcctc ctggtcactc gtcaggcctg tggcggcgcc
420
cactgcaact cggtgttgac cggctgggtg cgacgtcgct tgaggaatgc gggcagtcctc
480
ggcttcgaca atttggcacc tcgggcgacg gtgatagccg ccgggcgcag cacgttcata
540
cgggttgatga gctcgatctg aagcggacca ggatcatcgt ccaaccacg cacaatggcg
600
tcacgaagat aagcaagatc tgtcccaacg cgcaggaact ctaacgtgtg ccaccaccgg
660

t
661

<210> 1272
<211> 126
<212> PRT
<213> Homo sapiens

<400> 1272
Met Asn Thr Glu Gln Ile Leu Leu Ser Leu Thr Asp Leu Arg His Asn
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Leu Arg Gln Ala Gln Phe Pro Leu Asp Leu Pro Glu Ala Ile Thr Gln
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Ala Gly Leu Ala Arg Arg Ile Ala Asn Gln Leu Asn Asp Tyr Ile Leu
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Pro Arg Leu Glu Thr Ile Asp Ala Pro Leu Leu Ala Val Val Gly Gly
50 55 60
Ser Thr Gly Ala Gly Lys Ser Thr Leu Val Asn Ser Leu Val Gly His
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Met Val Thr Gln Pro Gly Val Ile Arg Pro Thr Thr Thr Ser Pro Val
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Leu Val His His Pro Asp Asp Ala Phe Trp Phe Asp Gly Asp Arg Val
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